

OK nucleic - nucleic search, using sw model

Run on: October 14, 2004, 09:12:14 ; Search time 3341.74 Seconds
(without alignments) 8443.595 Million cell updates/sec

Title: US-09-407-804A-5

Perfect score: 651
Sequence: 1 atgaacagagcaatacag.....acaagagagagattcaatga 651

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: +
1: gb_ba: +
2: gb_hg: +
3: gb_in: +
4: gb_cm: +
5: gb_ov: +
6: gb_pat: +
7: gb_ph: +
8: gb_pl: +
9: gb_pr: +
10: gb_ro: +
11: gb_scs: +
12: gb_sy: +
13: gb_un: +
14: gb_vl: +
15: em_da: +
16: em_fun: +
17: em_hum: +
18: em_in: +
19: em_mu: +
20: em_om: +
21: em_or: +
22: em_ov: +
23: em_pat: +
24: em_ph: +
25: em_pl: +
26: em_ro: +
27: em_scs: +

28: em_un: +
29: em_vl: +
30: em_hg_hum: +
31: em_hg_inv: +
32: em_hg_other: +
33: em_hg_mus: +
34: em_hg_pin: +
35: em_hg_rnd: +
36: em_hg_mam: +
37: em_hg_vrt: +
38: em_sy: +
39: em_hgco_hum: +
40: em_hgco_mus: +
41: em_hgco_other: +

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query				Description
	Score	Match	Length	ID	
1	651	100.0	651	6 BD245276	BD245276 Developme
2	651	100.0	41401	7 AB009866	AB009866 Bacterioph
3	651	100.0	41708	6 BD245281	BD245281 Developme
4	651	100.0	41708	6 AR368770	AR368770 Sequence
5	651	100.0	272850	1 AP004828	AP004828 Staphyloc
6	175.6	27.0	222887	1 AB063171	AB063171 Staphyloc
7	103.4	16.2	165118	2 AC119053	AC119053 Danio rer
8	103.4	15.9	155204	2 AC007926	AC007926 Trypanoso
9	102.2	15.7	110000	2 AL954295_2	Continuation (3 of
10	102.2	15.7	122838	2 BX248494	BX248494 Danio rer
11	99	15.2	146275	2 AL935272	AL935272 Danio rer
12	98.8	15.2	151802	3 AC114263	AC114263 Dictyoste
13	98.2	15.1	153751	3 AC116531	AC116531 Dictyoste
14	98	15.1	333321	3 AC116986	AC116986 Dictyoste
15	97.8	15.0	250029	3 AE014820	AE014820 Plasmodiu
16	96.2	14.8	116807	2 BX890614	BX890614 Danio rer
17	95.2	14.6	94534	5 AL929250	AL929250 Zebrafish
18	94.8	14.6	151341	5 AL929536	AL929536 Zebrafish
19	94.6	14.5	177595	2 AL933867	AL933867 Danio rer
20	94.4	14.5	349751	3 PFMAL4P3	PFMAL4P3 Danio rer
21	94.2	14.5	225581	2 BX537105	BX537105 Plasmodiu
22	93.6	14.4	171798	2 AC084397	AC084397 Danio rer
23	93.6	14.4	198743	2 BX530070	BX530070 Trypanoso
24	92.8	14.3	183584	3 AC012492	AC012492 Danio rer
25	92	14.1	110000	3 AC116957_2	Continuation (3 of
26	91.8	14.1	169841	9 AL607043	AL607043 Human DNA
27	91.6	14.1	245802	2 AC006279	AC006279 Plasmodiu
28	91.6	14.1	260929	3 AE014852	AE014852 Plasmodiu
29	91.2	14.0	4865	3 AF364131	AF364131 Anophel
30	91.2	14.0	199347	2 BX321884	BX321884 Danio rer
31	91.2	14.0	203204	2 AC092052	AC092052 Homo sapi
32	91	14.0	8056	6 AX595046	AX595046 Sequence
33	91	14.0	180023	2 BX897685	BX897685 Danio rer

c 34 90.4 13.9 60604 2 AC023466 Homo sapi
c 35 90.2 13.9 33321 3 AC116986 Dictyoste
c 36 89.6 13.8 384 3 AF201315 Dugesia p
c 37 89.6 13.8 8056 6 AX59046 Sequence
c 38 89.4 13.7 349980 6 AX344555 Sequence
c 39 88.6 13.6 183357 2 BX569779 Danto rer
c 40 88.2 13.5 17443 3 AC024806
c 41 88.2 13.5 111882 3 AC115612
c 42 88 13.5 104992 2 AC005504
c 43 88 13.5 169546 2 AC005504 Plasmodu
c 44 88 13.5 250421 3 AE014849 Plasmodu
c 45 87.6 13.5 348600 1 AB063521 Wt g1esmo

ALIGNMENTS

RESULT 1
BD245276 651 bp DNA linear PAT 17-JUL-2003
LOCUS BD245276
DEFINITION Development of novel antibiotics based on bacteriophage genomics.
ACCESSION BD245276
VERSION BD245276.1 GI:33055046
KEYWORDS JP 2002531107-A/11.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 651)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Development of novel antibiotics based on bacteriophage genomics
JOURNAL Patent: JP 2002531107-A 11 24-SEP-2002;
PHARTECH INC
COMMENT OS Staphylococcus aureus bacteriophage 77
PN JP 2002531107-A/11
PD 24-SEP-2002
PF 03-DEC-1999 JP 2000585456
PR 03-DEC-1999 US 60/110992,03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR
01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454232 PT JERRY
PELLETIER, PHILIPPE GROS, MICHAEL DUBOW
PC C12N15/09, A01N63/00, A61K45/00, A61P31/04, C07K14/005,
PC C12N15/09, A01N63/00, A61K38/00, A61K45/00, A61P31/04, C07K14/005,
PC C12N15/00,
PC C12N1/21, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/566, PC
C12N15/00,
PC A61K37/02
CC Coding Sequence
FH Key
FT source
FT aureus bacteriophage 77'

FEATURES
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ORIGIN

Query Match 100.0%; Score 651; DB 6; Length 651;
Best Local Similarity 100.0%; Pred. No. 3.58-72;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 481 GCTTATATCATATGATAGTTTATCATCTTCAAGATGACGAGAAAAATTAACGATTA 540
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QY 541 ATCTTATCTGATTAATTTGAAGACGTTTATGCTAAAGTTAAATTAACGAACT 600
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QY 601 TCGATTAAGAAAGATATATTAATTAATTAACGAGAGATTAATGA 651
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RESULT 2
AB009866 41401 bp DNA linear PHG 23-MAY-2000
LOCUS AB009866
DEFINITION Bacteriophage phi PVL proviral DNA, complete sequence.
ACCESSION AB009866
VERSION AB009866.2 GI:8051688
KEYWORDS dutPase; ssDNA binding protein; anti repressor; repressor;

integrases; LukF-PV; LukS-PV; holin; amidase (peptidoglycan hydrolase); capsid protein; portal protein.
SOURCE
ORGANISM
Staphylococcus aureus bacteriophage PV1
REFERENCE
AUTHORS
1 (sites)
Kaneke,J., Kimura,T., Kawakami,Y., Tomita,T. and Kamio,Y.
TITLE
Panton-Valentine leukocidin genes in a phage-like particle isolated from methicillin C-treated Staphylococcus aureus V8 (ATCC 49775) Blochl. Biotechnol. Biochem. 61 (11), 1960-1962 (1997)
JOURNAL
MEDLINE
98067870
PUBMED
940084
REFERENCE
AUTHORS
2 (sites)
Kaneke,J., Kimura,T., Narita,S., Tomita,T. and Kamio,Y.
TITLE
Complete nucleotide sequence and molecular characterization of the temperate staphylococcal bacteriophage phiPV1 carrying Panton-Valentine leukocidin genes
JOURNAL
Gene 215 (1), 57-67 (1998)
MEDLINE
98332719
PUBMED
9666077
REFERENCE
AUTHORS
3 (bases 1 to 41401)
Kaneke,J., Kimura,T., Narita,S., Tomita,T. and Kamio,Y.
TITLE
Direct Submision
JOURNAL
Submitted (17-DEC-1997) Jun Kaneke, Tohoku University, Dept. Appl. Biol. Chem., Faculty of Agriculture; 1-1 Tsurumi-dori Aamajimachi, Aoba-ku, Sendai, Miyagi 981, Japan (E-mail:j.kaneke@biochem.tohoku.ac.jp, tel:81-22-717-8781, fax:81-22-717-8780)
COMMENT
On May 24, 2000 this sequence version replaced gi:3341907.
Sequence updated (06-Feb-1998)
Sequence updated (22-May-2000).
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Query Match 100.0%; Score 651; DB 7; Length 41401;
Best Local Similarity 100.0%; Pred. No. 8.6e-73;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACGACCAATATAGGAAGCATATATACCTTAGACAGAGGTGTGCTTATTC A 60
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Db 39659 TCGATTAAGAAAGATATATTAATTTAAACAAGAGATTTAAATGA 39709

RESULT 3
BD245281 41708 bp DNA linear PAT 17-JUL-2003
LOCUS Development of novel antibiotics based on bacteriophage genomics.
DEFINITION BD245281
ACCESSION BD245281.1 GI:33055051
VERSION JP 2002531107-A/16.
KEYWORDS unidentfied
SOURCE unidentfied
ORGANISM unidentfied.
REFERENCE 1 (bases 1 to 41708)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Development of novel antibiotics based on bacteriophage genomics
JOURNAL Patient: JP 2002531107-A 16 24-SEP-2002;
PHARTECH INC
OS Staphylococcus aureus bacteriophage 77
PN JP 2002531107-A/16
PD 24-SEP-2002
PR 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR
01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454252 P1 JERRY
PELLETIER,PHILLIPE GROS,MICHAEL DUBOW
PC C12N15/09,A01N63/00,A61K38/00,A61K45/00,A61P31/04,C07K14/005,
PC C12M1/00,
PC C12N1/21,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/566,PC
C12N15/00,
PC A61K37/02
CC Genome Sequence
FH Key Location/Qualifiers
FT source 1..41708
FT aureus bacteriophage 77'
FT

FEATURES
source Location/Qualifiers
1..41708
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ORIGIN

Query Match 100.0%; Score 651; DB 6; Length 41708;
Best Local Similarity 100.0%; Pred. No. 8,66-73;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACGACAAATATATGAGACATATATACTTTAGACAGAGGTGTGCTTTATTC 60
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Db 39851 ATGACGACAAATATATGAGACATATATACTTTAGACAGAGGTGTGCTTTATTC 39910
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Db 39911 GTTAAAGATTTTGGTATTTTTCAGATCTTAACCTTAACGTAACAAAAATCAATTA 39970
QY 121 GACAAATATATCCGATATATTTAGATTTTAAAGGCTTAAAGATGATGGAGCT 180
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Db 39971 GACAAATATATCCGATATATTTAGATTTTAAAGGCTTAAAGATGATGGAGCT 40030
QY 181 TATATTTATCCAGACAGACATGAAATTTTATGATTTTGTATATGAGCTTTAAT 240
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Db 40031 TATATTTATCCAGACAGACATGAAATTTTATGATTTTGTATATGAGCTTTAAT 40090
QY 241 AATTTGATTAAGCAAGTAAAAAGCTATGAAATGTTATGATTAAGCAATGAT 300
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Db 40091 AATTTGATTAAGCAAGTAAAAAGCTATGAAATGTTATGATTAAGCAATGAT 40150
QY 301 AATTTATCAATATAGATTAAGCAATGAAATTTTAAAGATGATTAAGCAATGAT 360
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Db 40151 AATTTATCAATATAGATTAAGCAATGAAATTTTAAAGATGATTAAGCAATGAT 40210
QY 361 AGTACAAATCAATTTTATATCTTCTTTTGTATGAAACAAATGCTATTATTAAT 420
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Db 40211 AGTACAAATCAATTTTATATCTTCTTTTGTATGAAACAAATGCTATTATTAAT 40270
QY 421 GAATATCAAAAGATATCTATTTAAAAATATATTAATTAATGAATTAATGA 480
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Db 40271 GAATATCAAAAGATATCTATTTAAAAATATATTAATTAATGAATTAATGA 40330
QY 481 GCTTATATCATATGATAGTTTATCATCTGACGTACGACGAAAAATTAACGATTA 540
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Db 40331 GCTTATATCATATGATAGTTTATCATCTGACGTACGACGAAAAATTAACGATTA 40390
QY 541 AATCTTATCTTGATTAATTTGAGACAGTTAGTCAAAAGTTTAAATTAACAGACT 600
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Db 40391 AATCTTATCTTGATTAATTTGAGACAGTTAGTCAAAAGTTTAAATTAACAGACT 40450
QY 601 TCGATTAAGAAAGATATATTAATTTAAACAAGAGATTTAAATGA 651
|||||
Db 40451 TCGATTAAGAAAGATATATTAATTTAAACAAGAGATTTAAATGA 40501

RESULT 4
AR368770 41708 bp DNA linear PAT 12-SEP-2003
LOCUS AR368770
DEFINITION Sequence 3 from patent US 6376652.
ACCESSION AR368770
VERSION AR368770.1 GI:34603077
KEYWORDS

gene	<p>OROAATLPGSKESQLTLEALFAEKPVAKNDLKEI POLVTFRKNDVSESEETNTINDKTVK QKEAFENGVIYTRKADDETTNTTAVDKSGGQSKRTTPENRANAASASTNTTSCQKQ HKKSSGQAKKQSSSSKSTQKNNQTSNKSRTTNASSNAKSTFNALVAKNSKTEKR TEND"</p> <p>complement (1907. .2398) /gene="MM1682" complement (1907. .2398) /gene="MM1682" /note="ORFID:MM1682 hypothetical protein, similar to general stress protein homolog" /codon_start=1 /transl_table=1 /protein_id="BAB95547.1" /db_xref="GI:21204852" /translation="MDWILPIAGIIIAIAFLILICIGIVAVZSVKRLNDVAKTLDGV EQQVGGITRETTDLHAKVRLTEIDQGVDRHLSVVDVAKGIDSVQTINSSVRYTN SITHNISQNEDKISQVQVSWVAMEIADKMNHRHRSQANYKANNVATDANHSYTSR VDK"</p> <p>complement (2472. .3785) /gene="murC" complement (2472. .3785) /gene="murC" /note="ORFID:MM1683" /codon_start=1 /transl_table=1 /product="UDP-N-Acetylmutamate-alanine ligase" /protein_id="BAB95548.1" /db_xref="GI:21204853" /translation="MTYHFVGIKSGMSIAQIMHDLGHVQSGDIENVYFTEVALR NKGIKILPFDANNIKEDMVIQGNAPASSHEEIVRAHQLKLDVYVNDLQIIDYT SVAVTGANGKISTGTLSHWNGDKTSFLGGTGMLPESDYFAFACYRRHFLS YRQYAIMNTIDPDHDFKIDINDVFDAPQMAHNYKGI IAMGDDEHLRKI EADPI YTFGRSDDIYAKNIQTIDKGAEDVVDGEYDHFLEPQGDHVLNALAIALSY LEKLDVNIKEALETFGGVRRNETTIANQVVDYAHPREISATIEYARKYPRK EVVAVQPHFSRTOAFLEFASLSKADRVFLCEIFSGIRENTGALTIGDIDKIEG ASLIVDSINYLEQFDNAVVLPMGAGDIQKIDQNAVILDKLGMQNAF"</p> <p>complement (3809. .7633) /gene="MM1684" complement (3809. .7633) /note="DNA translocase stage III sporulation prot homolog ORFID:MM1684" /codon_start=1 /transl_table=1 /protein_id="BAB95549.1" /db_xref="GI:21204854" /translation="MSWFDKLFGEDINDSDLLHKKKKRQESQINDHDSLLPQNN DIYSHRGRFEPMSVAYENENYEQSADTISDEKEQHRDVRKQSHDSQRHRRR NOTTEQNYSEQRGSKISQOSI KYQHSYHNKPGTYVSAINGIEKTHKSTHAM YSNNTNHRADSPYHKESPTSEVPYATIGTKMKLNGRIPIYKRSKVESDQK KTDKYAKTOTSONKQLEQEKQDSVYKQFASKSDVENSTTKSNPYSKVNTIK INIIYASQIVEEIRREERAVLQKRFRKALQKREHNNEQDAIQRAIDEMAYQA ERNYDSSLINDSDLTINSTASQLHTNGIENETVNDENKQASIQNEEDNDITHVES PNYEEVLSNQVSTTKQSDDEVYVSNYSQHSALQHNVENDKELNQSRLIAS BEDGATKEEYSGSQIDDAEVEYINDTEADDTISNI EDNTNRYASQMAVQAPTQEH AYTESQANIDKTVNEIELAPRHKDQNTLVNNSLKTNDVNDGNAVYDSQMAEIK</p>	gene
CDS	<p>complement (9236. .9547) /gene="MM1687" complement (9236. .9547) /gene="MM1687" /note="ORFID:MM1687 thiorodoxin homolog" /codon_start=1 /transl_table=1 /protein_id="BAB95552.1" /db_xref="GI:21204857" /translation="MKQLSBOQFSLKQGAVFETFAACPCACVITEPDLPELARY PMRPTFVDRDKETDICTENGTMGIPSEFLYKNGSLGSLTGKSKSIEQIDAFLOY V"</p> <p>complement (9612. .10688)</p>	CDS
gene	<p>HNAAITENQNEABESKQVNEKTI ENNPKNQTEKSTLSKRPNNVMTPSDKRM DKRHSNVNPELKVQSKQAVSESKEASQAPSSRFDSQENTYAVKTNMKNVNE NNQILGHAEETENDYQNAQVSEQRSDSTQTEIFEESQDQNDLDEQVDSSTSSVS EVSDDIEESEETHPNNTSQQDNDQDQKDLPSQNDQEDTANENRRNTQODVATN QAVQTSKPMIRKGNRIKLPSVLSLEEQVIESDEDMITDKKEIDALFYNNPAAVQ DVEGPGSVTREFELSEVGYKVSRTIALODDQIMALLAKDRIEAPIRGTSTVGI EYRN QNTTNNLASITIEPSFRASBSKLTVMNGRINNEPMLMDIAKTPHALIAGATSGSKS VCINSLIKSLYKQHPPELNJLLIDPKNVEVLAVYNGLEHLVAVITDVKAATQSLMA VEEMERVKLEFAHYHVNITAFANKAPYDERPKIYVIDELADLMAAQAPEVEQSIA RIAQKARACGIMHVALTORPSVNVITGLIKANI PTRIAFVSSVSDSRT IISGGAE ILGQDMKLYSGGNKRPINVOGT FVSDDEIDVVDVDFIKQREPDYLFEEKELKKTGT QSODELFDVCAFMNNGHISTSLQHRRIQGNRAARIIDQLQGLQVSSANGSR DVYVTEADLNK"</p> <p>complement (7654. .8250) /gene="MM1685" complement (7654. .8250) /gene="MM1685" /note="ORFID:MM1685 phenylalanyl-tRNA synthetase (beta subunit) homolog" /codon_start=1 /transl_table=1 /protein_id="BAB95550.1" /db_xref="GI:21204855" /translation="MNLFPKRYGVDAFLQIEPVPEGRINNNKGVNVEITNEGNYG YNIFEISKQITIEKGIKLTDELNNPQKRSSEAGPYKTNADLSPTFVGYVERKQ KHPADKLSYLVNANGDITQIVCGANVEAQKVYAKVGAVPSGAVINDALELGV ASSQNTCSMKELNLENAPEKGIWYINDSEIQAFFB" complement (8279. .9136) /gene="MM1686" complement (8279. .9136) /gene="MM1686" /note="ORFID:MM1686" /codon_start=1 /transl_table=1 /product="conserved hypothetical protein" /protein_id="BAB95551.1" /db_xref="GI:21204856" /translation="MTTFQMRDKLEKLSHLDVDEKRNREEFLTAIYRTDNNKGITIK LNALVAKYEDKKEKIVDEIVYVDEALIAQADKTLIESISSQIMEVIAFSPDKTKQ GVPEIYDEHTAETAVYAVDLGKSYRLIDSNLEBDLKLTEQKIREMSLFNVRKLSNY TTDEVGNTFYFINSNGYDASRLINTAFINLET EAOQCGMLAVAPHQDVLI IADIRN KTGYDMALHMEFFTKGLVPTISLSPGYKQGLEPIFILGKNNQKRDVNIQRLBA NRKENKDK"</p> <p>complement (9236. .9547) /gene="MM1687" complement (9236. .9547) /gene="MM1687" /note="ORFID:MM1687 thiorodoxin homolog" /codon_start=1 /transl_table=1 /protein_id="BAB95552.1" /db_xref="GI:21204857" /translation="MKQLSBOQFSLKQGAVFETFAACPCACVITEPDLPELARY PMRPTFVDRDKETDICTENGTMGIPSEFLYKNGSLGSLTGKSKSIEQIDAFLOY V"</p> <p>complement (9612. .10688)</p>	gene

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endo-1,4-beta-glucanase homolog"
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/codon_start=1
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/translation="MTKLKTIPTIIYAVIISTISIIQYINKRKNPVNLEWKS
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/note="ORFID:NM1690"
/codon_start=1
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Best Local Similarity 100.0%; Pred. No. 4,5e-73;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAGAGAAATATAGAGCATATACCTTAGAGAGAGGTGTGCTTTATCA 60
DB 250006 ATGAAGAGAAATATAGAGCATATACCTTAGAGAGAGGTGTGCTTTATCA 24947
QY 61 GTTAAAGATTTTATAGTATTTACAGATTCTAACTTACACGCTTAAAAATCAATTA 120
DB 24946 GTTAAAGATTTTATAGTATTTACAGATTCTAACTTACACGCTTAAAAATCAATTA 24987
QY 121 GACAAATATATCCGATATATTTAGATTGTTAAAAAGCTAAAAAGATGATTGAGCT 180
DB 24986 GACAAATATATCCGATATATTTAGATTGTTAAAAAGCTAAAAAGATGATTGAGCT 24987

QY 181 TATATTATCCAGACAGACGATGAATTTTAAATTTTTGATTTGAGTCTTAAAT 240
DB 24982 TATATTATCCAGACAGACGATGAATTTTAAATTTTTGATTTGAGTCTTAAAT 249767
QY 241 AATTAGATTAAGCAAAAGTAAAAAGCGTATGAAAATGTTATGATTTAGCAAAATGAT 300
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QY 361 AGTACAAATCAGATTTTATATCCTCTTTGTATGGAACATTCGATATTAAT 420
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QY 421 GAATATCAAAAGATATATCTTATTTAAAAATATATTAATTAATGAATGAATAGA 480
DB 24958 GAATATCAAAAGATATATCTTATTTAAAAATATATTAATTAATGAATGAATAGA 249527
QY 481 GCTTATATCATATATGATGATTTATCATCTCAGATCAGACGAAAAATTAACGATTAAT 540
DB 24952 GCTTATATCATATATGATGATTTATCATCTCAGATCAGACGAAAAATTAACGATTAAT 249467
QY 541 AATCTTATCTGATTAATTTGAAGAACGTTAGTCAAAAAGTTAAAAATTAACGAAC 600
DB 24946 AATCTTATCTGATTAATTTGAAGAACGTTAGTCAAAAAGTTAAAAATTAACGAAC 249407
QY 601 TCGATTAAGAAAGAAATATATTTATTTAAACAAGAGATTTAAATGA 651
DB 24940 TCGATTAAGAAAGAAATATATTTATTTAAACAAGAGATTTAAATGA 249356
Search completed: October 14, 2004, 16:00:24
Job time : 3346.74 secs

OM nucleic - nucleic search, using mw model

Run on: October 14, 2004, 07:30:59 / Search time 434 Seconds
(without alignments)

6372.297 Million cell updates/sec

Title: US-09-407-804a-5

Perfect score: 651
Sequence: 1 atgaacgagcacaataatg.....acaagagagatttaataga 651

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

1: geneseqn1980a:*

2: geneseqn1990a:*

3: geneseqn2000a:*

4: geneseqn2001a:*

5: geneseqn2002a:*

6: geneseqn2003a:*

7: geneseqn2003a:*

8: geneseqn2003a:*

9: geneseqn2003a:*

10: geneseqn2004a:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	651	100.0	651	AAA68249	Aa668249 Bacterioph
2	651	100.0	41708	AAA68247	Aa668247 Bacterioph
3	651	100.0	41708	AAC86106	Aa686106 Complete
4	91.2	14.0	4985	AB075107	Ab075107 Mosquito
5	91.2	14.0	4985	ACF79720	AcF79720 Mosquito
6	91	14.0	8056	AB210246	Ab210246 Haematopo
7	89.6	13.8	8056	AB210246	Ab210246 Haematopo

8	83.2	12.8	8056	7	AB210100	Ab210100 Haematopo
9	82	12.6	8056	7	AB210100	Ab210100 Haematopo
10	80.2	12.3	1830	6	AB156243	Ab156243 AmePV met
11	80.2	12.3	32392	6	AB156203	Ab156203 AmePV gen
12	79.6	12.2	7892	6	ABK40056	Abk40056 Human che
13	78.6	12.1	50000	6	AB155643	Ab155643 AmePV gen
14	78	12.0	7695	6	AB133536	Ab133536 Human imm
15	78	12.0	7695	6	AB192258	Ab192258 Chemical1
16	77.4	11.9	11143	4	AB112834	Ab112834 Drosophila
17	77.2	11.9	34688	6	AB067060	Ab067060 Human ang
18	76.2	11.7	6437	6	AB133261	Ab133261 Human imm
19	76	11.7	7171	6	ABN80217	Abn80217 Human che
20	75.8	11.6	15743	6	ABK28395	Abk28395 DNA trans
21	75.4	11.6	6106	4	AA546429	Aa546429 Tumour su
22	75.4	11.6	6106	6	ABK40031	Abk40031 Human che
23	75.4	11.6	6106	6	AB133472	Ab133472 Human imm
24	75.4	11.6	15548	6	AB134155	Ab134155 Human imm
25	75.2	11.6	9810	6	AB132426	Ab132426 Human imm
26	74.8	11.5	6106	4	AA546429	Aa546429 Tumour su
27	74.8	11.5	6106	6	ABK40031	Abk40031 Human che
28	74.8	11.5	6106	6	AB133472	Ab133472 Human imm
29	74.8	11.5	19124	2	AA772882	Aa772882 Plasmodiu
30	74.8	11.5	19124	2	AA772882	Aa772882 Plasmodiu
31	74.8	11.5	50000	6	AB156202	Ab156202 AmePV gen
32	74.6	11.5	6106	4	AA546430	Aa546430 Tumour su
33	74.6	11.5	6106	6	ABK40032	Abk40032 Human che
34	74.6	11.5	6106	6	AB133473	Ab133473 Human imm
35	74.6	11.5	7722	3	AA770168	Aa770168 Plasmodiu
36	73.6	11.3	3255	2	AA598608	Aa598608 Nucleic a
37	73.6	11.3	9810	6	AB132427	Ab132427 Human imm
38	73.4	11.3	3567	3	AA770117	Aa770117 Plasmodiu
39	73.4	11.3	110000	6	ABK27873	Abk27873 Plasmodiu
40	73.2	11.2	7597	6	AB133013	Ab133013 Human imm
41	73.2	11.2	15548	6	AB134155	Ab134155 Human imm
42	72.8	11.2	969	6	AB039490	Ab039490 Oligonuc
43	72.8	11.2	969	6	AB039491	Ab039491 Oligonuc
44	72.4	11.1	831	6	AB156243	Ab156243 AmePV NTP
45	72.4	11.1	50000	6	AB155644	Ab155644 AmePV gen

ALIGNMENTS

RESULT 1	
AAA68249	
ID	AAA68249 standard; DNA; 651 BP.
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XX	
AC	AAA68249;
XX	
DT	15-SEP-2003 (revised)
DT	06-AUG-2003 (revised)
DT	27-OCT-2000 (first entry)
XX	
DE	Bacteriophage 77 77ORF019 nucleotide sequence.
XX	
KW	Bacteriophage; antimicrobial; genome; identification; antibacterial;
KW	Bacterial growth inhibition; bacterial infection; ds.

XX Staphylococcus aureus; bacteriophage 77.
OS
XX
PN WO200032825-A2.
XX
PD 08-JUN-2000.
XX
PF 03-DEC-1999; 99WO-1B002040.
XX
PR 03-DEC-1998; 98US-0110992P.
PR 03-JUN-1999; 99US-00326144.
PR 28-SEP-1999; 99US-00407804.
PR 30-SEP-1999; 99US-0157218P.
PR 01-DEC-1999; 99US-0168777P.
PR 02-DEC-1999; 99US-00454252.
XX
PA (PHAG-) PHAGETECH INC.
XX
PI Polletier J, Gros P, Dubow M;
XX
DR WPI, 2000-412361/35.
DR P-P5DB; AAB16524.
XX
XX
PT Identifying a bacteriophage coding region for treating bacterial
PT infections comprises identifying a nucleic acid encoding a product that
PT inhibits bacteria when a bacteriophage infects a bacterium.
XX
PS Disclosure; Page 153; 456pp; English.
XX
XX The present invention describes a method for identifying a bacteriophage
CC coding region encoding a product active on an essential bacterial target.
CC The method comprises identifying a nucleic acid sequence encoding a gene
CC product that provides a bacteria-inhibiting function when an
CC uncharacterized bacteriophage infects a pathogenic bacterium. The
CC compound active on a target of a bacteriophage inhibitor protein in a
CC bacteriophage is used to treat or prevent a bacterial infection in an animal.
CC AAB68243 to AAB69442 and AAB16523 to AAB16954 represent bacteriophage
CC nucleotide and protein sequences which are used in the exemplification of
CC the present invention. (Updated on 06-AUG-2003 to correct OS field.)
CC
CC (Updated on 15-SEP-2003 to standardise OS field)
XX
SQ Sequence 651 BP; 275 A; 57 C; 95 G; 224 T; 0 U; 0 other;
Query Match 100.0%; Score 651; DB 3; Length 651;
Best Local Similarity 100.0%; Pred. No. 2,4e-86;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAACGACGAATATATAGAGCATATATATAGAGGAGGTGTGCTTTATTC 60
DB 1 ATGAACGACGAATATATAGAGCATATATATAGAGGAGGTGTGCTTTATTC 60
QY 61 GTTAAAGATTTTATAGTATTTTACGATTCCTACCAAGTAAAAATCAATTTA 120
DB 61 GTTAAAGATTTTATAGTATTTTACGATTCCTACCAAGTAAAAATCAATTTA 120
QY 121 GAACAAATATATCCATATATTTAGATTGTTTAAAAAGGCTAAAAAGATGAGCT 180
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DB 121 GAACAAATATATCCATATATTTAGATTGTTTAAAAAGGCTAAAAAGATGAGCT 180
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DB 181 TATATTATCCACAGACGATGATTTTATAGATTTTATGATGAGCTTTAT 240
QY 241 AATTAGATAGCAAGTAAAAAGGCTATGAAAAATGTTATGATTAACAAATGAT 300
DB 241 AATTAGATAGCAAGTAAAAAGGCTATGAAAAATGTTATGATTAACAAATGAT 300
QY 301 AATTATCAATATAGTATAGCAATGCAATTTTAAAGTATGATTAACAAATGAT 360
DB 301 AATTATCAATATAGTATAGCAATGCAATTTTAAAGTATGATTAACAAATGAT 360
QY 361 AATTATCAATATAGTATAGCAATGCAATTTTAAAGTATGATTAACAAATGAT 420
DB 361 AATTATCAATATAGTATAGCAATGCAATTTTAAAGTATGATTAACAAATGAT 420
QY 421 GATATCAAAAAGATATCTTATTTAAAAATATATATATATATATATATATAT 480
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QY 481 GCTTATATCATATTTGATTTTATATATATATATATATATATATATATATAT 540
DB 481 GCTTATATCATATTTGATTTTATATATATATATATATATATATATATATAT 540
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DB 541 AATCTTATCTGATATATTTGAGAACAGTTTATGTCAAAAGTTTAAATTAACGACT 600
QY 601 TCAATTAAGAAAGATTTATTTATTTAAACAGAGGATTTAAATGA 651
DB 601 TCAATTAAGAAAGATTTATTTATTTAAACAGAGGATTTAAATGA 651
RESULT 2
ID AAB68247 standard; DNA; 41708 BP.
XX
AC AAB68247;
XX
DT 15-SEP-2003 (revised)
DT 06-AUG-2003 (revised)
DT 27-OCT-2000 (first entry)
XX
DE Bacteriophage 77 complete genome sequence.
XX
KW Bacteriophage; antimicrobial; genome; identification; antibacterial;
KW bacterial growth inhibition; bacterial infection; ds.
XX
XX Staphylococcus aureus; bacteriophage 77.
XX
PN WO200032825-A2.
XX
PD 08-JUN-2000.
XX
PF 03-DEC-1999; 99WO-1B002040.

XX Novel DnaI polypeptides useful for treating and diagnosing microbial,
PT preferably bacterial, diseases such as those caused by *Staphylococcus*
PT aureus.
PS
XX
XX Disclosure: Fig 2, 107pp; English.

CC This sequence represents the genome of Bacteriophage 77. The growth
CC inhibitory gene product of ORF 104 interacts with DnaI derived from *S.*
CC aureus, to form the basis of a screening assay. DnaI polypeptides and
CC polynucleotides are useful for treating microbial, preferably bacterial,
CC especially *Staphylococcus*, infections. DnaI polypeptides and
CC polynucleotides are useful for biological, diagnostic, prophylactic,
CC clinical and therapeutic use, and as components in databases useful for
CC search analyses as well as in sequence analysis algorithms. (Updated on
CC 06-AUG-2003 to correct OS field.)
XX
XX

SQ Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 U; 0 other;

Query Match 100.0%; Score 651; DB 4; Length 41708;
Best Local Similarity 100.0%; Pred. No. 1.5e-86;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 39851 ATGAACGACAAATATAGAGCATATATACCTTACGAGAGGTGTGCTTTATCA 39910
QY 61 GTAAAGAGATTTTAGATTTTACAGATCTTACAGCTTAAATCAATTTA 120
DB 39911 GTAAAGAGATTTTAGATTTTACAGATCTTACAGCTTAAATCAATTTA 39970
QY 121 GAACAATATATCGATATATTTAGATTTTAAAGGCTTAAAGATGATGGAGCT 180
DB 39971 GAACAATATATCGATATATTTAGATTTTAAAGGCTTAAAGATGATGGAGCT 40030
QY 181 TATATTATCCAAAGCAAGCATGATTTTGAATTTTGAATTTGAATGCTTTAT 240
DB 40031 TATATTATCCAAAGCAAGCATGATTTTGAATTTTGAATTTGAATGCTTTAT 40090
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DB 40091 AATTAGATACCAAGTAAAAAGCTATGAAATGTTATGATTTAGCAATGANT 40150
QY 301 AATTATCAATATAGTTAAGCAATGAAAGATTTTAAAGATTTCAACATGAATT 360
DB 40151 AATTATCAATATAGTTAAGCAATGAAAGATTTTAAAGATTTCAACATGAATT 40210
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DB 40211 AGTCAAAATCAGATTTTAAATCCTTCTTTGTTATGAAACATTCGATTATTAAT 40270
QY 421 GAATATCAAAAAGATATATCTTATTTAAATATATTAATTAATGAATGAATTA 480
DB 40271 GAATATCAAAAAGATATATCTTATTTAAATATATTAATTAATGAATGAATTA 40330
QY 481 GCTTATATCATATTTGATTTTATCATCTGAGTACGAGCAAAAATAACGATTAT 540
DB 40331 GCTTATATCATATTTGATTTTATCATCTGAGTACGAGCAAAAATAACGATTAT 40390

DB 40391 GCTTATATCATATTTGATTTTATCATCTGAGTACGAGCAAAAATAACGATTAT 40390
QY 541 AATCTTATCTGTAAATTTGAGAACAGTTTACGAAAGTTTAAATTAACAGACT 600
DB 40391 AATCTTATCTGTAAATTTGAGAACAGTTTACGAAAGTTTAAATTAACAGACT 40450
QY 601 TCGATTAAGAAAGATATTTATTTATTTAAACAAAGAGATTTAAATGA 651
DB 40451 TCGATTAAGAAAGATATTTATTTATTTAAACAAAGAGATTTAAATGA 40501
Search completed: October 14, 2004, 12:48:12
Job time : 436 secs

OK nucleole - nucleole search, using sw model

Run on: October 14, 2004, 12:03:47 ; Search time 3040.61 Seconds

(without alignments)
6393.544 Million cell updates/sec

SUMMARIES

28: gb_gss1:.*
29: gb_gss2:.*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Title: US-09-407-804A-5
Perfect score: 651
Sequence: 1 atgacagcagcacaataatga.....acagagagagattcaatga 651
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_gss1:.*
2: em_gss2:.*
3: em_gss3:.*
4: em_gss4:.*
5: em_gss5:.*
6: em_gss6:.*
7: em_gss7:.*
8: em_gss8:.*
9: gb_gss1:.*
10: gb_gss2:.*
11: gb_gss3:.*
12: gb_gss4:.*
13: gb_gss5:.*
14: gb_gss6:.*
15: gb_gss7:.*
16: gb_gss8:.*
17: em_gss9:.*
18: em_gss10:.*
19: em_gss11:.*
20: em_gss12:.*
21: em_gss13:.*
22: em_gss14:.*
23: em_gss15:.*
24: em_gss16:.*
25: em_gss17:.*
26: em_gss18:.*
27: em_gss19:.*

Result No.	Score	Query		DB ID	Description
		Match	Length		
1	121.6	18.7	1101	29	CNS00EVL
2	105.2	16.2	1201	9	AL536104
3	104.8	16.1	1200	13	BK437758
4	102	15.7	1200	13	BK415878
5	100.8	15.5	1201	13	BK443774
6	100	15.4	1201	13	BK439779
7	99.2	15.2	1101	29	CNS003BD
8	98.8	15.2	1200	13	BK415878
9	98.6	15.1	1101	29	CNS00E07
10	98	15.1	1056	13	BK415058
11	98	15.1	1201	9	AL536104
12	97.4	15.0	999	13	BK380865
13	97.2	14.9	1201	13	BK420717
14	97	14.9	1201	13	BK426629
15	96.6	14.8	1277	28	CC253231
16	96.6	14.8	781	29	BK145762
17	96.2	14.8	1064	13	BK361825
18	94.2	14.5	1101	29	CNS00E07
19	93.8	14.4	1201	13	BK458623
20	93.6	14.4	964	13	BK341256
21	92.2	14.2	1098	13	BK377526
22	91.2	14.0	1348	29	CG749499
23	91	14.0	829	29	BK173672
24	90.8	13.9	641	28	AQ946120
25	90.6	13.9	707	29	CG403361
26	90.2	13.9	893	12	BP507314
27	90.2	13.9	1092	29	CNS020K7
28	89.6	13.8	886	28	BH177277
29	89.6	13.8	886	29	CNS07JUX
30	89.6	13.8	886	29	CNS07JUX
31	89.6	13.8	1201	13	BK462660
32	89.4	13.7	1201	9	AL565455
33	89.4	13.7	1201	13	BK340226
34	89.4	13.7	1272	28	CC264939
35	89.4	13.7	1392	29	CG757503
36	89	13.7	1200	13	BK437739
37	88.8	13.6	660	28	BH183498
38	88.8	13.6	660	29	CNS07JUX
39	88.8	13.6	670	28	BK388480
40	88.8	13.6	975	13	BK414927
41	88.8	13.6	1201	13	BK366070
42	88.4	13.6	1101	29	CNS003BD
43	88.4	13.6	1133	13	BK444099
44	88.2	13.5	700	28	AQ940248
45	87.4	13.4	1206	28	BZ695529

Search completed: October 14, 2004, 18:55:08
Job time : 3043.61 sec

OK nucleic - nucleic search, using sw model

Run on: October 14, 2004, 09:12:14 ; Search time 1339.78 Seconds
(without alignments)

8443.595 Million cell updates/sec

Title: US-09-407-804A-6

Perfect score: 261
Sequence: 1 atgtattcgaatacagcga.....acttgatcagtaagtag 261

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: 1: gb_ba: 2: gb_hvg: 3: gb_in: 4: gb_cm: 5: gb_ov: 6: gb_pat: 7: gb_ph: 8: gb_pl: 9: gb_pr: 10: gb_ro: 11: gb_scs: 12: gb_sy: 13: gb_un: 14: gb_vl: 15: em_ba: 16: em_fm: 17: em_hum: 18: em_in: 19: em_mu: 20: em_cm: 21: em_or: 22: em_ov: 23: em_pat: 24: em_ph: 25: em_pl: 26: em_ro: 27: em_scs:

28: em_un: 29: em_vl: 30: em_hvg_hum: 31: em_hvg_inv: 32: em_hvg_other: 33: em_hvg_mus: 34: em_hvg_pin: 35: em_hvg_rtd: 36: em_hvg_mam: 37: em_hvg_vrt: 38: em_sy: 39: em_hvg_hum: 40: em_hvg_mus: 41: em_hvg_other:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query				Description
	Score	Match	Length	ID	
1	261	100.0	261	6	BD245277 Developme
2	261	100.0	297	6	BD245280 Developme
3	261	100.0	41708	6	BD245281 Developme
4	261	100.0	41708	6	AR368770 Sequence
5	257.8	98.8	41401	7	AB009866 Bacterioph
6	256.2	98.2	42942	7	AB045978 Bacterioph
7	256.2	98.2	348527	1	AP003360 Bacterioph
8	254.6	97.3	45636	7	AB044534 Bacterioph
9	253	96.9	43081	7	AP001553 Bacterioph
10	133	51.0	348650	1	AP003364 Bacterioph
11	131.4	50.3	580	6	AR355085 Sequence
12	131.4	50.3	43594	6	BD245634 Developme
13	131.4	50.3	43604	7	AR424781 Developme
14	128.4	49.2	258	6	AK618548 Sequence
15	121.8	46.7	42722	7	AF424783 Bacterioph
16	121.8	46.7	272850	1	AP004828 Bacterioph
17	118.8	45.5	267	6	AK618246 Sequence
18	101	38.7	291150	1	AP003135 Bacterioph
19	47.4	18.2	82281	8	AC025295 Bacterioph
20	47.4	18.2	192780	9	AL162723 Human DNA
21	45.8	17.5	207726	2	AC024953 Human DNA
22	45.8	17.5	209287	2	AC012077 Human DNA
23	45.2	17.3	200473	2	AC133762 Bacterioph
24	45.2	17.3	254977	2	AC117353 Bacterioph
25	45	17.2	110000	2	AC112311_2 Bacterioph
26	45	17.2	175406	5	BK000522 Zebrafish
27	45	17.2	241807	2	AC126077 Bacterioph
28	45	17.2	248933	2	AC109773 Bacterioph
29	44.4	17.0	156060	2	AC004153 Bacterioph
30	44.4	17.0	184090	10	AC122304 Bacterioph
31	44.4	17.0	250707	3	AE014848 Bacterioph
32	44.2	16.9	138807	9	AL161650 Human DNA
33	44	16.9	238646	2	AC099463 Bacterioph

ALIGNMENTS

RESULT 1

COMMENT

C12N15/00,
PC 861K37

FEATURES	Location/Qualifiers
SOURCE	1. .261

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Dib

BD245280

COMMENT

FT aureus bacteriophage 77' /organism='Staphylococcus aureus bacteriophage 77'

FEATURES source Location/Qualifiers 1..297 /organism="unidentified" /mol_type="genomic DNA" /db_xref="taxon:32644"

ORIGIN

Query Match 100.0%; Score 261; DB 6; Length 297; Best Local Similarity 100.0%; Pred. No. 6.7e-45; Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATTAAGAAATAGCGCAATCATACGCAAAATATTCATGTAAAGGATTCGATTT 60
DB 37 ATGATTAAGAAATAGCGCAATCATACGCAAAATATTCATGTAAAGGATTCGATTT 96
QY 61 AAGCTATCATTTTAAAGGTCATATGGCATATCATACAGTAAAGATGAAAC 120
DB 97 AAGCTATCATTTTAAAGGTCATATGGCATATCATACAGTAAAGATGAAAC 156
QY 121 GTACCAATTAACATGCTTATGTCTAGATGAGATGACTTAAGTGGCATCACTTA 180
DB 157 GTACCAATTAACATGCTTATGTCTAGATGAGATGACTTAAGTGGCATCACTTA 216
QY 181 TTTAACCAAGCATAGATGATGATGAAAGAAACAGACAGACAGACTTA 240
DB 217 TTTAACCAAGCATAGATGATGATGAAAGAAACAGACAGACAGACTTA 276
QY 241 AACTAGTCATGAATGGTAG 261
DB 277 AACTAGTCATGAATGGTAG 297

RESULT 3 BD245281 41708 bp DNA linear PAT 17-JUL-2003
LOCUS BD245281 Development of novel antibiotics based on bacteriophage genomics.
DEFINITION BD245281
ACCESSION BD245281.1 GI:33055051
VERSION JP 2002531107-A/16.
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 41708)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Development of novel antibiotics based on bacteriophage genomics
JOURNAL Patent: JP 2002531107-A 16 24-SEP-2002;
PHARTECH INC
COMMENT OS Staphylococcus aureus bacteriophage 77
PN JP 2002531107-A/16
PD 24-SEP-2002
PF 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR
01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454252 PI JERRY

PELLETIER, PHILIPPE, GROS, MICHAEL, DUBOW
PC C12N13/09,A01N63/00,A61K38/00,A61K45/00,A61P31/04,C07K14/005,
PC C12M1/00,
PC C12N1/21,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/566, PC
C12N15/00,
PC A61K37/02
CC Genome Sequence
FH Key
FT source Location/Qualifiers
FT aureus bacteriophage 77' /organism='Staphylococcus aureus bacteriophage 77'

FEATURES source Location/Qualifiers 1..41708 /organism="unidentified" /mol_type="genomic DNA" /db_xref="taxon:32644"

ORIGIN

Query Match 100.0%; Score 261; DB 6; Length 41708; Best Local Similarity 100.0%; Pred. No. 3.8e-45; Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATTAAGAAATAGCGCAATCATACGCAAAATATTCATGTAAAGGATTCGATTT 60
DB 29304 ATGATTAAGAAATAGCGCAATCATACGCAAAATATTCATGTAAAGGATTCGATTT 29363
QY 61 AAGCTATCATTTTAAAGGTCATATGGCATATCATACAGTAAAGATGAAAC 120
DB 29364 AAGCTATCATTTTAAAGGTCATATGGCATATCATACAGTAAAGATGAAAC 29423
QY 121 GTACCAATTAACATGCTTATGTCTAGATGAGATGACTTAAGTGGCATCACTTA 180
DB 29424 GTACCAATTAACATGCTTATGTCTAGATGAGATGACTTAAGTGGCATCACTTA 29483
QY 181 TTTAACCAAGCATAGATGATGATGAAAGAAACAGACAGACAGACTTA 240
DB 29484 TTTAACCAAGCATAGATGATGATGAAAGAAACAGACAGACAGACTTA 29543
QY 241 AACTAGTCATGAATGGTAG 261
DB 29544 AACTAGTCATGAATGGTAG 29564

RESULT 4 AR368770 41708 bp DNA linear PAT 12-SEP-2003
LOCUS AR368770
DEFINITION AR368770 Sequence 3 from patent US 637652.
ACCESSION AR368770
VERSION AR368770.1 GI:34603077
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 41708)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Compositions and methods involving an essential Staphylococcus

Journal Patent: US 6376652-A 3 23-APR-2002;
Location/Qualifiers
1..41708
/orgnism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 261; DB 6; Length 41708;
Best Local Similarity 100.0%; Pred. No. 3,86-45;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATTACGAATAGGCGAAATCTACGCAAAATATCATGTACGGATTCGATTTT 60
DB 29304 ATGATTACGAATAGGCGAAATCTACGCAAAATATCATGTACGGATTCGATTTT 29363
QY 61 AACGATATCTTTTAAAGGTCATAGGCGATATCAATACATGTTAAAGATGAAC 120
DB 29364 AACGATATCTTTTAAAGGTCATAGGCGATATCAATACATGTTAAAGATGAAC 29423
QY 121 GTACCAATTAACATGCTTATGTGCTAGATGAGATGACTAGATATGGCATCACTTA 180
DB 29424 GTACCAATTAACATGCTTATGTGCTAGATGAGATGACTAGATATGGCATCACTTA 29483
QY 181 TTACCAAGCAATGATGATGATGAGATGAGATGAGATGAGATGAGATGAGAT 240
DB 29484 TTACCAAGCAATGATGATGATGAGATGAGATGAGATGAGATGAGATGAGAT 29543
QY 241 AACTAGTCATGAATGCTAG 261
DB 29544 AACTAGTCATGAATGCTAG 29564

RESULT 5
AB009866 41401 bp DNA linear PHG 23-MAY-2000
LOCUS Bacteriophage phi PVL proviral DNA, complete sequence.
DEFINITION AB009866
ACCESSION AB009866
VERSION AB009866.2 GI:8031688
KEYWORDS dUTPase; ssDNA binding protein; anti repressor; repressor; integrase; lusk-PV; lusk-PV; holin; amidase (peptidoglycan hydrolase); capsid protein; portal protein.
SOURCE Staphylococcus aureus bacteriophage PVL
ORGANISM Staphylococcus aureus bacteriophage PVL
REFERENCE 1 Vituase; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
AUTHORS Kaneo, J., Kimura, T., Kawakami, Y., Tomita, T. and Kamio, Y.
TITLE Pantom-valentine leukocidin genes in a phage-like particle isolated from mitomycin C-treated Staphylococcus aureus V8 (ATCC 49775)
JOURNAL Biosci. Biotechnol. Biochem. 61 (11), 1960-1962 (1997)
MEDLINE 98067870
PUBMED 9404084
REFERENCE 2 (dites)
AUTHORS Kaneo, J., Kimura, T., Narita, S., Tomita, T. and Kamio, Y.
TITLE Complete nucleotide sequence and molecular characterization of the temperate staphylococcal bacteriophage phiPVL carrying Pantom-Valentine leukocidin genes

JOURNAL Gene 215 (1), 57-67 (1998)
MEDLINE 98332719
PUBMED 9666077
REFERENCE 3 (bases 1 to 41401)
AUTHORS Kaneo, J., Kimura, T., Narita, S., Tomita, T. and Kamio, Y.
TITLE Direct Submission
JOURNAL Submitted (17-DEC-1997) Jun Kaneo, Tohoku University, Dept. Appl. Biol. Chem., Faculty of Agriculture, 1-1 Tsurumi-dori, Aomiyamae, Aoba-ku, Sendai, Miyagi 981, Japan (E-mail: jkaneob@biochem.tohoku.ac.jp, Tel: 81-22-717-8781, Fax: 81-22-717-8780)

COMMENT On May 24, 2000 this sequence version replaced gi:3341907.
Sequence updated (06-Feb-1998)
Sequence updated (22-May-2000).
Location/Qualifiers

FEATURES

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Query Match 98.8%; Score 257.8; DB 7; Length 41401;
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RESULT 6
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 VERSION
 AB045978.1 GI:12697822
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 ORGANISM
 Staphylococcus aureus temperate phage phiSLT
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 Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
 REFERENCE
 1 (altes)
 Narita,S., Kaneko,J., Chiba,J., Piemont,Y., Jarraud,S., Etienne,J.
 and Kamio,Y.
 Phage conversion of Panton-Valentine leukocidin in Staphylococcus
 aureus: molecular analysis of a PVL-converting phage, phiSLT
 TITLE
 JOURNAL
 MEDLINE
 PUBLISHED
 11368915
 2 (bases 1 to 42942)
 Kaneko,J., Narita,S. and Kamio,Y.
 TITLE
 JOURNAL
 Submitted (12-JUL-2000) Jun Kaneko, Tohoku University, Graduate
 school of Agricultural Science, 1-1, Tsutsunodori Aomiyamachi,

Sendai, Miyagi 981-8555, Japan
 (E-mail: jkaneko@biochem.tohoku.ac.jp, Tel:81-22-717-8781,
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OY 61 AACGATTCATTTTAAAGGTCATATGGGCAATTCATACATAGTTAAAGATGAAAC 120
DB 230734 AACGATTCATTTTAAAGGTCATATGGGCAATTCATACATAGTTAAAGATGAAAC
230793

OY 121 GTACCAATTAAACGCTTATGTCTGATAGATGAGAAATGATGATGCGATCAGCTTA 180
DB 230794 GTACCAATTAAACGCTTATGTCTGATAGATGAGAAATGATGATGCGATCAGCTTA
230853

OY 181 TTTAACCAAGCATATGATGATGATGAAAGAAACAGACAGACAGACAGATTA 240
DB 230854 TTTAACCAAGCATATGATGATGATGAAAGAAACAGACAGACAGACAGATTA
230913

OY 241 AACTTAGTCATGAATGCTAG 261
DB 230914 AACTTAGTCATGAATGCTAG 230934

RESULT 8
LOCUS AB044554 45636 bp DNA linear PHG 04-JUL-2000
DEFINITION Staphylococcus aureus prophage phiPV83 proviral DNA, complete
sequence.
ACCESSION AB044554
VERSION AB044554.1 GI:8918747
KEYWORDS
SOURCE Staphylococcus aureus prophage phiPV83
ORGANISM Staphylococcus aureus prophage phiPV83
1 (sites)
REFERENCE
AUTHORS Kaneko,J., Kimura,T., Kawakami,Y., Tomita,T. and Kamio,Y.
TITLE Pantom-valentine leukocidin genes in a phage-like particle isolated
from mitomycin C-treated Staphylococcus aureus V8 (ATCC 49775)
JOURNAL Biotec. Biotechnol. Biochem. 61 (11), 1960-1962 (1997)
MEDLINE 98067870
PUBMED 9404084
REFERENCE 2 (sites)
AUTHORS Zou,D., Kaneko,J., Narita,S. and Kamio,Y.

TITLE Complete nucleotide sequence and molecular characterization of
prophage PV83pro carrying lukM-lukF-PV(p83) gene cluster in
Staphylococcus aureus strain P83
JOURNAL 3 (bases 1 to 45636)
REFERENCE
AUTHORS Kaneko,J., Zou,D. and Kamio,Y.
TITLE Direct Submission
JOURNAL Submitted (09-JUN-2000) Jun Kaneko, Tohoku University, Graduate
school of Agricultural Science, 1-1 Tsutsumi-dori Aamiyamachi,
Aoba-ku, Sendai, Miyagi 981-8555, Japan
(E-mail:jkaneko@biochem.tohoku.ac.jp, Tel:81-22-717-8781,
Fax:81-22-717-8780)

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Query Match 97.5%; Score 254.6; DB 7; Length 45636;
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Matches 257; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DB 7035 AAGCTATTCATTTTAAAGGTCAATGGGCAATCATACAGTTAAAGATGAAACAAC 7094
QY 121 GTACCAATTAACATGCTTATGTGCTAGATGAGATGACTTATGGCATCGACTTA 180
DB 7095 GTACCAATTAACATGCTTATGTGCTAGATGAGATGACTTATGGCATCGACTTA 7154
QY 181 TTAAACCAAGCATGATGATGATGATGAGAACACACACACACACACATATT 240
DB 7155 TTAAACCAAGCATGATGATGATGATGAGAACACACACACACACACATATT 7214
QY 241 AACTTACTCATGAATGCTAG 261
DB 7215 AACTTACTCATGAATGCTAG 7235

RESULT 9
LOCUS AP001553 43081 bp DNA circular PHG 14-MAR-2001
DEFINITION Bacteriophage phi ETA DNA, complete genome.
ACCESSION AP001553
VERSION AP001553.1 GI:8918415
KEYWORDS
SOURCE Bacteriophage phi ETA
ORGANISM Bacteriophage phi ETA
REFERENCE 1 (sites)
Yamaguchi, T., Hayashi, T., Takami, H., Nakasone, K., Ohnishi, M.,
Nakayama, K., Yamada, S., Komatsuwa, H., and Sugai, M.,
Phage conversion of enterofoliate toxin A production in
Staphylococcus aureus
JOURNAL Mol. Microbiol. 38 (4), 694-705 (2000)
MEDLINE 20566787
PUBMED 11135106
REFERENCE 2 (bases 1 to 43081)
Sugai, M., Yamaguchi, T., Hayashi, T., Nakasone, K. and Takami, H.

TITLE Direct Submission
JOURNAL Submitted (28-Mar-2000) Motoyuki Sugai, Hiroshima University
Faculty of Dentistry, Microbiology/ Kaasumi 1-2-3, Hiroshima,
Hiroshima 734-8553, Japan (E-mail: sugai@hiroshima-u.ac.jp,
Tel:81-82-257-5637, Fax:81-82-257-5639)
FEATURES
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CDS

CDS

CDS

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Matches 256; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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DB 6936 ATGATTACGAATAGCGAAATCATACGCAAAATATTCATGTAAAGATTCGATTT 6995
QY 61 AAGCTATTCATTTAAAGGTCATATGGGATATCATATACAGTTAAAGATTAACAAC 120
DB 6996 AAAATATTCATTTAAAGGTCATATGGGATATCATATACAGTTAAAGATTAACAAC 7055
QY 121 GTACCAATTAAACATGCTATGTCCTATGATGAGATGCTTATGCTATGCTTAA 180
DB 7056 GTACCAATTAAACATGCTATGTCCTATGATGAGATGCTTATGCTATGCTTAA 7115
QY 181 TTAAACCAACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
DB 7116 TTAAACCAACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7175
QY 241 AACTTAGTCAATGAATGATG 261
DB 7176 AACTTAGTCAATGAATGATG 7196

Search completed: October 14, 2004, 16:00:28
Job time : 1343.78 secs

GenCore version 5.1.6
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OM nucleole - nucleole search, using sw model

Run on: October 14, 2004, 07:30:59 ; Search time 174 Seconds
(without alignments)
6372.297 Million cell updates/sec

Title: US-09-407-804A-6

Perfect score: 261

Sequence: 1 atgattacgaatagcgaa.....acttagcatgaatgtag 261

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:.*
1: geneseqn1980s:.*
2: geneseqn1990s:.*
3: geneseqn2000s:.*
4: geneseqn2001s:.*
5: geneseqn2001bs:.*
6: geneseqn2002s:.*
7: geneseqn2003s:.*
8: geneseqn2003bs:.*
9: geneseqn2003cs:.*
10: geneseqn2004s:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	261	100.0	261	3	AAA68250
2	261	100.0	297	3	AAA68253 Bacterioph
3	261	100.0	41708	3	AAA68247 Bacterioph
4	261	100.0	41708	4	AA086106 Bacterioph
5	131.4	50.3	380	2	AAV75514 Complete
6	131.4	50.3	43576	3	AAA68609 Bacterioph
7	128.4	49.2	258	7	ACF73076 Bacterioph

8	118.8	45.5	267	ACF72925	AcF72925	Staphylococcus aureus; bacteriophage 77.
9	41.4	15.9	50000	ABIS55643	Abi55643	ABIS55643
10	38.6	14.8	3365	ABIS55643	Abi55643	ABIS55643
11	38.4	14.7	110000	ABA90521_07	Abi90521_07	ABA90521_07
12	38.4	14.7	110000	ABA90521_08	Abi90521_08	ABA90521_08
13	37.8	14.5	7341	ABIS1395	Abi1395	ABIS1395
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16	37.8	14.5	32392	ABIS6203	Abi6203	ABIS6203
17	37.6	14.4	2685	ABIS6203	Abi6203	ABIS6203
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22	37.2	14.3	6835	ABX14745	Abi14745	ABX14745
23	37	14.2	3449	ABX14745	Abi14745	ABX14745
24	37	14.2	9731	ABX14745	Abi14745	ABX14745
25	37	14.2	10467	ABX14745	Abi14745	ABX14745
26	36.8	14.1	7319	ABX14745	Abi14745	ABX14745
27	36.6	14.0	3534	ACA28380	Abi28380	ACA28380
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30	36.4	13.9	6048	AAV74570	Abi74570	AAV74570
31	36.2	13.9	924	AAV70276	Abi70276	AAV70276
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35	36	13.8	17848	AAV45322	Abi45322	AAV45322
36	36	13.8	17848	ABK39975	Abi39975	ABK39975
37	36	13.8	17848	ABK28163	Abi28163	ABK28163
38	35.8	13.7	994	AAV27429	Abi27429	AAV27429
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40	35.8	13.7	994	ABO84897	Abi84897	ABO84897
41	35.8	13.7	1033	AAV27419	Abi27419	AAV27419
42	35.8	13.7	1033	ABO84897	Abi84897	ABO84897
43	35.8	13.7	1033	ABO84897	Abi84897	ABO84897
44	35.8	13.7	1110	ABX06325	Abi06325	ABX06325
45	35.8	13.7	1112	AAV05427	Abi05427	AAV05427

ALIGNMENTS

RESULT 1
 ID AAA68250 standard; DNA; 261 BP.
 AC AAA68250;
 XX
 DT 15-SEP-2003 (revised)
 DT 06-AUG-2003 (revised)
 DT 27-OCT-2000 (first entry)
 XX
 DE Bacteriophage 77 77ORF043 nucleotide sequence.
 XX
 KW Bacteriophage; antimicrobial; genome; identification; antibacterial;
 bacterial growth inhibition; bacterial infection; ds.

XX	Staphylococcus aureus; bacteriophage 77.
OS	WO200032825-A2.
XX	08-JUN-2000.
XX	03-DEC-1999; 99WO-1B002040.
XX	03-DEC-1998; 98US-0110992P.
PR	03-JUN-1999; 99US-00326144.
PR	28-SEP-1999; 99US-00407804.
PR	30-SEP-1999; 99US-0157218P.
PR	01-DEC-1999; 99US-0168777P.
PR	02-DEC-1999; 99US-00454252.
PA	(PHAG-) PHAGEGEN INC.
XX	Pelletier J, Gros P, Dubow M,
DR	WPI; 2000-412361/35.
DR	P-PSDB; AAB16525.
XX	Identifying a bacteriophage coding region for treating bacterial
PT	infections comprises identifying a nucleic acid encoding a product that
PT	inhibits bacteria when a bacteriophage infects a bacterium.
XX	Disclosure; Page 157; 456pp; English.
XX	The present invention describes a method for identifying a bacteriophage
CC	coding region encoding a product active on an essential bacterial target.
CC	The method comprises identifying a nucleic acid sequence encoding a gene
CC	product that provides a bacteria-inhibiting function when an
CC	uncharacterized bacteriophage infects a pathogenic bacterium. The
CC	compound active on a target of a bacteriophage inhibitor protein in a
CC	bacteria is used to treat or prevent a bacterial infection in an animal.
CC	AA68243 to AA69442 and AAB16923 to AAB16954 represent bacteriophage
CC	nucleotide and protein sequences which are used in the exemplification of
CC	the present invention. (Updated on 06-AUG-2003 to correct OS field.)
CC	(Updated on 15-SEP-2003 to standardise OS field)
XX	Sequence 261 BP; 105 A; 36 C; 49 G; 71 T; 0 U; 0 Other;
XX	Query Match 100.0%; Score 261; DB 3; Length 261;
XX	Best Local Similarity 100.0%; Pred. No. 9.2e-57;
XX	Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ATGTATACGAAATAGCGAAATATCGAAATATTCATGTTAAGGATTCATTTT 60
DB	1 ATGTATACGAAATAGCGAAATATCGAAATATTCATGTTAAGGATTCATTTT 60
QY	61 AAGCTATTCATTTTAAAGGTCATATGGGATTCATCAATGTAAGATTAAGAAC 120
DB	61 AAGCTATTCATTTTAAAGGTCATATGGGATTCATCAATGTAAGATTAAGAAC 120
QY	121 GTACCAATTAACATGCTATGCTAGATGAGATGACTGATGATGATGATGATG 180
DB	121 GTACCAATTAACATGCTATGCTAGATGAGATGACTGATGATGATGATGATG 180

Db 121 GTACCAATTAACGCTATGTCGATGAAATGACTATGATGGCATCAGACTTA 180

QY 181 TTAAACCAAGCATATGATGATGATTTGAAGAAACAGACAGAGAGACTTAT 240

Db 181 TTAAACCAAGCATATGATGATGATTTGAAGAAACAGACAGAGAGACTTAT 240

QY 241 AACTTAGTCATGAATGGTAG 261

Db 241 AACTTAGTCATGAATGGTAG 261

RESULT 2

AAA68253

ID AAA68253 standard; DNA; 297 BP.

XX

AC AAA68253;

XX

DT 15-SEP-2003 (revised)

DT 06-AUG-2003 (revised)

DT 27-OCT-2000 (first entry)

XX

DE Bacteriophage 77 77ORF182 nucleotide sequence.

XX

KW Bacteriophage; antimicrobial; genome; identification; antibacterial;

KW bacterial growth inhibition; bacterial infection; ds.

XX

OS Staphylococcus aureus; bacteriophage 77.

XX

FN WO200032825-A2.

XX

PD 08-JUN-2000.

XX

PF 03-DEC-1999; 99WO-1B002040.

XX

PR 03-DEC-1998; 98US-0110992P.

PR 03-JUN-1999; 99US-00326144.

PR 28-SEP-1999; 99US-00407804.

PR 30-SEP-1999; 99US-0157218P.

PR 01-DEC-1999; 99US-0168777P.

PR 02-DEC-1999; 99US-00454252.

XX

PA (PHAG-) PHAGETECH INC.

XX

PI Polletier J, Gros P, Dubow M;

XX

DR WPI, 2000-412361/35.

DR P-PSDB; AAB16528.

XX

XX Identifying a bacteriophage coding region for treating bacterial

PT infections comprises identifying a nucleic acid encoding a product that

PT inhibits bacteria when a bacteriophage infects a bacterium.

XX

PS Disclosure; Page 165; 456pp; English.

XX

CC The present invention describes a method for identifying a bacteriophage

CC coding region encoding a product active on an essential bacterial target.

CC The method comprises identifying a nucleic acid sequence encoding a gene

CC product that provides a bacteria-inhibiting function when an

CC uncharacterised bacteriophage infects a pathogenic bacterium. The

CC compound active on a target of a bacteriophage inhibitor protein in a

CC bacteria is used to treat or prevent a bacterial infection in an animal.

CC AAA68243 to AAA69442 and AAB16523 to AAB16954 represent bacteriophage

CC nucleotide and protein sequences which are used in the exemplification of

CC the present invention. (updated on 06-AUG-2003 to correct 05 field.)

CC (updated on 15-SEP-2003 to standardise 05 field)

XX

SQ Sequence 297 BP; 123 A; 40 C; 57 G; 77 T; 0 U; 0 Other;

Query Match 100.0%; Score 261; DB 3; Length 297;

Best Local Similarity 100.0%; Pred. No. 9.5e-57;

Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATATTACGAATATAGCGCAATCATACGCAAAATATCATGTAAAGGATTCATTT 60

Db 37 ATGATATTACGAATATAGCGCAATCATACGCAAAATATCATGTAAAGGATTCATTT 96

QY 61 AAGCTATTGATTTTAAAGGTCATATGGCATATCAATACAAAGTTAAAGATGAACAC 120

Db 97 AAGCTATTGATTTTAAAGGTCATATGGCATATCAATACAAAGTTAAAGATGAACAC 156

QY 121 GTACCAATTAACGCTATGTCGATGAAATGACTATGATGGCATCAGACTTA 180

Db 157 GTACCAATTAACGCTATGTCGATGAAATGACTATGATGGCATCAGACTTA 216

QY 181 TTAAACCAAGCATATGATGATGATTTGAAGAAACAGACAGAGAGACTTAT 240

Db 217 TTAAACCAAGCATATGATGATGATTTGAAGAAACAGACAGAGAGACTTAT 276

QY 241 AACTTAGTCATGAATGGTAG 261

Db 277 AACTTAGTCATGAATGGTAG 297

RESULT 3

AAA68247

ID AAA68247 standard; DNA; 41708 BP.

XX

AC AAA68247;

XX

DT 15-SEP-2003 (revised)

DT 06-AUG-2003 (revised)

DT 27-OCT-2000 (first entry)

XX

DE Bacteriophage 77 complete genome sequence.

XX

KW Bacteriophage; antimicrobial; genome; identification; antibacterial;

KW bacterial growth inhibition; bacterial infection; ds.

XX

OS Staphylococcus aureus; bacteriophage 77.

XX

FN WO200032825-A2.

XX

PD 08-JUN-2000.

XX

PF 03-DEC-1999; 99WO-1B002040.
XX
PR 03-DEC-1998; 98US-0110992P.
PR 03-JUN-1999; 99US-00326144.
PR 28-SEP-1999; 99US-00407804.
PR 30-SEP-1999; 99US-0157218P.
PR 01-DEC-1999; 99US-0168777P.
PR 02-DEC-1999; 99US-00454252.
XX
PA (PHAG-) PHAGETECH INC.
XX
PI Pelletier J, Gros P, Dubow M;
XX
DR WPI, 2000-412361/35.
XX
XX
PT Identifying a bacteriophage coding region for treating bacterial
PT infections comprises identifying a nucleic acid encoding a product that
PT inhibits bacteria when a bacteriophage infects a bacterium.
XX
PS Example 3; Page 141-151; 456pp; English.
XX
CC The present invention describes a method for identifying a bacteriophage
CC coding region encoding a product active on an essential bacterial target.
CC The method comprises identifying a nucleic acid sequence encoding a gene
CC product that provides a bacteria-inhibiting function when an
CC uncharacterised bacteriophage infects a pathogenic bacterium. The
CC compound active on a target of a bacteriophage inhibitor protein in a
CC bacteria is used to treat or prevent a bacterial infection in an animal.
CC AAA68243 to AAA69442 and AAB16523 to AAB16954 represent bacteriophage
CC nucleotide and protein sequences which are used in the exemplification of
CC the present invention. (Updated on 06-AUG-2003 to correct OS field.)
CC (Updated on 15-SEP-2003 to standardise OS field)
XX
SQ Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 U; 0 Other;
Query Match 100.0%; Score 261; DB 3; Length 41708;
Best Local Similarity 100.0%; Pred. No. 2,5e-56;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTATTACGAAATAGCGAATTCATACGCAAAATATTATGTTAGCGATTGATTTT 60
DB 29304 ATGTATTACGAAATAGCGAATTCATACGCAAAATATTATGTTAGCGATTGATTTT 29363
QY 61 AAGCTATTCATTTTAAAGGTCATATGGCATATCATATCAAGTTTAAAGATATGAAAC 120
DB 29364 AAGCTATTCATTTTAAAGGTCATATGGCATATCATATCAAGTTTAAAGATATGAAAC 29423
QY 121 GTACCAATTAACATGCTATATGTCGTAGATGAGATGACTTATGATGGCATGCACTTA 180.
DB 29424 GTACCAATTAACATGCTATATGTCGTAGATGAGATGACTTATGATGGCATGCACTTA 29483
QY 181 TTACCAAGCAATGATGATGATGAGGAAACAGACAGCAAGCAAGCAAGCAAT 240
DB 29484 TTACCAAGCAATGATGATGATGAGGAAACAGACAGCAAGCAAGCAAGCAAT 29543
QY 241 AACTTAGTCATGAATGCTAG 261
|||||

DB 29544 AACTTAGTCATGAATGCTAG 29564
RESULT 4
ID AAC86106 standard; cDNA; 41708 BP.
XX
XX AAC86106;
AC
XX
XX 06-AUG-2003 (revised)
DT 29-AUG-2001 (first entry)
XX
XX Complete genome of bacteriophage 77.
XX
XX DnaI; S. aureus; inhibitor; bacteriophage 77; ORF 104; phage 77ORF104;
XX screening assay; ss.
XX
OS Bacteriophage.
XX
XX WO200146383-A2.
XX
XX 28-JUN-2001.
PD
XX 21-DEC-2000; 2000WO-US035180.
PF
XX 22-DEC-1999; 99US-00470512.
PR 12-OCT-2000; 2000US-00689952.
XX
XX (PHAG-) PHAGETECH INC.
PA (WILL/) WILLIAMS K M.
XX
XX Pelletier J, Gros P, Dubow M;
PI
XX
XX WPI, 2001-418052/44.
DR
XX
XX Novel DnaI polypeptides useful for treating and diagnosing microbial,
PT preferably bacterial, diseases such as those caused by Staphylococcus
PT aureus.
XX
XX Disclosure; Fig 2; 107pp; English.
XX
XX This sequence represents the genome of Bacteriophage 77. The growth
CC inhibitory gene product of ORF 104 interacts with DnaI derived from S.
CC aureus, to form the basis of a screening assay. DnaI polypeptides and
CC polynucleotides are useful for treating microbial, preferably bacterial,
CC especially Staphylococcal, infections. DnaI polypeptides and
CC polynucleotides are useful for biological, diagnostic, prophylactic,
CC clinical and therapeutic use, and as components in databases useful for
CC search analyses as well as in sequence analysis algorithms. (Updated on
CC 06-AUG-2003 to correct OS field.)
XX
SQ Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 U; 0 Other;
Query Match 100.0%; Score 261; DB 4; Length 41708;
Best Local Similarity 100.0%; Pred. No. 2,5e-56;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATATACGAAATAGCGAAATCATACGCAAAATATTCATGTACGATTCATTT 60
 |||||||
 Db 29304 ATGATATACGAAATAGCGAAATCATACGCAAAATATTCATGTACGATTCATTT 29363
 |||||||
 QY 61 AAGCATTCATTTTAAAGGTCATATGGCATTCATACAGATTAAGATATGACAC 120
 |||||||
 Db 29364 AAGCATTCATTTTAAAGGTCATATGGCATTCATACAGATTAAGATATGACAC 29423
 |||||||
 QY 121 GTACCAATTAACATGCTATGTGTGTAGATGAGATGACTTAATGGCATCACTTA 180
 |||||||
 Db 29424 GTACCAATTAACATGCTATGTGTGTAGATGAGATGACTTAATGGCATCACTTA 29483
 |||||||
 QY 181 TTAAACCAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 |||||||
 Db 29484 TTAAACCAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 29543
 |||||||
 QY 241 AACTTAGTCATGAATGCTAG 261
 |||||||
 Db 29544 AACTTAGTCATGAATGCTAG 29564
 |||||||

Search completed: October 14, 2004, 12:48:14
 Job time : 176 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using SW model

Run on: October 14, 2004, 12:03:47 ; Search time 1219.05 Seconds
 (without alignments)
 6393.544 Million cell updates/sec

Title: US-09-407-804A-6

Perfect score: .261

Sequence: 1 atgtattacgaataagcgga.....acttagcatgaatgtag 261

Scoring table: IDENTITY NUC
 Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
 Listing first 45 summaries

Database : EST:*

1: em_estba:*

2: em_esthum:*

3: em_estlin:*

4: em_estnu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estcom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pin:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rtd:*

26: em_gss_phg:*

27: em_gss_vr1:*

28: gb_gsa1:++
29: gb_gsa2:++

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	46.4	17.8	1083	29	CNS009YO	AL054505 Drosophila
2	45.6	17.5	328	28	AZ923265	AZ923265 4908.gf20
3	43.6	16.7	700	28	BH371930	BH371930 AG-ND-132
4	42.6	16.3	1101	29	CNS001FB	AL060732 Drosophila
5	42.4	16.2	509	28	BZ842685	BZ842685 CH240.276
6	42.2	16.2	1044	13	BK415231	BK415231 BX415231
7	41.8	16.0	519	28	AZ525518	AZ525518 244PBH11
8	41.8	16.0	571	28	AZ526884	AZ526884 260PB612
9	41.6	15.9	706	28	BH954338	BH954338 cdh21b04.
10	41.6	15.9	924	28	AZ674753	AZ674753 ENTHU31TR
11	41.4	15.9	988	13	BK410403	BK410403 BX410403
12	41.4	15.9	1101	29	CNS00HOT	AL072991 Drosophila
13	41.2	15.8	801	14	CA508813	CA508813 UT-R-F50-
14	41.1	15.7	1097	29	CNS01235	AL101630 Drosophila
15	40.8	15.6	561	14	CD526186	CD526186 kw31f06.y
16	40.6	15.6	523	14	CF263276	CF263276 AUA IPTes
17	40.6	15.6	954	14	CA788983	CA788983 AGENCOURT
18	40.4	15.5	538	28	BH296850	BH296850 CH230-13P
19	40.4	15.5	592	12	BJ368128	BJ368128 BJ368128
20	40.4	15.5	692	28	BZ011251	BZ011251 oet17a10.
21	40.2	15.4	1453	28	CC294053	CC294053 CH261-175
22	39.8	15.2	284	10	BB381549	BB381549 BB381549
23	39.8	15.2	523	28	AA550417	AA550417 1568m3 gm
24	39.8	15.2	737	12	BM160122	BM160122 EST562645
25	39.8	15.2	759	29	CNS060XY	AL411257 T7 end of
26	39.6	15.2	621	28	AZ178178	AZ178178 SP_0149.A
27	39.6	15.2	948	12	BG286502	BG286502 602382994
28	39.6	15.2	1101	29	CNS007AB	AL066914 Drosophila
29	39.4	15.1	549	9	AL388772	AL388772 MCB50F05
30	39.4	15.1	880	13	BK464942	BK464942 BX464942
31	39.4	15.1	926	28	AZ137368	AZ137368 SP_0175.B
32	39.4	15.1	1287	14	CF222655	CF222655 AGENCOURT
33	39.2	15.0	425	13	BU496326	BU496326 PESToc0
34	39.2	15.0	430	9	AV879351	AV879351 AV879351
35	39.2	15.0	623	29	CE633602	CE633602 tigr-gsa-
36	39.2	15.0	644	29	DR28C4T	AL984585 Danilo rer
37	39.2	15.0	661	29	AG153453	AG153453 Pan trogl
38	39.2	15.0	849	14	CB943202	CB943202 AGENCOURT
39	39.2	15.0	286	10	BB514506	BB514506 BB514506
40	39	14.9	292	10	BB065040	BB065040 BB065040
41	39	14.9	296	10	BB156700	BB156700 BB156700
42	39	14.9	297	10	BB485740	BB485740 BB485740
43	39	14.9	318	10	BB273660	BB273660 BB273660
44	39	14.9	369	9	AU270532	AU270532 AU270532
45	39	14.9	588	29	AG238463	AG238463 Lotus cor

Search completed: October 14, 2004, 18:55:12
Job time : 1223.05 secs

OK nucleic - nucleic search, using sw model

Run on: October 14, 2004, 19:00:14 ; Search time 831.658 Seconds
(without alignments)
8442.862 Million cell updates/sec

Title: US-09-407-804A-7

Perfect score: 162
Sequence: 1 atgagcaacattatataaag.....aatgctttctcaagaataa 162

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 2167151695 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : GenEmbl:
1: gb_ba:.*
2: gb_hgt:.*
3: gb_in:.*
4: gb_ov:.*
5: gb_ov:.*
6: gb_pat:.*
7: gb_ph:.*
8: gb_pl:.*
9: gb_pr:.*
10: gb_ro:.*
11: gb_sta:.*
12: gb_sy:.*
13: gb_un:.*
14: gb_vl:.*
15: em_da:.*
16: em_fun:.*
17: em_hum:.*
18: em_in:.*
19: em_mu:.*
20: em_om:.*
21: em_or:.*
22: em_ov:.*
23: em_pat:.*
24: em_ph:.*
25: em_pl:.*
26: em_ro:.*
27: em_sta:.*

28: em_un:.*
29: em_vl:.*
30: em_hgt_hum:.*
31: em_hgt_inv:.*
32: em_hgt_other:.*
33: em_hgt_mus:.*
34: em_hgt_pin:.*
35: em_hgt_rnd:.*
36: em_hgt_mam:.*
37: em_hgt_vrt:.*
38: em_sy:.*
39: em_hgtc_hum:.*
40: em_hgtc_mus:.*
41: em_hgtc_other:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			ID	Description
	Score	Match	Length		
1	162	100.0	162	6	BD245278
2	162	100.0	41708	6	BD245281
3	162	100.0	41708	6	AR368770
4	74	45.7	159	6	AX583668
5	67	41.4	159	6	AX618544
6	67	41.4	1408	6	AR354422
7	67	41.4	43604	7	AF424781
8	67	41.4	291150	1	AP003135
9	65	40.1	43095	6	BD245282
10	55	34.0	43594	6	BD245634
11	50	30.9	45636	7	AB044554
12	41	25.3	348527	1	AP003360
13	36	22.2	42722	7	AF424783
14	36	22.2	27850	1	AP004828
15	36	22.2	348650	1	AP003364
16	35	21.6	41401	7	AB009866
17	32	19.8	333750	1	AP004827
18	28	17.3	43081	7	AP001553
19	26	16.0	2049	6	AR354173
20	26	16.0	27650	1	AC090967
21	26	16.0	42942	7	AB045978
22	26	16.0	44970	7	AF424782
23	23	14.2	25	6	BD245934
24	21	13.0	25	6	BD245869
25	20	12.3	195607	2	AC117567
26	20	12.3	222621	2	AC119890
27	19	11.7	4279	9	BC035013
28	19	11.7	4725	9	BC028603
29	19	11.7	4983	6	AX056364
30	19	11.7	5181	9	AB023182
31	19	11.7	13484	1	AF400047
32	19	11.7	13484	1	AY044156
33	19	11.7	110283	9	AC093245

34	c	19	11.7	116783	9	AC092829	AC092829 Homo sapi	91	18	11.1	173359	2	AC021536	AC021536 Homo sapi
35	c	19	11.7	132775	10	AL671899	AL671899 Mouse DNA	92	18	11.1	173746	2	AC024040	AC024040 Homo sapi
36	c	19	11.7	141819	5	AL935063	AL935063 Zebrafish	93	18	11.1	176046	2	BX601643	BX601643 Danto rer
37	c	19	11.7	145021	2	AC093257	AC093257 Homo sapi	c 94	18	11.1	176048	5	AL929314	AL929314 Zebrafish
38	c	19	11.7	158588	2	AC092273	AC092273 Homo sapi	c 95	18	11.1	182297	2	BX571738	BX571738 Danto rer
39	c	19	11.7	160984	9	AC092453	AC092453 Homo sapi	c 96	18	11.1	188848	10	AC116709	AC116709 Homo sapi
40	c	19	11.7	161823	2	AC136647	AC136647 Homo sapi	c 97	18	11.1	190732	2	AC142150	AC142150 Homo sapi
41	c	19	11.7	161970	2	AC021737	AC021737 Homo sapi	c 98	18	11.1	194170	2	AC138401	AC138401 Homo sapi
42	c	19	11.7	163693	9	AC087879	AC087879 Homo sapi	c 99	18	11.1	202438	2	AC116145	AC116145 Mus muscu
43	c	19	11.7	168434	2	BX294123	BX294123 Danto rer	c 100	18	11.1	203212	2	AC122469	AC122469 Mus muscu
44	c	19	11.7	192400	2	AC022712	AC022712 Homo sapi	c 101	18	11.1	206470	2	AC135811	AC135811 Rattus no
45	c	19	11.7	201437	2	AC015981	AC015981 Homo sapi	c 102	18	11.1	206966	9	AC021850	AC021850 Homo sapi
46	c	19	11.7	221526	10	AC117668	AC117668 Mus muscu	c 103	18	11.1	210998	2	AC146105	AC146105 Pan trogl
47	c	19	11.7	233320	2	AC106175	AC106175 Rattus no	c 104	18	11.1	211465	2	AC103070	AC103070 Rattus no
48	c	19	11.7	233327	2	AC093463	AC093463 Rattus no	c 105	18	11.1	212359	2	AC101667	AC101667 Mus muscu
49	c	19	11.7	239624	2	AC093365	AC093365 Mus muscu	c 106	18	11.1	212445	10	AC108419	AC108419 Mus muscu
50	c	19	11.7	245146	2	AC130643	AC130643 Rattus no	c 107	18	11.1	214256	10	AC118007	AC118007 Mus muscu
51	c	19	11.7	245323	2	AC111925	AC111925 Rattus no	c 108	18	11.1	214468	2	AC123108	AC123108 Rattus no
52	c	19	11.7	248333	2	AC097869	AC097869 Rattus no	c 109	18	11.1	220495	10	AL732525	AL732525 Mouse DNA
53	c	19	11.7	253903	2	AC121208	AC121208 Rattus no	c 110	18	11.1	228355	10	AL731839	AL731839 Mouse DNA
54	c	19	11.7	254975	2	AC095125	AC095125 Rattus no	c 111	18	11.1	234595	2	AC110204	AC110204 Mus muscu
55	c	19	11.7	254975	2	AC095125	AC095125 Rattus no	c 112	18	11.1	234950	2	AC109079	AC109079 Rattus no
56	c	19	11.7	262183	1	CJ11168X4	AF135975 Papio ham	c 113	18	11.1	237754	10	AC125576	AC125576 Rattus no
57	c	18	11.1	538	8	AY189701	AY189701 Pheillus	c 114	18	11.1	241610	2	AC093465	AC093465 Mus muscu
58	c	18	11.1	33498	3	CEZK593	CEZK593 Human DNA	c 115	18	11.1	247108	2	AC123333	AC123333 Rattus no
59	c	18	11.1	57578	9	AL589825	AL589825 Human DNA	c 116	18	11.1	252283	2	AC126977	AC126977 Rattus no
60	c	18	11.1	59441	9	AC109588	AC109588 Homo sapi	c 117	18	11.1	258484	2	AC125555	AC125555 Rattus no
61	c	18	11.1	60791	9	AC004749	AC004749 Homo sapi	c 118	18	11.1	262050	2	AC105575	AC105575 Rattus no
62	c	18	11.1	79041	9	AC009016	AC009016 Homo sapi	c 119	18	11.1	265423	2	AC128960	AC128960 Rattus no
63	c	18	11.1	79851	9	AC034252	AC034252 Homo sapi	c 120	18	11.1	272627	2	AC097289	AC097289 Rattus no
64	c	18	11.1	80402	8	AB025636	AB025636 Azeblidops	c 121	18	11.1	281660	2	AC127837	AC127837 Rattus no
65	c	18	11.1	89017	2	AC135193	AC135193 Rattus no	c 122	18	11.1	281957	2	AC095956	AC095956 Rattus no
66	c	18	11.1	111701	2	AC144405	AC144405 Medicago	c 123	18	11.1	318115	2	AC098550	AC098550 Rattus no
67	c	18	11.1	113567	8	AF058626	AF058626 Azeblidops	c 124	17	10.5	546	11	BV067122	BV067122 S212P6015
68	c	18	11.1	113567	8	AF058626	AF058626 Azeblidops	c 125	17	10.5	609	11	G91194	G91194 S208P6396R2
69	c	18	11.1	116261	9	AL555357	AL555357 Human DNA	c 126	17	10.5	674	14	AB057066	AB057066 Helicobac
70	c	18	11.1	122557	2	AC011429	AC011429 Homo sapi	c 127	17	10.5	834	14	AB086272	AB086272 Human imm
71	c	18	11.1	129608	8	OSJN00214	AL663013 Oryza sat	c 128	17	10.5	835	14	AB086272	AB086272 Human imm
72	c	18	11.1	132119	9	AC008497	AC008497 Homo sapi	c 129	17	10.5	1067	3	AF438039	AF438039 Chlaenius
73	c	18	11.1	133345	9	AL356294	AL356294 Human DNA	c 130	17	10.5	1379	6	BD249104	BD249104 49 human
74	c	18	11.1	138094	8	AC141113	AC141113 Medicago	c 131	17	10.5	1529	5	BC054177	BC054177 Xenopus 1
75	c	18	11.1	138224	9	AC096562	AC096562 Homo sapi	c 132	17	10.5	1923	8	AK064446	AK064446 Oryza sat
76	c	18	11.1	139401	2	AC124406	AC124406 Mus muscu	c 133	17	10.5	3000	1	AF525506	AF525506 Fusobacte
77	c	18	11.1	139490	2	BX640536	BX640536 Danto rer	c 134	17	10.5	6477	6	AK653060	AK653060 Sequence
78	c	18	11.1	145115	8	AC096690	AC096690 Oryza sat	c 135	17	10.5	10410	1	AE010782	AE010782 Methanosa
79	c	18	11.1	148088	4	AC096883	AC096883 Sus scrofa	c 136	17	10.5	10717	1	AE010553	AE010553 Fusobacte
80	c	18	11.1	149273	10	AL928732	AL928732 Mouse DNA	c 137	17	10.5	11730	1	AE010579	AE010579 Fusobacte
81	c	18	11.1	157530	9	AC146247	AC146247 Pan trogl	c 138	17	10.5	11815	1	AE001262	AE001262 Treponeema
82	c	18	11.1	158472	9	AC110612	AC110612 Homo sapi	c 139	17	10.5	12500	1	AE001261	AE001261 Treponeema
83	c	18	11.1	161341	2	AL929055	AL929055 Mus muscu	c 140	17	10.5	16341	1	AF178757	AF178757 Arabidema
84	c	18	11.1	163828	8	AC104433	AC104433 Oryza sat	c 141	17	10.5	18092	9	AL590874	AL590874 Human DNA
85	c	18	11.1	166074	5	AL645307	AL645307 Zebrafish	c 142	17	10.5	38231	8	AB072893	AB072893 Penicill111
86	c	18	11.1	167168	2	AC115907	AC115907 Mus muscu	c 143	17	10.5	39709	2	AC145431	AC145431 Homo sapi
87	c	18	11.1	168049	2	AC022830	AC022830 Homo sapi	c 144	17	10.5	50737	2	AC020294	AC020294 Drosophila
88	c	18	11.1	168353	2	AC146598	AC146598 Mus muscu	c 145	17	10.5	54355	6	AK695644	AK695644 Sequence
89	c	18	11.1	168527	2	AC040993	AC040993 Homo sapi	c 146	17	10.5	62464	9	AL139164	AL139164 Human DNA
90	c	18	11.1	172337	8	AC133007	AC133007 Oryza sat	c 147	17	10.5	68273	9	AL138695	AL138695 Human DNA

c 148	17	10.5	68678	2	AC126334	Homo sapi	c 205	17	10.5	152309	9	AC138185	AC138185 Homo sapi
c 149	17	10.5	70282	2	AC091141	Homo sapi	c 206	17	10.5	152905	2	AC104480	AC104480 Sus scrofa
c 150	17	10.5	70983	2	AC134259	Rattus no	c 207	17	10.5	153472	9	AC011179	AC011179 Homo sapi
c 151	17	10.5	90440	2	AC123574	Medicago	c 208	17	10.5	153814	9	AC095063	AC095063 Homo sapi
c 152	17	10.5	90657	2	AC131755	Homo sapi	c 209	17	10.5	154055	9	AC157774	AC157774 Homo sapi
c 153	17	10.5	90696	2	AC017624	Drosophila	c 210	17	10.5	155348	5	AL1928820	AL1928820 Zebrafish
c 154	17	10.5	91155	2	AC026450	Homo sapi	c 211	17	10.5	155466	2	AL139181	AL139181 Homo sapi
c 155	17	10.5	95553	4	AC124804	Equus cab	c 212	17	10.5	157023	9	AL165360	AL165360 Homo sapi
c 156	17	10.5	96396	6	AC095395	Sequence	c 213	17	10.5	157306	9	AL161417	AL161417 Human DNA
c 157	17	10.5	101098	8	AC002427	Arabidops	c 214	17	10.5	157534	2	AC090100	AC090100 Homo sapi
c 158	17	10.5	107271	8	ATT8M16	Arabidops	c 215	17	10.5	157706	5	AL1928936	AL1928936 Zebrafish
c 159	17	10.5	109476	9	AL133548	Human DNA	c 216	17	10.5	158213	2	AC016865	AC016865 Homo sapi
c 160	17	10.5	110000	2	AC098456	Rattus no	c 217	17	10.5	158486	2	BX649350	BX649350 Danto rer
c 161	17	10.5	110000	2	AC129939	Mus muscu	c 218	17	10.5	159565	9	AP001318	AP001318 Homo sapi
c 162	17	10.5	110000	2	AC143189	Continuation (3 of	c 219	17	10.5	160004	9	AL133318	AL133318 Homo sapi
c 163	17	10.5	110000	2	AY294423	Continuation (2 of	c 220	17	10.5	160013	9	AL133325	AL133325 Human DNA
c 164	17	10.5	110000	9	AY129465	Continuation (3 of	c 221	17	10.5	160180	10	AL129016	AL129016 Homo sapi
c 165	17	10.5	111876	8	ATF4110	Arabidops	c 222	17	10.5	160502	2	AC139369	AC139369 Mus muscu
c 166	17	10.5	113148	8	HSBG54N10	Human DNA	c 223	17	10.5	160612	2	AP005856	AP005856 Homo sapi
c 167	17	10.5	113266	8	AC092262	Oryza sat	c 224	17	10.5	160739	9	AP001092	AP001092 Homo sapi
c 168	17	10.5	115224	9	AL1356234	Human DNA	c 225	17	10.5	160922	2	AC104848	AC104848 Oryza sat
c 169	17	10.5	115306	9	AC008615	Homo sapi	c 226	17	10.5	162246	10	BX000428	BX000428 Mouse DNA
c 170	17	10.5	119974	9	AC018763	Homo sapi	c 227	17	10.5	162739	9	AL1353788	AL1353788 Human DNA
c 171	17	10.5	122630	2	AC012434	Homo sapi	c 228	17	10.5	162976	9	AC114301	AC114301 Homo sapi
c 172	17	10.5	123109	2	AC007149	Drosophila	c 229	17	10.5	164117	5	ALB45313	ALB45313 Zebrafish
c 173	17	10.5	123889	2	AC115872	Mus muscu	c 230	17	10.5	164404	2	AC027149	AC027149 Homo sapi
c 174	17	10.5	124786	9	AC115285	Homo sapi	c 231	17	10.5	164620	9	AC110721	AC110721 Homo sapi
c 175	17	10.5	126323	8	AC132215	Genomic s	c 232	17	10.5	164735	2	AC090475	AC090475 Homo sapi
c 176	17	10.5	128749	2	AC145811	Oryza sat	c 233	17	10.5	164907	3	AC007146	AC007146 Drosophila
c 177	17	10.5	129167	8	AC113433	Oryza sat	c 234	17	10.5	165178	2	AC025355	AC025355 Homo sapi
c 178	17	10.5	129398	8	AL1596276	Human DNA	c 235	17	10.5	165178	2	AC024255	AC024255 Homo sapi
c 179	17	10.5	130218	2	CNS08C81	Human DNA	c 236	17	10.5	165236	9	AC011352	AC011352 Homo sapi
c 180	17	10.5	130372	2	CNS08C92	Oryza sat	c 237	17	10.5	166444	9	AC011352	AC011352 Homo sapi
c 181	17	10.5	130801	2	AC141188	Rattus no	c 238	17	10.5	166653	2	AC115862	AC115862 Mus muscu
c 182	17	10.5	131042	10	AC110166	Mus muscu	c 239	17	10.5	167099	2	AC104486	AC104486 Sus scrofa
c 183	17	10.5	131577	2	AC146333	Medicago	c 240	17	10.5	167604	2	AC084017	AC084017 Homo sapi
c 184	17	10.5	131577	2	AC146333	Medicago	c 241	17	10.5	167629	9	AL1353595	AL1353595 Homo sapi
c 185	17	10.5	133028	8	AP003447	Oryza sat	c 242	17	10.5	167629	9	AL1353595	AL1353595 Homo sapi
c 186	17	10.5	133400	2	AC134521	Medicago	c 243	17	10.5	168010	2	AC132984	AC132984 Rattus no
c 187	17	10.5	134725	2	AC091852	Mus muscu	c 244	17	10.5	168259	2	AC009936	AC009936 Homo sapi
c 188	17	10.5	139754	2	AC124322	Mus muscu	c 245	17	10.5	168484	9	AC113366	AC113366 Homo sapi
c 189	17	10.5	140597	9	AC074270	Homo sapi	c 246	17	10.5	168484	9	AC067848	AC067848 Homo sapi
c 190	17	10.5	140934	9	AC009491	Homo sapi	c 247	17	10.5	168728	2	AC026183	AC026183 Homo sapi
c 191	17	10.5	141459	2	BX539347	Danto rer	c 248	17	10.5	169891	2	AC114479	AC114479 Homo sapi
c 192	17	10.5	141834	8	AP003445	Oryza sat	c 249	17	10.5	169988	2	BX321875	BX321875 Danto rer
c 193	17	10.5	145009	2	AC141949	Rattus no	c 250	17	10.5	170114	9	AC044790	AC044790 Homo sapi
c 194	17	10.5	145122	9	AC025588	Homo sapi	c 251	17	10.5	171127	2	AC024527	AC024527 Homo sapi
c 195	17	10.5	146368	2	AC022651	Medicago	c 252	17	10.5	171744	9	CNS01D99	CNS01D99 Homo sapi
c 196	17	10.5	148247	10	AL1935057	Mouse DNA	c 253	17	10.5	172061	2	AC027136	AC027136 Homo sapi
c 197	17	10.5	148841	9	AC110794	Homo sapi	c 254	17	10.5	172366	9	AC004949	AC004949 Homo sapi
c 198	17	10.5	149391	9	AC093825	Mus muscu	c 255	17	10.5	172618	2	AC144822	AC144822 Danto rer
c 199	17	10.5	149646	10	AC122482	Mus muscu	c 256	17	10.5	172627	2	AC142134	AC142134 Rattus no
c 200	17	10.5	149849	9	AL1590678	Human DNA	c 257	17	10.5	173154	2	AC0919132	AC0919132 Homo sapi
c 201	17	10.5	150547	2	AC102787	Mus muscu	c 258	17	10.5	173481	9	AL1932423	AL1932423 Homo sapi
c 202	17	10.5	150934	2	AC022252	Homo sapi	c 259	17	10.5	173520	9	AL1932423	AL1932423 Homo sapi
c 203	17	10.5	150955	2	AL156111	Human DNA	c 260	17	10.5	174383	5	AL1929216	AL1929216 Zebrafish
c 204	17	10.5	151682	2	AC147146	Mus muscu	c 261	17	10.5	175100	2	AC132241	AC132241 Mus muscu

262	17	10.5	175158	2	AC120531	Oryza sat
263	17	10.5	175483	9	AL445258	Human DNA
264	17	10.5	175965	10	AC121921	Mus muscu
265	17	10.5	175977	3	AC007470	Drosophill
266	17	10.5	177662	2	AC013665	Homo sapi
267	17	10.5	178273	2	AC099620	Mus muscu
268	17	10.5	178414	2	AC025341	Homo sapi
269	17	10.5	178448	2	AC134419	Mus muscu
270	17	10.5	179138	9	CNS076GV	Human chr
271	17	10.5	179798	9	AL359532	Human DNA
272	17	10.5	179862	9	CNS05TEE	Human chr
273	17	10.5	180192	2	AC058810	Homo sapi
274	17	10.5	180213	3	AC010847	Drosophill
275	17	10.5	181058	2	AC068118	Homo sapi
276	17	10.5	181463	10	AC122452	Mus muscu
277	17	10.5	181852	2	AC120866	Mus muscu
278	17	10.5	183619	2	AC104485	Sus scrofa
279	17	10.5	183976	9	AC100821	Homo sapi
280	17	10.5	184032	9	AC079926	Homo sapi
281	17	10.5	184701	2	AC136630	Homo sapi
282	17	10.5	184732	2	AC125845	Homo sapi
283	17	10.5	185212	2	BK572088	Mus muscu
284	17	10.5	185324	2	AC026265	Homo sapi
285	17	10.5	186321	2	AC134738	Rattus no
286	17	10.5	191081	2	AC023143	Homo sapi
287	17	10.5	191634	2	AC112755	Rattus no
288	17	10.5	192651	2	AC142465	Rattus no
289	17	10.5	193826	9	AL131379	Human DNA
290	17	10.5	194808	2	AL120857	Mus muscu
291	17	10.5	194869	2	AL954136	Zebrafish
292	17	10.5	196591	2	AC091082	Homo sapi
293	17	10.5	196617	2	AC115134	Rattus no
294	17	10.5	198190	2	AC136446	Homo sapi
295	17	10.5	198386	9	AC079789	Homo sapi
296	17	10.5	199280	8	ATC079364	Mus muscu
297	17	10.5	199536	8	ATC079364	Mus muscu
298	17	10.5	199913	2	AC121308	Arabidops
299	17	10.5	200512	2	AC135358	Mus muscu
300	17	10.5	201429	2	AC109375	Mus muscu
301	17	10.5	202229	2	AC128611	Rattus no
302	17	10.5	202774	2	AC108851	Rattus no
303	17	10.5	202915	10	AC116703	Mus muscu
304	17	10.5	203047	10	AL928922	Mouse DNA
305	17	10.5	203226	9	AC105479	Rattus no
306	17	10.5	203300	9	AC000134	Homo sapi
307	17	10.5	207050	4	AC123667	Mus muscu
308	17	10.5	207304	4	AC125499	Equus cab
309	17	10.5	207411	2	AC084746	Mus muscu
310	17	10.5	207625	2	AC140270	Mus muscu
311	17	10.5	208670	9	AC103588	Homo sapi
312	17	10.5	209003	2	AC073724	Mus muscu
313	17	10.5	211041	2	AC116413	Mus muscu
314	17	10.5	212246	10	AC123686	Mus muscu
315	17	10.5	212253	2	AC140184	Mus muscu
316	17	10.5	213375	2	AC129581	Mus muscu
317	17	10.5	213721	9	HS172820	Human DNA
318	17	10.5	215435	10	AC124752	Mus muscu
319	17	10.5	215850	2	AC138285	Mus muscu
320	17	10.5	216386	2	AC113795	Rattus no
321	17	10.5	217097	2	AC112080	Rattus no
322	17	10.5	218131	2	AC105635	Rattus no
323	17	10.5	222964	2	AC117649	Mus muscu
324	17	10.5	223711	2	AC126979	Rattus no
325	17	10.5	223794	2	AC145076	Mus muscu
326	17	10.5	224044	10	AL935326	Mouse DNA
327	17	10.5	224346	2	BK530018	Danio rer
328	17	10.5	225490	2	AC140213	Mus muscu
329	17	10.5	225538	2	AC108577	Rattus no
330	17	10.5	225648	2	AC133459	Mus muscu
331	17	10.5	225782	2	AC109529	Rattus no
332	17	10.5	227459	2	AC127039	Rattus no
333	17	10.5	227682	2	AC131460	Rattus no
334	17	10.5	228080	2	AC134938	Rattus no
335	17	10.5	230127	10	AL691481	Mouse DNA
336	17	10.5	230567	2	AC116966	Rattus no
337	17	10.5	232842	2	AC109880	Rattus no
338	17	10.5	235024	2	AC120681	Rattus no
339	17	10.5	235129	2	AC130145	Rattus no
340	17	10.5	236237	2	AC106297	Rattus no
341	17	10.5	238543	2	AC133701	Rattus no
342	17	10.5	238560	2	AC114016	Rattus no
343	17	10.5	239475	2	AC122116	Mus muscu
344	17	10.5	240181	2	AC098105	Rattus no
345	17	10.5	240272	2	AC097809	Rattus no
346	17	10.5	241100	2	AC095453	Rattus no
347	17	10.5	243613	2	AC105517	Rattus no
348	17	10.5	243822	2	AC094751	Rattus no
349	17	10.5	244866	2	AC097571	Rattus no
350	17	10.5	246401	2	AC094195	Rattus no
351	17	10.5	248835	2	AC097256	Rattus no
352	17	10.5	249181	2	AC130997	Rattus no
353	17	10.5	249995	3	AE014840	plemmodiu
354	17	10.5	250360	2	AC106965	Rattus no
355	17	10.5	250586	2	AC094879	Rattus no
356	17	10.5	252230	2	AC114944	Homo sapi
357	17	10.5	252374	2	AC105618	Rattus no
358	17	10.5	254366	2	AC125987	Rattus no
359	17	10.5	254578	10	AC109253	Mus muscu
360	17	10.5	258545	2	AC135666	Rattus no
361	17	10.5	259790	2	AC106956	Rattus no
362	17	10.5	261216	2	AC119381	Rattus no
363	17	10.5	262718	2	AC106366	Rattus no
364	17	10.5	265750	2	BK539323	Drosophill
365	17	10.5	266175	3	AE003633	Drosophill
366	17	10.5	266188	2	AC103296	Rattus no
367	17	10.5	268342	2	AC144457	Homo sapi
368	17	10.5	273959	2	AC118114	Rattus no
369	17	10.5	281085	2	AC123455	Rattus no
370	17	10.5	281926	2	AC094818	Rattus no
371	17	10.5	283769	2	AC094777	Rattus no
372	17	10.5	285841	2	AC126476	Rattus no
373	17	10.5	302529	1	AE016851	Tropheym
374	17	10.5	324050	1	BK251410	Tropheym

c 375	17	10.5	332869	2	AC098450	AC098450 Rattus no	432	16	9.9	1354	3	DAM538207	AJ538207 Drosophila
376	17	10.5	334120	2	AC114017	AC114017 Rattus no	433	16	9.9	1354	3	DAM538211	AJ538211 Drosophila
377	17	10.5	339193	2	AC098394	AC098394 Rattus no	434	16	9.9	1354	3	DAM538213	AJ538213 Drosophila
378	17	10.5	342650	1	AP003582	AP003582 Neotoma sp	435	16	9.9	1354	3	DAM538216	AJ538216 Drosophila
379	17	10.5	346474	3	AE003512	AE003512 Drosophila	436	16	9.9	1354	3	DAM538219	AJ538219 Drosophila
380	16	9.9	25	6	BD456696	BD456696 Drosophila	437	16	9.9	1354	3	DAM538225	AJ538225 Drosophila
381	16	9.9	149	9	565841504	565841504 gamma-actin	438	16	9.9	1354	3	DAM538228	AJ538228 Drosophila
382	16	9.9	250	11	GJ5137	GJ5137 human STS S	439	16	9.9	1354	3	DAM538201	AJ538201 Drosophila
c 383	16	9.9	253	11	BK276154	BK276154 Arabidopsis	440	16	9.9	1354	3	DAM538204	AJ538204 Drosophila
384	16	9.9	284	11	GJ5786	GJ5786 human STS C	441	16	9.9	1354	3	DAM538205	AJ538205 Drosophila
c 385	16	9.9	302	11	BY072730	BY072730 S208P6815	442	16	9.9	1354	3	DAM538208	AJ538208 Drosophila
c 386	16	9.9	334	8	AY19611	AY19611 Arabidopsis	443	16	9.9	1354	3	DAM538209	AJ538209 Drosophila
c 387	16	9.9	361	11	BK663978	BK663978 Arabidopsis	444	16	9.9	1354	3	DAM538210	AJ538210 Drosophila
c 388	16	9.9	400	6	AR356817	AR356817 Sequence	445	16	9.9	1354	3	DAM538218	AJ538218 Drosophila
c 389	16	9.9	403	1	MGU01787	MGU01787 Mycoplasma	446	16	9.9	1354	3	DAM538228	AJ538228 Drosophila
390	16	9.9	427	6	AR427627	AR427627 Sequence	447	16	9.9	1354	3	DAM538230	AJ538230 Drosophila
391	16	9.9	427	6	BD123180	BD123180 EST and e	448	16	9.9	1354	3	DAM538212	AJ538212 Drosophila
392	16	9.9	468	1	UPR318208	UPR318208 Unculture	449	16	9.9	1354	3	DAM538215	AJ538215 Drosophila
393	16	9.9	495	6	AX874669	AX874669 Sequence	450	16	9.9	1354	3	DAM538222	AJ538222 Drosophila
394	16	9.9	495	6	BD154731	BD154731 Primer fo	451	16	9.9	1354	3	DAM538227	AJ538227 Drosophila
395	16	9.9	592	8	AJ586321	AJ586321 Fagus cre	452	16	9.9	1354	3	DAM538224	AJ538224 Drosophila
396	16	9.9	649	11	G66008	G66008 sy885 Mlase	453	16	9.9	1489	6	AX882999	AX882999 Sequence
c 397	16	9.9	649	11	BY062522	BY062522 S212P6243	454	16	9.9	1489	6	BD160056	BD160056 Primer fo
c 398	16	9.9	660	11	G67144	G67144 233F8-R Hum	455	16	9.9	1489	6	AK023592	AK023592 Homo sapi
c 399	16	9.9	684	11	BY064590	BY064590 S212P6035	456	16	9.9	1515	5	AF201348	AF201348 Oreochrom
400	16	9.9	702	3	AB107990	AB107990 POLYandro	457	16	9.9	1722	6	AR379576	AR379576 Sequence
401	16	9.9	755	9	AY459026	AY459026 Pan trogl	458	16	9.9	1782	8	AK071245	AK071245 Oryza sat
402	16	9.9	755	9	AY459027	AY459027 Pan trogl	459	16	9.9	1794	8	AK071245	AK071245 Oryza sat
403	16	9.9	755	9	AY459028	AY459028 Pan trogl	460	16	9.9	1814	1	AF190223	AF190223 Polinetel
404	16	9.9	755	9	AY459029	AY459029 Pan trogl	461	16	9.9	1896	6	AX618652	AX618652 Sequence
405	16	9.9	755	9	AY459030	AY459030 Pan trogl	462	16	9.9	2046	9	AK094627	AK094627 Homo sapi
406	16	9.9	755	9	AY459031	AY459031 Pan trogl	463	16	9.9	2212	6	AX881562	AX881562 Sequence
407	16	9.9	755	9	AY459032	AY459032 Pan trogl	464	16	9.9	2212	6	BD159124	BD159124 Primer fo
408	16	9.9	755	9	AY459033	AY459033 Pan trogl	465	16	9.9	2212	9	AK021757	AK021757 Homo sapi
409	16	9.9	755	9	AY459034	AY459034 Pan trogl	466	16	9.9	2269	8	SCESBP6	SCESBP6 S. cerevisia
410	16	9.9	755	9	AY459035	AY459035 Pan trogl	467	16	9.9	2298	9	HSGAT1MR	HSGAT1MR Homo sapi
411	16	9.9	755	9	AY459036	AY459036 Pan trogl	468	16	9.9	2349	3	560739	560739 cEGRHecdy
412	16	9.9	755	9	AY459037	AY459037 Pan trogl	469	16	9.9	2366	10	BC014810	BC014810 Mus muscu
413	16	9.9	755	9	AY459038	AY459038 Pan trogl	470	16	9.9	2394	2	AC019569	AC019569 Drosophila
414	16	9.9	755	9	AY459039	AY459039 Pan trogl	471	16	9.9	2407	5	BC057507	BC057507 Dario rer
415	16	9.9	795	6	AX434330	AX434330 Sequence	472	16	9.9	2630	1	AY036014	AY036014 Bacillus
c 416	16	9.9	837	11	BY039632	BY039632 S212P6009	473	16	9.9	2744	9	BC063868	BC063868 Homo sapi
c 417	16	9.9	846	11	BY035787	BY035787 S212P6046	474	16	9.9	2915	5	BC060000	BC060000 Xenopus 1
418	16	9.9	1084	3	AF438064	AF438064 Dypa sp	475	16	9.9	3027	3	AY061587	AY061587 Drosophila
c 419	16	9.9	1091	3	AF398659	AF398659 Desera au	476	16	9.9	3124	8	SCN1L28C	SCN1L28C BC029230
c 420	16	9.9	1198	3	AF129083	AF129083 Drosophila	477	16	9.9	3322	10	BC029230	BC029230 Mus muscu
c 421	16	9.9	1201	3	AF132563	AF132563 Drosophila	478	16	9.9	3327	1	CPPLASPC1	CPPLASPC1 X62079 C.coli plas
422	16	9.9	1349	3	DAM538226	DAM538226 Drosophila	479	16	9.9	3330	3	AT29885751	AT29885751 X62080 C.coli plas
423	16	9.9	1350	3	DAM538229	DAM538229 Drosophila	480	16	9.9	3571	1	PH077788	PH077788 Pasteurella
424	16	9.9	1352	3	DAM538206	DAM538206 Drosophila	481	16	9.9	3628	1	PASSAIA	PASSAIA M62363 S. pneumoniae
425	16	9.9	1352	3	DAM538206	DAM538206 Drosophila	482	16	9.9	3779	9	BC009650	BC009650 Homo sapi
426	16	9.9	1353	3	DAM538200	DAM538200 Drosophila	483	16	9.9	3920	3	AY119444	AY119444 Drosophila
427	16	9.9	1353	3	DAM538217	DAM538217 Drosophila	484	16	9.9	4438	10	PMU500673	PMU500673 Mus muscu
428	16	9.9	1353	3	DAM538217	DAM538217 Drosophila	485	16	9.9	4455	5	X1LCTRM	X1LCTRM X65256 X. laevis
429	16	9.9	1353	3	DAM538223	DAM538223 Drosophila	486	16	9.9	4455	5	X1LCTRM	X1LCTRM X65256 X. laevis
430	16	9.9	1354	3	DAM538202	DAM538202 Drosophila	487	16	9.9	4455	5	X1LCTRM	X1LCTRM X65256 X. laevis
431	16	9.9	1354	3	DAM538203	DAM538203 Drosophila	488	16	9.9	4455	5	X1LCTRM	X1LCTRM X65256 X. laevis

489	16	9.9	4470	3	AF001796	AF001796 Drosophila	c 546	16	9.9	43081	7	AP001553	AP001553 Bacterioph
490	16	9.9	4493	9	BC033904	BC033904 Homo sapi	c 547	16	9.9	43331	9	HSX297824	AJ297824 Homo sapi
c 491	16	9.9	4687	7	AF513856	AF513856 Stephyloc	c 548	16	9.9	43481	8	SCCKHIV43	Z46843 S. cerevisiae
c 492	16	9.9	5177	9	AB014548	AB014548 Homo sapi	c 549	16	9.9	43594	6	BD245634	BD245634 Drosophila
c 493	16	9.9	5561	9	HMM12B	K02056 Human Inter	c 550	16	9.9	43604	7	AF424781	AF424781 Stephyloc
c 494	16	9.9	5693	8	AF533704	AF533704 Pyrenoph	c 551	16	9.9	43927	9	HS024460	HS024460 Stephyloc
c 495	16	9.9	5742	7	PIHORS	L77215 Bacterioph	c 552	16	9.9	45878	9	AP003773	AP003773 Human DNA
c 496	16	9.9	6086	8	SCNLI26W	Z77402 S. cerevisiae	c 553	16	9.9	46508	1	AP005352	AP005352 Vibrio vu
c 497	16	9.9	6103	8	AF533703	AF533703 Pyrenoph	c 554	16	9.9	48940	5	AY298859	AY298859 Xiphophor
c 498	16	9.9	6684	9	HSIL105	X00699 Human Inter	c 555	16	9.9	53336	9	AC092600	AC092600 Homo sapi
c 499	16	9.9	6744	9	AF294791	AF294791 Homo sapi	c 556	16	9.9	54874	2	AC013691	AC013691 Homo sapi
c 500	16	9.9	6752	9	AF359939	AF359939 Homo sapi	c 557	16	9.9	55021	6	AC025815	AC025815 Arabidops
c 501	16	9.9	7035	1	LIU60336	U60336 Lactococcus	c 558	16	9.9	55417	2	AL390915	AL390915 Homo sapi
c 502	16	9.9	7120	7	AF195902	AF195902 Lactobac	c 559	16	9.9	55564	3	AB000109	AB000109 Dicyoste
c 503	16	9.9	7608	3	PTA51DN	X85133 P. tetraurel	c 560	16	9.9	55715	2	AC135912	AC135912 Homo sapi
c 504	16	9.9	8154	3	PAR51A	M65163 P. tetraurel	c 561	16	9.9	55741	2	AC008293	AC008293 Drosophila
c 505	16	9.9	8415	8	OSAS35044	AJ35044 Oryza sat	c 562	16	9.9	56328	2	AC068514	AC068514 Homo sapi
c 506	16	9.9	8415	8	OSAS35044	AF292555 Gfp marke	c 563	16	9.9	56333	2	AC020257	AC020257 Drosophila
c 507	16	9.9	8850	12	AF292555	AF292555 Yfp marke	c 564	16	9.9	58970	2	AC101231	AC101231 Mus muscu
c 508	16	9.9	8850	12	AF292555	AF292560 Gfp marke	c 565	16	9.9	59356	9	AC115109	AC115109 Homo sapi
c 509	16	9.9	8950	12	AF292555	AF292556 Gfp marke	c 566	16	9.9	59463	9	AC107486	AC107486 Homo sapi
c 510	16	9.9	8974	12	AF292555	AF292557 Yfp marke	c 567	16	9.9	59800	2	AC100183	AC100183 Mus muscu
c 511	16	9.9	8974	12	AF292555	AF292558 Gfp marke	c 568	16	9.9	59800	2	AC100183	AC100183 Mus muscu
c 512	16	9.9	9330	5	AY298856	AY298856 Xiphophor	c 569	16	9.9	61199	2	AC100497	AC100497 Mus muscu
c 513	16	9.9	9621	2	AC020370	AC020370 Drosophila	c 570	16	9.9	61419	2	AC014418	AC014418 Drosophila
c 514	16	9.9	10210	1	AE000558	AE000558 Helicobac	c 571	16	9.9	61550	2	AC069038	AC069038 Homo sapi
c 515	16	9.9	10266	12	ACSHUTVEC	A001494 Artificia	c 572	16	9.9	62092	2	AC092282	AC092282 Homo sapi
c 516	16	9.9	10470	6	AR353902	AR353902 Sequence	c 573	16	9.9	62874	2	AC130374	AC130374 Homo sapi
c 517	16	9.9	10823	1	AE000641	AE000641 Helicobac	c 574	16	9.9	63181	2	AC087443	AC087443 Homo sapi
c 518	16	9.9	11135	3	PAR1DNA	U67495 Methanococ	c 575	16	9.9	63866	2	AC116462	AC116462 Homo sapi
c 519	16	9.9	11743	1	U67495	AE007516 Clostridi	c 576	16	9.9	67124	9	AC026415	AC026415 Homo sapi
c 520	16	9.9	12119	1	AE007516	U39689 Mycoplasma	c 577	16	9.9	67497	4	BX649310	BX649310 Smilthops
c 521	16	9.9	12285	1	U39689	AE011441 Leptospir	c 578	16	9.9	68196	2	AC108407	AC108407 Mus muscu
c 522	16	9.9	12732	3	DDID16466	DI6466 Dicyoste	c 579	16	9.9	69146	9	AC068668	AC068668 Homo sapi
c 523	16	9.9	13320	3	PTALPHA51	X96400 P. tetraurel	c 580	16	9.9	69749	9	AY341031	AY341031 Homo sapi
c 524	16	9.9	15561	6	AX076016	AX076016 Sequence	c 581	16	9.9	70564	9	HS034662	HS034662 Homo sapi
c 525	16	9.9	22212	9	AC015979	AC015979 Homo sapi	c 582	16	9.9	72030	2	AC083987	AC083987 Homo sapi
c 526	16	9.9	22442	3	CEFA9A5	Z81542 Caenorhabd	c 583	16	9.9	72576	10	BX005243	BX005243 Mus muscu
c 527	16	9.9	24342	3	CEFA9A5	AL117199 Caenorhab	c 584	16	9.9	73397	2	AC101427	AC101427 Homo sapi
c 528	16	9.9	24686	2	AC014976	AC014976 Drosophila	c 585	16	9.9	73427	9	HS324L9	HS324L9 Homo sapi
c 529	16	9.9	24764	8	AY101381	AY101381 Cryptococ	c 586	16	9.9	73908	9	AL1596112	AL1596112 Homo sapi
c 530	16	9.9	24874	8	AY101381	AC114739 Homo sapi	c 587	16	9.9	74315	2	AC136287	AC136287 Homo sapi
c 531	16	9.9	29657	6	AX695329	Z82262 Caenorhabd	c 588	16	9.9	74315	2	AC136287	AC136287 Homo sapi
c 532	16	9.9	32767	6	AX695329	Z82262 Caenorhabd	c 589	16	9.9	74560	9	HS433B8	HS433B8 Homo sapi
c 533	16	9.9	32873	3	CECA359	AC091630 Homo sapi	c 590	16	9.9	74568	8	OSR243961	OSR243961 Homo sapi
c 534	16	9.9	33365	2	AC091630	AC139089 Homo sapi	c 591	16	9.9	76568	3	MREYV	MREYV Homo sapi
c 535	16	9.9	36160	2	AC139089	U42836 Caenorhabd	c 592	16	9.9	78170	2	AC015396	AC015396 Homo sapi
c 536	16	9.9	36971	10	AL358774	Z69382 S. cerevisiae	c 593	16	9.9	78260	2	AC015438	AC015438 Homo sapi
c 537	16	9.9	37386	3	SCCKHIV38K	AL312875 Human DNA	c 594	16	9.9	78746	9	AC024289	AC024289 Homo sapi
c 538	16	9.9	37800	8	SCCKHIV38K	AC138522 Homo sapi	c 595	16	9.9	78874	2	AL355521	AL355521 Homo sapi
c 539	16	9.9	37897	9	AL312875	AC138522 Homo sapi	c 596	16	9.9	79418	2	AC005429	AC005429 Drosophila
c 540	16	9.9	38735	9	AC138522	AC025155 Homo sapi	c 597	16	9.9	79718	8	AFAL2H2	AFAL2H2 Homo sapi
c 541	16	9.9	40307	9	AC025155	AC138521 Homo sapi	c 598	16	9.9	79867	8	ATT18N14	ATT18N14 Homo sapi
c 542	16	9.9	40915	9	AC138521	AC139074 Homo sapi	c 599	16	9.9	80514	9	AC004454	AC004454 Homo sapi
c 543	16	9.9	41733	2	AC139074	AC084425 Caenorhab	c 600	16	9.9	80845	9	AC090821	AC090821 Homo sapi
c 544	16	9.9	42310	3	CBRC01B5	BX324221 Mouse DNA	c 601	16	9.9	81056	2	AP0096441_3	AP0096441_3 of Continuation (4 of
c 545	16	9.9	42786	10	BX324221	BX324221 Mouse DNA	c 602	16	9.9	81580	8	AP000736	AP000736 Arabidops

603	16	9.9	81835	8	ATTCa8	297344 Arabidopsis	660	16	9.9	110000	2	BK649394_2	Continuation (3 of
604	16	9.9	82061	9	AC025180	AC025180 Homo sapi	661	16	9.9	110000	6	AR271569_10	Continuation (11 of
605	16	9.9	83385	2	AL590104	AL590104 Homo sapi	662	16	9.9	110000	6	AR300198_1	Continuation (2 of
606	16	9.9	85710	8	AL137080	AL137080 Arabidops	663	16	9.9	110394	8	AC130808	AC130808 Medicago
607	16	9.9	86358	2	AP003739	AP003739 Oryza sat	664	16	9.9	110855	2	AC142095	AC142095 Medicago
608	16	9.9	87095	10	AL928770	AL928770 Mouse DNA	665	16	9.9	111075	2	AC114337	AC114337 Medicago
609	16	9.9	87350	10	BK284690	BK284690 Mouse DNA	666	16	9.9	112171	10	ALB837306	ALB837306 Homo sapi
610	16	9.9	88871	10	MM58105	U88105 Mus musculu	667	16	9.9	112268	9	AC116653	AC116653 Homo sapi
611	16	9.9	90688	9	AC119732	AC119732 Homo sapi	668	16	9.9	112780	2	AC027274	AC027274 Homo sapi
612	16	9.9	90840	8	AC091913	AC091913 Homo sapi	669	16	9.9	112864	2	AC024127	AC024127 Homo sapi
613	16	9.9	90923	8	AF527808	AF527808 Sorghum b	670	16	9.9	113167	8	AC144539	AC144539 Medicago
614	16	9.9	91883	8	CNS08CDY	BX000508 Oryza sat	671	16	9.9	113284	9	AP003382	AP003382 Medicago
615	16	9.9	92809	9	AC073618	AC073618 Homo sapi	672	16	9.9	113733	9	AP003139	AP003139 Homo sapi
616	16	9.9	93476	2	AC112352_3	Continuation (4 of	673	16	9.9	114620	2	AC013815	AC013815 Homo sapi
617	16	9.9	94349	8	ATF26013	AL133452 Arabidops	674	16	9.9	115281	9	AC013815	AC013815 Homo sapi
618	16	9.9	95107	9	AL591242	AL591242 Homo sapi	675	16	9.9	115304	2	BK548251	BK548251 Dario rer
619	16	9.9	95214	9	AC012457	AC012457 Homo sapi	676	16	9.9	116275	2	AP003993	AP003993 Oryza sat
620	16	9.9	95643	8	FGN15	AF069299 Arabidops	677	16	9.9	116772	2	AC141228	AC141228 Homo sapi
621	16	9.9	95692	2	AC015534	AC015534 Homo sapi	678	16	9.9	116793	10	AC079990	AC079990 Homo sapi
622	16	9.9	95786	2	BX571801	BX571801 Homo sapi	679	16	9.9	117824	9	AL389886	AL389886 Homo sapi
623	16	9.9	95921	9	AC004141	AC004141 Homo sapi	680	16	9.9	119377	2	AC133691	AC133691 Rattus no
624	16	9.9	96618	9	HS34781	AL035670 Human DNA	681	16	9.9	120187	9	AC005884	AC005884 Homo sapi
625	16	9.9	98017	8	AC027033	AC027033 Arabidops	682	16	9.9	120538	9	AC004815	AC004815 Homo sapi
626	16	9.9	98109	9	AC025777	AC025777 Homo sapi	683	16	9.9	120709	9	AL445123	AL445123 Human DNA
627	16	9.9	98190	2	AC125738_3	Continuation (4 of	684	16	9.9	121436	2	AC142023	AC142023 Rattus no
628	16	9.9	98345	2	BK649394_3	Continuation (4 of	685	16	9.9	121799	8	OSN00054	AL060609 Oryza sat
629	16	9.9	98461	8	ATF6H20	AL066859 Arabidops	686	16	9.9	121848	9	AC109456	AC109456 Homo sapi
630	16	9.9	99661	2	AC137530	AL035670 Takifuu	687	16	9.9	121902	9	AC008386	AC008386 Homo sapi
631	16	9.9	100443	9	AL731532	AL731532 Human DNA	688	16	9.9	123023	9	AC104788	AC104788 Homo sapi
632	16	9.9	101270	9	HS48316	AL034374 Human DNA	689	16	9.9	123169	9	AC008771	AC008771 Homo sapi
633	16	9.9	102146	2	AC133396	AL031396 Felle cat	690	16	9.9	123551	9	AC026361	AC026361 Homo sapi
634	16	9.9	103181	9	HS97820	AL031397 Human DNA	691	16	9.9	123567	9	AC091958	AC091958 Homo sapi
635	16	9.9	103216	9	HS093918	AL080251 Human DNA	692	16	9.9	123925	9	AC003976	AC003976 Homo sapi
636	16	9.9	103566	9	AC003087	AC003087 Homo sapi	693	16	9.9	124170	8	AC135501	AC135501 Oryza sat
637	16	9.9	104307	8	AL929560	AL929560 Zabrufish	694	16	9.9	124582	8	AC114828	AC114828 Oryza sat
638	16	9.9	104307	8	CNS08CDY	BX000504 Oryza sat	695	16	9.9	125147	2	AC074081	AC074081 Homo sapi
639	16	9.9	105001	9	AC105287	AC105287 Homo sapi	696	16	9.9	125693	9	AL354774	AL354774 Human DNA
640	16	9.9	106123	9	AC109821	AC109821 Homo sapi	697	16	9.9	125766	2	AC013137	AC013137 Homo sapi
641	16	9.9	106420	9	AC002546	AC002546 Homo sapi	698	16	9.9	126052	9	AC018764	AC018764 Homo sapi
642	16	9.9	106795	9	AC004864	AC004864 Homo sapi	699	16	9.9	126349	2	AC101076	AC101076 Mus muscu
643	16	9.9	107027	8	ATF14L2	AL353818 Arabidops	700	16	9.9	126838	9	AC125609	AC125609 Homo sapi
644	16	9.9	107826	2	AC124968	AC124968 Medicago	701	16	9.9	127514	9	AC004417	AC004417 Homo sapi
645	16	9.9	109431	8	AC035249	AC035249 Arabidops	702	16	9.9	127587	9	AC006448	AC006448 Homo sapi
646	16	9.9	109887	10	AL845169	AL845169 Mouse DNA	703	16	9.9	127833	9	AC003958	AC003958 Homo sapi
647	16	9.9	110000	2	AC09180_5	Continuation (6 of	704	16	9.9	127997	2	AC143890	AC143890 Macaca mu
648	16	9.9	110000	2	AC096441_2	Continuation (3 of	705	16	9.9	128622	2	AC114968	AC114968 Homo sapi
649	16	9.9	110000	2	AC098250_2	Continuation (3 of	706	16	9.9	128945	9	AL449083	AL449083 Human DNA
650	16	9.9	110000	2	AC106549_3	Continuation (4 of	707	16	9.9	129575	9	AL160159	AL160159 Human DNA
651	16	9.9	110000	2	AC112373_08	Continuation (9 of	708	16	9.9	129626	2	AC040929	AC040929 Homo sapi
652	16	9.9	110000	2	AC12162_3	Continuation (4 of	709	16	9.9	129638	9	AC094083	AC094083 Homo sapi
653	16	9.9	110000	2	AC125156_0	AC125156 Mus muscu	710	16	9.9	129638	9	AC094083	AC094083 Homo sapi
654	16	9.9	110000	2	AC125726_1	Continuation (2 of	711	16	9.9	130469	9	AC006367	AC006367 Homo sapi
655	16	9.9	110000	2	AC128488_0	AC128488 Rattus no	712	16	9.9	130499	8	OSN00142	AL662940 Oryza sat
656	16	9.9	110000	2	AC139485_1	Continuation (2 of	713	16	9.9	131287	8	OSN6015	AL117264 Oryza sat
657	16	9.9	110000	2	AC146410_0	AC146410 Pan trogl	714	16	9.9	131408	9	AC112914	AC112914 Homo sapi
658	16	9.9	110000	2	AC146410_1	Continuation (2 of	715	16	9.9	131903	9	HS360E18	282203 Human DNA
659	16	9.9	110000	2	BX005127_3	Continuation (4 of	716	16	9.9	132438	9	HS0575N6	AL109741 Human DNA

c 717	16	9.9 132508	8	AC141323	AC141323 Medicago	c 774	16	9.9 145564	2	AC134794	AC134794 Mus muscu
c 718	16	9.9 133276	2	AC087147	AC087147 Mus muscu	c 775	16	9.9 145659	2	AC008531	AC008531 Homo sapi
c 719	16	9.9 133508	9	AF241728	AF241728 Homo sapi	c 776	16	9.9 146071	10	AL929061	AL929061 Mouse DNA
c 720	16	9.9 133780	2	AL356293	AL356293 Homo sapi	c 777	16	9.9 146267	2	AC008815	AC008815 Homo sapi
c 721	16	9.9 134082	2	CNS08CAY	AL844875 Oryza sat	c 778	16	9.9 146377	9	AC083963	AC083963 Homo sapi
c 722	16	9.9 134226	14	JH1CG	MT5116 lctcalurid h	c 779	16	9.9 146413	2	AC051652	AC051652 Homo sapi
c 723	16	9.9 135690	2	BX323089	BX323089 Dantio rer	c 780	16	9.9 146454	14	AF410153	AF410153 Swinepox
c 724	16	9.9 135793	8	CNS08CAY	AL177247 Oryza sat	c 781	16	9.9 146690	2	AC102254	AC102254 Mus muscu
c 725	16	9.9 135850	2	AC130193	AC130193 Felis cat	c 782	16	9.9 147205	8	AC146702	AC146702 Genomic s
c 726	16	9.9 136111	9	AC092980	AC092980 Homo sapi	c 783	16	9.9 148248	2	AC147347	AC147347 SILLURANA
c 727	16	9.9 136249	2	AC143739	AC143739 Macaca mu	c 784	16	9.9 148326	2	AC103619	AC103619 Mus muscu
c 728	16	9.9 136877	9	AL390788	AL390788 Homo sapi	c 785	16	9.9 148454	2	AC007023	AC007023 Homo sapi
c 729	16	9.9 136968	9	AL390788	AL390788 Homo sapi	c 786	16	9.9 148623	2	AC068582	AC068582 Homo sapi
c 730	16	9.9 137481	2	AC027207	AC027207 Homo sapi	c 787	16	9.9 148715	2	BX511217	BX511217 Dantio rer
c 731	16	9.9 137930	2	AC141193	AC141193 Rattus no	c 788	16	9.9 148844	9	AL161738	AL161738 Human DNA
c 732	16	9.9 137941	2	AC128149	AC128149 Rattus no	c 789	16	9.9 149008	2	BX296524	BX296524 Dantio rer
c 733	16	9.9 137995	2	AC008596	AC008596 Homo sapi	c 790	16	9.9 149096	2	AC025083	AC025083 Homo sapi
c 734	16	9.9 138145	9	HS1121J1B	AL031653 Human DNA	c 791	16	9.9 149109	2	AC023181	AC023181 Homo sapi
c 735	16	9.9 138498	2	BX088562	BX088562 Dantio rer	c 792	16	9.9 149198	9	AC007034	AC007034 Homo sapi
c 736	16	9.9 139327	2	AC025017	AC025017 Homo sapi	c 793	16	9.9 149252	9	AC066580	AC066580 Homo sapi
c 737	16	9.9 139327	2	AC025017	AC025017 Homo sapi	c 794	16	9.9 149309	9	AC079895	AC079895 Homo sapi
c 738	16	9.9 139330	8	AC119415	AC119415 Medicago	c 795	16	9.9 149332	2	AC068833	AC068833 Homo sapi
c 739	16	9.9 139388	9	AC007666	AC007666 Homo sapi	c 796	16	9.9 149347	8	AC073392	AC073392 Oryza sat
c 740	16	9.9 139708	2	AC134609	AC134609 Mus muscu	c 797	16	9.9 149527	2	AC147264	AC147264 Mus muscu
c 741	16	9.9 139774	2	AC069339	AC069339 Homo sapi	c 798	16	9.9 149950	9	AC113173	AC113173 Homo sapi
c 742	16	9.9 139823	8	AC104321	AC104321 Oryza sat	c 799	16	9.9 149984	2	AC109789	AC109789 Bos tauru
c 743	16	9.9 139843	2	AL158145	AL158145 Homo sapi	c 800	16	9.9 150332	2	AC004921	AC004921 Lemur cat
c 744	16	9.9 139929	8	AC146525	AC146525 Oryza sat	c 801	16	9.9 150587	2	AC140021	AC140021 Homo sapi
c 745	16	9.9 140098	2	AC024510	AC024510 Homo sapi	c 802	16	9.9 150681	9	AC006011	AC006011 Homo sapi
c 746	16	9.9 140120	2	AL390237	AL390237 Human DNA	c 803	16	9.9 150831	9	AC007719	AC007719 Homo sapi
c 747	16	9.9 140186	2	AC125559	AC125559 Rattus no	c 804	16	9.9 150906	2	AC113550	AC113550 Mus muscu
c 748	16	9.9 140842	2	AC144747	AC144747 Pan trogl	c 805	16	9.9 150936	2	BX255899	BX255899 Dantio rer
c 749	16	9.9 140999	9	AL356415	AL356415 Human DNA	c 806	16	9.9 150994	2	AC024054	AC024054 Homo sapi
c 750	16	9.9 141194	9	AC092611	AC092611 Homo sapi	c 807	16	9.9 151008	2	AC035146	AC035146 Homo sapi
c 751	16	9.9 141350	8	AC135500	AC135500 Oryza sat	c 808	16	9.9 151289	9	AL158164	AL158164 Human DNA
c 752	16	9.9 141420	10	AC133078	AC133078 Mus muscu	c 809	16	9.9 151382	9	AC112221	AC112221 Homo sapi
c 753	16	9.9 141450	2	AC015148	AC015148 Drosophill	c 810	16	9.9 151408	10	AL1732318	AL1732318 Mouse DNA
c 754	16	9.9 141504	2	AC022295	AC022295 Homo sapi	c 811	16	9.9 152118	2	AC013263	AC013263 Homo sapi
c 755	16	9.9 141597	2	AC008455	AC008455 Homo sapi	c 812	16	9.9 152137	2	AP001932	AP001932 Homo sapi
c 756	16	9.9 142037	9	AC025171	AC025171 Homo sapi	c 813	16	9.9 152246	9	AC023473	AC023473 Homo sapi
c 757	16	9.9 142126	2	AC026139	AC026139 Homo sapi	c 814	16	9.9 152281	10	AL672066	AL672066 Mouse DNA
c 758	16	9.9 142420	9	AL138816	AL138816 Human DNA	c 815	16	9.9 152519	2	AC108898	AC108898 Felis cat
c 759	16	9.9 142658	2	AC129074	AC129074 Felis cat	c 816	16	9.9 152572	2	AC067788	AC067788 Homo sapi
c 760	16	9.9 142751	9	AC093714	AC093714 Homo sapi	c 817	16	9.9 152937	2	AC024350	AC024350 Homo sapi
c 761	16	9.9 143093	9	AL442635	AL442635 Human DNA	c 818	16	9.9 153082	2	AC142533	AC142533 Homo sapi
c 762	16	9.9 143192	9	AL954247	AL954247 Pan trogl	c 819	16	9.9 153305	2	AC139606	AC139606 Homo sapi
c 763	16	9.9 143823	9	AC019195	AC019195 Homo sapi	c 820	16	9.9 153426	10	AC121949	AC121949 Mus muscu
c 764	16	9.9 144233	2	AC068103	AC068103 Homo sapi	c 821	16	9.9 153485	2	AC090757	AC090757 Homo sapi
c 765	16	9.9 144343	2	AC121027	AC121027 Rattus no	c 822	16	9.9 153950	8	AC104429	AC104429 Oryza sat
c 766	16	9.9 144437	2	AC019273	AC019273 Homo sapi	c 823	16	9.9 154034	2	AC133311	AC133311 Rattus no
c 767	16	9.9 144683	9	AC096554	AC096554 Homo sapi	c 824	16	9.9 154308	10	AC105065	AC105065 Mus muscu
c 768	16	9.9 144962	2	AP005425	AP005425 Oryza sat	c 825	16	9.9 154653	9	AC146050	AC146050 Pan trogl
c 769	16	9.9 145023	2	AC074380	AC074380 Homo sapi	c 826	16	9.9 154671	2	AC021680	AC021680 Homo sapi
c 770	16	9.9 145307	2	AP004745	AP004745 Oryza sat	c 827	16	9.9 154733	2	AC127462	AC127462 Dantio rer
c 771	16	9.9 145366	5	AL299327	AL299327 Zebrafish	c 828	16	9.9 154792	2	AC116603	AC116603 Mus muscu
c 772	16	9.9 145437	2	AC139985	AC139985 Rattus no	c 829	16	9.9 154795	2	AC144678	AC144678 Homo sapi
c 773	16	9.9 145504	2	AC141023	AC141023 Rattus no	c 830	16	9.9 154959	9	AC004925	AC004925 Homo sapi

c 831	16	9.9 155015	2	AC144700	AC144700 Oryza sat	888	16	9.9 161635	9	AC083873	AC083873 Homo sapi
c 832	16	9.9 155239	2	AC013618	AC013618 Homo sapi	889	16	9.9 161821	10	AL645968	AL645968 Mouse DNA
833	16	9.9 155364	5	BX088582	BX088582 Zebrafish	c 890	16	9.9 161826	2	AC026157	AC026157 Homo sapi
834	16	9.9 155411	10	AC133602	AC133602 Mus muscu	c 891	16	9.9 162237	2	AC115050	AC115050 Mus muscu
835	16	9.9 155420	8	AC025906	AC025906 Oryza sat	c 892	16	9.9 162249	8	AF061282	AF061282 Sorghum b
c 836	16	9.9 155544	8	AP005799	AP005799 Oryza sat	c 893	16	9.9 162325	9	AC103585	AC103585 Homo sapi
c 837	16	9.9 155856	10	BX572626	BX572626 Mouse DNA	894	16	9.9 162437	10	AL928829	AL928829 Mouse DNA
838	16	9.9 156313	2	AL359702	AL359702 Homo sapi	895	16	9.9 162738	9	AC083812	AC083812 Homo sapi
839	16	9.9 156392	2	AC026341	AC026341 Homo sapi	896	16	9.9 162775	2	AC023006	AC023006 Homo sapi
840	16	9.9 156485	9	AC007422	AC007422 Homo sapi	897	16	9.9 162955	9	AC012527	AC012527 Homo sapi
c 841	16	9.9 156527	9	AL161439	AL161439 Human DNA	c 898	16	9.9 163056	5	AC144826	AC144826 Danio rer
842	16	9.9 156598	2	AC012040	AC012040 Homo sapi	c 899	16	9.9 163083	9	AC103773	AC103773 Homo sapi
843	16	9.9 156754	9	AC021055	AC021055 Homo sapi	c 900	16	9.9 163096	9	CNS01DU1	CNS01DU1 Human chr
844	16	9.9 156958	9	AC013460	AC013460 Homo sapi	c 901	16	9.9 163100	2	AC145421	AC145421 Human chr
c 845	16	9.9 157195	2	AC122770	AC122770 Mus muscu	c 902	16	9.9 163104	2	AC110672	AC110672 Mus muscu
c 846	16	9.9 157417	2	AC136261	AC136261 Rattus no	c 903	16	9.9 163132	2	AC121312	AC121312 Mus muscu
c 847	16	9.9 157557	9	AC098808	AC098808 Papio anu	c 904	16	9.9 163355	2	AC117927	AC117927 Mus muscu
c 848	16	9.9 157799	2	AC128320	AC128320 Rattus no	c 905	16	9.9 163473	2	AC144870	AC144870 Pan trogl
849	16	9.9 157836	2	AC060228	AC060228 Homo sapi	c 906	16	9.9 163539	9	AC096916	AC096916 Homo sapi
c 850	16	9.9 158312	2	AC083922	AC083922 Homo sapi	c 907	16	9.9 163631	9	AC009276	AC009276 Homo sapi
c 851	16	9.9 158321	2	AC064610	AC064610 Homo sapi	c 908	16	9.9 163713	2	AC069432	AC069432 Homo sapi
852	16	9.9 158392	9	CNS07EGN	AL591770 Human chr	c 909	16	9.9 163731	9	AC008949	AC008949 Homo sapi
c 853	16	9.9 158412	2	AP001134	AP001134 Homo sapi	c 910	16	9.9 163979	9	CNS01RGM	AL158800 Human chr
c 854	16	9.9 158482	14	AY126275	AY126275 Mamestra	c 911	16	9.9 164013	9	AL360088	AL360088 Human DNA
855	16	9.9 158544	2	AC023658	AC023658 Homo sapi	c 912	16	9.9 164125	9	AC018693	AC018693 Homo sapi
856	16	9.9 158579	2	AC012657	AC012657 Homo sapi	c 913	16	9.9 164176	2	AC080147	AC080147 Homo sapi
857	16	9.9 158759	9	AC144916	AC144916 Homo sapi	c 914	16	9.9 164280	2	AC025391	AC025391 Homo sapi
858	16	9.9 158913	10	AL645928	AL645928 Mouse DNA	c 915	16	9.9 164288	2	AC016500	AC016500 Homo sapi
859	16	9.9 159059	2	AC093000	AP005470 Oryza sat	c 916	16	9.9 164290	9	BS000061	BS000061 Pan trogl
860	16	9.9 159061	2	AP005470	AP005470 Oryza sat	c 917	16	9.9 164304	9	BS000061	BS000061 Pan trogl
861	16	9.9 159339	10	AC127277	AC127277 Mus muscu	c 918	16	9.9 164396	2	AC016519	AC016519 Homo sapi
c 862	16	9.9 159371	2	AC011876	AC011876 Homo sapi	c 919	16	9.9 164462	9	AC008522	AC008522 Homo sapi
c 863	16	9.9 159435	9	AC116564	AC116564 Homo sapi	c 920	16	9.9 164566	2	AC068559	AC068559 Homo sapi
c 864	16	9.9 159521	9	AC098647	AC098647 Homo sapi	c 921	16	9.9 164611	2	AC128858	AC128858 Homo sapi
865	16	9.9 159624	2	AC011021	AC011021 Homo sapi	c 922	16	9.9 164805	8	OSJN00174	OSJN00174 Homo sapi
c 866	16	9.9 159653	2	AC115908	AC115908 Mus muscu	c 923	16	9.9 164839	8	AP002844	AP002844 Oryza sat
c 867	16	9.9 159656	5	AL929243	AL929243 Zebrafish	c 924	16	9.9 165112	2	AC026920	AC026920 Homo sapi
868	16	9.9 159735	2	AC022627	AC022627 Homo sapi	c 925	16	9.9 165307	10	AC132116	AC132116 Mus muscu
c 869	16	9.9 159767	2	AC080178	AC080178 Homo sapi	c 926	16	9.9 165365	2	AC011959	AC011959 Homo sapi
870	16	9.9 159775	10	AC131787	AC131787 Mus muscu	c 927	16	9.9 165617	5	AL845526	AL845526 Zebrafish
c 871	16	9.9 159946	9	AC104840	AC104840 Homo sapi	c 928	16	9.9 165749	9	AC007966	AC007966 Homo sapi
c 872	16	9.9 160073	2	AC025532	AC025532 Homo sapi	c 929	16	9.9 165777	10	BX004852	BX004852 Mouse DNA
c 873	16	9.9 160179	2	AC092930	AC092930 Homo sapi	c 930	16	9.9 165843	2	AC135548	AC135548 Papio anu
c 874	16	9.9 160440	10	AC126245	AC126245 Mus muscu	c 931	16	9.9 165920	9	AC010232	AC010232 Homo sapi
c 875	16	9.9 160603	8	AC084818	AC084818 Oryza sat	c 932	16	9.9 165988	2	AC113573	AC113573 Canis fam
876	16	9.9 160636	2	AC024991	AC024991 Homo sapi	c 933	16	9.9 166045	2	AC018543	AC018543 Homo sapi
877	16	9.9 160746	2	AC044853	AC044853 Homo sapi	c 934	16	9.9 166118	9	AL355495	AL355495 Human DNA
c 878	16	9.9 160920	8	AC137072	AC137072 Genomic s	c 935	16	9.9 166119	2	AC105169	AC105169 Mus muscu
879	16	9.9 160946	5	AL935188	AL935188 Zebrafish	c 936	16	9.9 166447	9	AC021723	AC021723 Homo sapi
c 880	16	9.9 160961	2	AC145794	AC145794 Silurana	c 937	16	9.9 166451	9	AC018994	AC018994 Homo sapi
c 881	16	9.9 160962	2	AC022862	AC022862 Homo sapi	c 938	16	9.9 166540	2	AC142445	AC142445 Homo sapi
882	16	9.9 161180	2	AC146771	AC146771 Canis fam	c 939	16	9.9 166679	2	AC105366	AC105366 Rattus no
883	16	9.9 161309	9	AC0100839	AC0100839 Homo sapi	c 940	16	9.9 166944	2	AC145117	AC145117 Rattus no
c 884	16	9.9 161376	2	BX511150	BX511150 Danio rer	c 941	16	9.9 167030	2	AC025646	AC025646 Homo sapi
885	16	9.9 161416	2	AC026857	AC026857 Homo sapi	c 942	16	9.9 167065	2	AC018266	AC018266 Homo sapi
c 886	16	9.9 161461	10	AC124355	AC124355 Mus muscu	c 943	16	9.9 167099	9	AC100779	AC100779 Homo sapi
c 887	16	9.9 161602	9	AC022634	AC022634 Homo sapi	c 944	16	9.9 167159	2	AC073481	AC073481 Homo sapi

c 945	16	9.9	167416	9	AC023856	Homo sapi
c 946	16	9.9	167611	9	AL583859	Human DNA
c 947	16	9.9	167613	5	AL5928670	Zebrafish
c 948	16	9.9	167658	2	BX537110	Danio rer
c 949	16	9.9	167728	2	AC109240	Mus muscu
c 950	16	9.9	168008	9	AC142334	Pan trogl
c 951	16	9.9	168380	9	AC063933	Homo sapi
c 952	16	9.9	168479	3	AC093454	Drosophi
c 953	16	9.9	168335	9	AC021302	Homo sapi
c 954	16	9.9	168334	2	AC011650	Homo sapi
c 955	16	9.9	168688	9	AC118557	Homo sapi
c 956	16	9.9	168696	9	AC018469	Homo sapi
c 957	16	9.9	168805	2	AC027523	Homo sapi
c 958	16	9.9	168870	2	AC146201	Pan trogl
c 959	16	9.9	168982	2	AC020669	Homo sapi
c 960	16	9.9	169190	9	AC114776	Homo sapi
c 961	16	9.9	169391	9	AC093746	Homo sapi
c 962	16	9.9	169402	2	AC027715	Homo sapi
c 963	16	9.9	169515	2	AC023213	Homo sapi
c 964	16	9.9	169646	9	AL160269	Human DNA
c 965	16	9.9	169888	9	AL356754	Human DNA
c 966	16	9.9	169911	2	AC138383	Mus muscu
c 967	16	9.9	169950	2	AC084049	Homo sapi
c 968	16	9.9	169966	2	AC053521	Homo sapi
c 969	16	9.9	170181	9	AC069353	Homo sapi
c 970	16	9.9	170184	3	AC009911	Drosophi
c 971	16	9.9	170202	9	AC110792	Homo sapi
c 972	16	9.9	170796	2	AC069416	Homo sapi
c 973	16	9.9	170855	10	AC132605	Mus muscu
c 974	16	9.9	170861	2	AC025698	Homo sapi
c 975	16	9.9	170885	2	AC024378	Homo sapi
c 976	16	9.9	170923	2	AC016181	Homo sapi
c 977	16	9.9	170944	2	AC027230	Homo sapi
c 978	16	9.9	171012	2	AC016061	Homo sapi
c 979	16	9.9	171307	2	AL355820	Homo sapi
c 980	16	9.9	171376	3	AC007929	Drosophi
c 981	16	9.9	171426	2	AL391664	Homo sapi
c 982	16	9.9	171490	2	AC068209	Homo sapi
c 983	16	9.9	171593	10	AL672074	Mouse DNA
c 984	16	9.9	171643	2	AC116803	Mus muscu
c 985	16	9.9	171744	9	AC025472	Homo sapi
c 986	16	9.9	171793	5	BX005479	Zebrafish
c 987	16	9.9	172016	10	AC128671	Mus muscu
c 988	16	9.9	172077	10	BX005171	Mouse DNA
c 989	16	9.9	172103	2	AC021871	Homo sapi
c 990	16	9.9	172208	2	BX510322	Danio rer
c 991	16	9.9	172481	2	AL357692	Homo sapi
c 992	16	9.9	172812	10	AC137877	Mus muscu
c 993	16	9.9	172984	2	AC117788	Mus muscu
c 994	16	9.9	173025	2	AL391596	Homo sapi
c 995	16	9.9	173066	9	AC093495	Homo sapi
c 996	16	9.9	173288	10	AF532117	Mus muscu
c 997	16	9.9	173295	9	AC099744	Papilo anu
c 998	16	9.9	173471	2	AC101841	Mus muscu
c 999	16	9.9	173623	2	AC144872	Pan trogl
c 1000	16	9.9	173915	9	AP001254	Homo sapi

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	
BD245278	BD245278	Development of novel antibiotics based on bacteriophage genomics.	BD245278	BD245278.1	GI:33055048	JP 2002531107-A/13.	unidentified	1 (bases 1 to 162)	Pelletier,J., Gros,P. and Dubow,M.	Development of novel antibiotics based on bacteriophage genomics	Patent: JP 2002531107-A/13 24-SEP-2002; PHAGETECH INC	OS StepHyLococcus aureus bacteriophage 77 PN JP 2002531107-A/13 PD 24-SEP-2002 PF 03-DEC-1999 JP 2000585456 PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR 28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR 01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454252 PI JERRY PELLETIER,PHILIPPE GROS,MICHAEL DUBOW PC C12N15/09,A01N63/00,A61K38/00,A61K45/00,A61P31/04,C07K14/005,PC C12M1/00 PC C12N1/21,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/566,PC C12N15/00 CC A61K37/02 CC Coding Sequence FH Key FT source FT aureus bacteriophage 77'. FT FT	
FEATURES	source	Location/Qualifiers	1..162	/organism="unidentified"	/mol_type="genomic DNA"	/db_xref="taxon:32644"	ORIGIN	Query Match	100.0%; Score 162; DB 6; Length 162;	Best Local Similarity	100.0%; Pred. No. 7.7e-73;	Matches	162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1	ATAGCAACATTATATTAAGGCTACGAGTATATGCTTACAGCTTACGAGTT	60				Db	1	ATAGCAACATTATATTAAGGCTACGAGTATATGCTTACAGCTTACGAGTT	60			60
QY	61	GTAAGCAACATTATATTAAGGCTACGAGTATATGCTTACAGCTTACGAGTT	120				Db	61	GTAAGCAACATTATATTAAGGCTACGAGTATATGCTTACAGCTTACGAGTT	120			120

QY 121 GCAACATTCATGTAACAAAGATGCTTTTCAAGATTA 162
DB 121 GCAACATTCATGTAACAAAGATGCTTTTCAAGATTA 162

RESULT 2
BD245281 41708 bp DNA linear PAT 17-JUL-2003
LOCUS BD245281
DEFINITION Development of novel antibiotics based on bacteriophage genomics.
ACCESSION BD245281
VERSION BD245281.1 GI:33055051
KEYWORDS JP 2002531107-A/16.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 41708)
AUTHORS Pelletier, J., Gros, P. and Dubow, M.
TITLE Development of novel antibiotics based on bacteriophage genomics
JOURNAL PHARMATECH INC
COMMENT 05 Staphylococcus aureus bacteriophage 77
PN JP 2002531107-A/16
PD 24-SEP-2002
PR 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992, 03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804, 30-SEP-1999 US 60/157218 PR
01-DEC-1999 US 60/168777, 02-DEC-1999 US 09/454252 PI JERRY
PELLETIER, PHILLIPE GROS, MICHAEL DUBOW
PC C12N15/09, A01N63/00, A61K38/00, A61K45/00, A61P31/04, C07K14/005,
PC C12N1/00,
PC C12N1/21, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/566, PC
C12N15/00,
PC A61K37/02
CC Genome Sequence
FH Key
FT source
FT aureus bacteriophage 77
FT

FEATURES
source Location/Qualifiers
1..41708
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 100.0%; Score 162; DB 6; Length 41708;
Best Local Similarity 100.0%; Pred. No. 2.7e-73;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAGCAACATTATATAAGCTAGTACAGATATTGCTTCAAGTCTTAGCGATT 60
DB 29051 ATAGCAACATTATATAAGCTAGTACAGATATTGCTTCAAGTCTTAGCGATT 29110
QY 61 GTACTATGCGCTTCTATATCTTCACTACAGACAGATGCGGGAATCGCAAGTATC 120
DB 29111 GTACTATGCGCTTCTATATCTTCACTACAGACAGATGCGGGAATCGCAAGTATC 29170

QY 121 GCAACATTCATGTAACAAAGATGCTTTTCAAGATTA 162
DB 29171 GCAACATTCATGTAACAAAGATGCTTTTCAAGATTA 29212

RESULT 3
AR368770 41708 bp DNA linear PAT 12-SEP-2003
LOCUS AR368770
DEFINITION Sequence 3 from patent US 6376652.
ACCESSION AR368770
VERSION AR368770.1 GI:34603077
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 41708)
AUTHORS Pelletier, J., Gros, P. and Dubow, M.
TITLE Compositions and methods involving an essential Staphylococcus aureus gene and its encoded protein
JOURNAL Patent: US 6376652-A 3 23-Apr-2002;
FEATURES Location/Qualifiers
source 1..41708
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 162; DB 6; Length 41708;
Best Local Similarity 100.0%; Pred. No. 2.7e-73;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAGCAACATTATATAAGCTAGTACAGATATTGCTTCAAGTCTTAGCGATT 60
DB 29051 ATAGCAACATTATATAAGCTAGTACAGATATTGCTTCAAGTCTTAGCGATT 29110
QY 61 GTACTATGCGCTTCTATATCTTCACTACAGACAGATGCGGGAATCGCAAGTATC 120
DB 29111 GTACTATGCGCTTCTATATCTTCACTACAGACAGATGCGGGAATCGCAAGTATC 29170
QY 121 GCAACATTCATGTAACAAAGATGCTTTTCAAGATTA 162
DB 29171 GCAACATTCATGTAACAAAGATGCTTTTCAAGATTA 29212

RESULT 4
AX583668 159 bp DNA linear PAT 10-JAN-2003
LOCUS AX583668
DEFINITION Sequence 45 from Patent W002059148.
ACCESSION AX583668
VERSION AX583668.1 GI:27655478
KEYWORDS
SOURCE Staphylococcus aureus
ORGANISM Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE 1
AUTHORS Melnik, A., Nagy, E., von Absen, U., Klede, C., Henics, T., Zauner, W., Minn, D. B., Vytvytska, O., Etz, H., Dryla, A., Welohart, T., Hafner, M.,

Tempelmeier, B., Fraser, C.M. and Gill, S.
A method for identification, isolation and production of antigens
to a specific pathogen
JOURNAL Patent: WO 02059148-A 45 01-AUG-2002;
Clatam Biotechnologies GmbH (AT)
FEATURES Location/Qualifiers
source 1..159
/organism="Staphylococcus aureus"
/mol_type="unassigned DNA"
/db_xref="taxon:1280"

ORIGIN

Query Match 45.7%; Score 74; DB 6; Length 159;
Best Local Similarity 100.0%; Pred. No. 2.9e-27;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 ATTGCTATATCCGTTTCTATATCTACATGAGCATGGTCAATTGCGGATTCGCAGAT 117
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DB 58 ATTGCTATATCCGTTTCTATATCTACATGAGCATGGTCAATTGCGGATTCGCAGAT 117
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QY 118 ATCCGACATTCAT 131
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DB 118 ATCCGACATTCAT 131
|||||

RESULT 5
AX618544 159 bp DNA linear PAT 20-FEB-2003
LOCUS
DEFINITION Sequence 1507 from Patent WO02094868.
ACCESSION AX618544
VERSION AX618544.1 GI:28448591
KEYWORDS
SOURCE Staphylococcus aureus
ORGANISM Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcus.

REFERENCE 1
AUTHORS Masignani, V.C., Mora, M.C. and Scarselli, M.C.
TITLE Staphylococcus aureus proteins and nucleic acids
JOURNAL Patent: WO 02094868-A 1507 28-NOV-2002;
Chiron Spa (IT)
FEATURES Location/Qualifiers
source 1..159
/organism="Staphylococcus aureus"
/mol_type="unassigned DNA"
/db_xref="taxon:1280"

ORIGIN

Query Match 41.4%; Score 67; DB 6; Length 159;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 TATGCTTACAGCTCTAGCGATGTACTATATGCCGTTTCTATATCTACTACAGCATGGT 97
|||||
DB 38 TATGCTTACAGCTCTAGCGATGTACTATATGCCGTTTCTATATCTACTACAGCATGGT 97
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QY 98 CAATGTC 104
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DB 98 CAATGTC 104

RESULT 6
AR354422/c 1408 bp DNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 540 from patent US 6593114.
ACCESSION AR354422
VERSION AR354422.1 GI:33760506
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1408)
AUTHORS Rosen, C.A., Choi, G.H., Barash, S., Dillon, P.J., Fannon, M.R. and
Rosen, C.A.

TITLE Staphylococcus aureus polynucleotides and sequences
JOURNAL Patent: US 6593114-A 540 15-JUL-2003;
FEATURES Location/Qualifiers
source 1..1408
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 41.4%; Score 67; DB 6; Length 1408;
Best Local Similarity 100.0%; Pred. No. 8.1e-24;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 TATGCTTACAGCTCTAGCGATGTACTATATGCCGTTTCTATATCTACTACAGCATGGT 97
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DB 302 TATGCTTACAGCTCTAGCGATGTACTATATGCCGTTTCTATATCTACTACAGCATGGT 243
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QY 98 CAATGTC 104
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DB 242 CAATGTC 236
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RESULT 7
AF424781 43604 bp DNA linear PHG 10-JUN-2002
LOCUS
DEFINITION Staphylococcus aureus phage phi 11, complete genome.
ACCESSION AF424781
VERSION AF424781.1 GI:18920487
KEYWORDS
SOURCE Staphylococcus aureus phage phi 11
ORGANISM Staphylococcus aureus phage phi 11
VIRUSES; dsDNA Viruses; no RNA stage; Caudovirales; Siphoviridae.

REFERENCE 1 (bases 1 to 43604)
AUTHORS Iandolo, J.J., Worrell, V., Grelicher, K.H., Qian, Y., Tian, R.,
Kenton, S., Dorman, A., Ji, H., Lin, S., Loh, P., Qi, S., Zhu, H. and
Roe, B.A.
TITLE Comparative analysis of the genomes of the temperate bacteriophages
JOURNAL phi11, phi12 and phi13 of Staphylococcus aureus 8325
MEDLINE Gene 289 (1-2), 109-116 (2002)
PUBMED 22032962
12036589
REFERENCE 2 (bases 1 to 43604)

AUTHORS Iandolo,J.J., Worrell,V., Roe,B., Qian,Y., Dorman,A., Tian,R., Lin,S. and Jia,H.
TITLE Direct Submission
JOURNAL Submitted (26-SEP-2001) Microbiology and Immunology, Univ. of Oklahoma Health Sciences Center, 940 S.L. Young Bvd, Oklahoma City, OK 73190, USA

FEATURES Location/Qualifiers
1..43604
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/proviral
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/db_xref="GI:18920488"

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/protein_id="AAL8246.1"
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/protein_id="AAL8254.1"
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/db_xref="GI:18920498"
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VMK"
7566..8345
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/db_xref="GI:18920498"
/translation="MTERTQVDILQGLGVKDISKQNNKFEKATVGRGTGTF
LTKNNALVDINEDGTTEDEAVVOIKVKKFSATIMLPKITEQLBNGKIDV
VETIQKLADITDDIDNGSKKPTFNMGCASTRVSYIKIEKQEHYPLATISG
HGIKRDDEGSTINPTITIEAODIKKAVTSQDLARTIEHEQDGEKTYQVL
NAEPNLETKIRHSSNKKNNRFINSDVVAQIRNG"
8375..8929
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/protein_id="AL82241.1"
/db_xref="GI:18920500"
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RYETIVENNEGKQYKNOYPPFOODQEQYIELSLGIKINLPDITDPTOLIN
KIGTIVLKNENEGCKRYRLSYVMKKDDEVNKKPEPTDEMQKQDQNGKPT
NSQSNFPANANGPIEINDDLFP"
8942..9634
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/db_xref="GI:18920501"
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PNNKLSIEQRKIFAKCRDIELHGEVESTRKLQTELEIKGVEEISLRDSKV
ARELEILAFNEHQIPMSVETSKLSEDAALLVATINNCVIGRPHADLAREV
VGRGNINKNHYDHYVALCRQHNEQHALGVSPDKYHLDSWIKYDERLIMKLC
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YNEGYTMSLSENPNEBMLNENPNINSRLAQTEFTLAMEKVNGLKVTNWK
NOSLSVAKHKEKNLQOQYREKQKLEKLNVTYLRDTEEEERKEEKEEK
NKEEREAVFSSIKYIINLIDKLTVMQKOLGFAIDIGTNAFVYVGYETTSK
SAHGGYLIKVLNNMAKENVTKEDAKKIAPRNTTDVIAQKEKELSD"
10765..12006
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/product="helicase DnaB"
/protein_id="AL82244.1"
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/translation="NNGOFEISTITATLKQPDVLEKIRVDWNTKERTFN
VMDYKIDHQEYLYKATDKERLADPTIKLNDSICGFERYQGLISSYQJAK
NELVTERKQOPNQNINLIDELADLTITNKEDGKKEVEEVEELYSQPKQIK

1GKLMYKIGLEPQLIVIAAPSVGKTGFALMMMLNIHQNGYKTSFSLERTGS
VLKMLSTTIGLEIKIKELINLPDILTKLNADKIMKIGDISDSNTTPQDRA
QAMRSRQOVFIIDYQLMDTDVADVRRAVAKISRLKIKINETGAIYTLISQNR
GVSRQDRPMLSIDKESGGIEADSLAMLYNHDYVNRBDSITGNSIYECNIAN
KDEGTGIEEFYKTKTORFT"
12222..12443
/codon_start=1
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/db_xref="GI:18920504"
/translation="WPKRYLYKREDGETDIKIVIKYKIMNVEYSILGAFSDEKIM

Query Match 41.4%; Score 67; DB 7; Length 43604;
Best Local Similarity 100.0%; Pred. No. 4.2e-24;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 TATGCTTACAGCTTACGATTTGACTTATCCGTTTCTACTTACGACGATGCT 97
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Db 6232 TATGCTTACAGCTTACGATTTGACTTATCCGTTTCTACTTACGACGATGCT 6291
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Qy 98 CAATTC 104
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Db 6292 CAATTC 6298

RESULT 8
AP003135/c
LOCUS AP003135 291150 bp DNA linear BCT 11-JAN-2003
DEFINITION Staphylococcus aureus subsp. aureus N315 genomic DNA, complete
genome, section 7/10.
ACCESSION AP003135 BA000018
VERSION AP003135.2 GI:14349227
KEYWORDS
SOURCE
ORGANISM
Staphylococcus aureus subsp. aureus N315
Staphylococcus aureus subsp. aureus N315
Bacteria; Firmicutes; Bacillales; Staphylococcus.

REFERENCE
AUTHORS
1 Kuroda,M., Ohta,T., Uchiyama,I., Baba,T., Yuzawa,H., Kobayashi,I.,
Cui,L., Oguchi,A., Aoki,K., Nagai,Y., Iino,J., Ito,T., Kanamori,M.,
Matsumaru,H., Maruyama,A., Murakami,H., Hosoyama,A.,
Mizutani-Uji,Y., Takahashi,N.K., Sekano,T., Inoue,R., Kato,C.,
Sekimizu,K., Hirakawa,H., Kohara,S., Goto,S., Yabuzaki,J.,
Kanehisa,M., Yamashita,A., Oshima,K., Furuya,K., Yoshino,C.,
Shiba,T., Hattori,M., Ogasawara,N., Hayashi,H. and Hiramatsu,K.
Whole genome sequencing of methicillin-resistant Staphylococcus
aureus
Lancet 357 (9264), 1223-1240 (2001)

JOURNAL
MEDLINE
21311952
PUBMED
11418146
REFERENCE
2 (bases 1 to 291150)
DIRECTOR-GENERAL, Biotechnology Center, Aoki,K., Oguchi,A.,
Hosoyama,A., Nagai,Y., Kuroda,M., Hiramatsu,K. and Kikuchi,H.
TITLE
JOURNAL
Direct Submission
Submitted (30-JAN-2001) Director-General, Biotechnology Center,
National Institute of Technology and Evaluation,
Center, 2Chome 49-10 Nishihara, Shibuya-Ku, Tokyo 151-0066, Japan

(E-mail:bl@nate.go.jp, URL:http://www.bio.nite.go.jp/,
Tel:81-3-3481-1933, Fax:81-3-3481-8424)
On Jun 12, 2001 this sequence version replaced gi:13701545.
Location/Qualifiers
1. 291150
/organism="Staphylococcus aureus subsp. aureus N315"
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/strain="N315"
/sub_species="aureus N315"
/db_xref="taxon:158879"
complement(357. .1205)
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complement(357. .1205)
/gene="SA1571"
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/transl_table=11
/product="D-alanine aminotransferase"
/protein_id="BAB42839.1"
/db_xref="GI:13701546"
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Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 10
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LOCUS
DEFINITION Development of novel antibiotics based on bacteriophage genomics.
ACCESSION BD245634
VERSION BD245634.1 GI:33055404
KEYWORDS JP 2002331107-A/369.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 43594)
AUTHORS Pelletier, V., Gros, P. and Dubow, M.
TITLE Development of novel antibiotics based on bacteriophage genomics
JOURNAL
PHARMETECH INC
PATENT: JP 2002331107-A 369 24-SEP-2002;
COMMENT
OS Staphylococcus aureus bacteriophage 96
PN JP 2002331107-A/369
PD 24-SEP-2002
PF 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992, 03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804, 30-SEP-1999 US 60/157218 PR
01-DEC-1999 US 60/168777, 02-DEC-1999 US 09/454252 PI JERRY
PELLETIER, PHILIPPE GROS, MICHAEL DUBOW
PC C12N15/09, A01N63/00, A61K38/00, A61K45/00, A61P31/04, C07K14/005,
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PC C12N1/21, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/566, PC
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CC Genome Sequence
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Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS
DEFINITION Staphylococcus aureus prophage phiPV83
ACCESSION AB044554
VERSION AB044554.1 GI:8918747
KEYWORDS
SOURCE
ORGANISM Staphylococcus aureus prophage phiPV83
REFERENCE 1 (bases 1 to 45636)
AUTHORS Kaneko, J., Kimura, T., Kawakami, Y., Tomita, T. and Kamio, Y.
TITLE Panton-Valentine leukocidin genes in a phage-like particle isolated from mitomycin C-treated Staphylococcus aureus V8 (ATCC 49775)
JOURNAL Biosci. Biotechnol. Biochem. 61 (11), 1960-1962 (1997)
MEDLINE 98067870
PUBMED 9404084
REFERENCE 2 (sites)
AUTHORS Zou, D., Kaneko, J., Narita, S. and Kamio, Y.
TITLE Complete nucleotide sequence and molecular characterization of prophage PV83pro carrying lukM-lukF-PV(p83) gene cluster in Staphylococcus aureus strain p83
JOURNAL
REFERENCE 3 (bases 1 to 45636)
AUTHORS Kaneko, J., Zou, D. and Kamio, Y.
TITLE Direct Submission
JOURNAL Submitted (09-JUN-2000) Jun Kaneko, Tohoku University, Graduate School of Agricultural Science; 1-1 Taishu-1-dori Aomiyamachi, Aoba-ku, Sendai, Miyagi 981-8555, Japan
(E-mail: jkaneko@biochem.tohoku.ac.jp, Tel: 81-22-717-8781, Fax: 81-22-717-8780)
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Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 12
AP003360 348527 bp DNA linear BCT 07-FEB-2002
LOCUS
DEFINITION *Staphylococcus aureus* subsp. *aureus* Mu50 genomic DNA, complete
SEQUENCE, section 3/9.
ACCESSION AP003360 BA000017
VERSION AP003360.2 GI:14246388
KEYWORDS
SOURCE *Staphylococcus aureus* subsp. *aureus* Mu50
ORGANISM *Staphylococcus aureus* subsp. *aureus* Mu50

REFERENCE
AUTHORS
1 Kuroda, M., Ohta, T., Uchiyama, I., Baba, T., Yuzawa, H., Kobayashi, I.,
Cui, L., Oguchi, A., Aoki, K., Nagai, Y., Iian, D., Ito, T., Kanamori, M.,
Matsumaru, H., Maruyama, A., Murakami, H., Hosoyama, A.,
Mizutani-U, Y., Takahashi, N. K., Sawano, T., Inoue, R., Kaito, C.,
Sekizawa, K., Hirakawa, H., Kohara, S., Goto, S., Yabuzaki, J.,
Kanehisa, M., Yamashita, A., Oshima, K., Furuya, K., Yoshino, C.,
Shiba, T., Hattori, M., Ogasawara, N., Hayashi, H. and Hiramatsu, K.
Whole genome sequencing of methicillin-resistant *Staphylococcus*
aureus
JOURNAL Lancet 357 (9264), 1225-1240 (2001)
MEDLINE 21311952
PUBMED 11418146
REFERENCE 2 (bases 1 to 348527)
AUTHORS Ohta, T.
TITLE Direct Submission
JOURNAL Submitted (28-FEB-2001) Toshiko Ohta, University of Tsukuba College
of Medical Technology and Nursing, Department of Medical
Technology; 1-1-1 Ten-nodai, Tsukuba, Ibaraki 305-8577, Japan
(E-mail: tohta@sakura.cc.tsukuba.ac.jp, Tel:81-298-53-3454,
Fax:81-298-53-3454)
On May 29, 2001 this sequence version replaced gi:13874937.
COMMENT
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 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 230191 TACTCTACACAGCATGCTCAATTCGGGATTCCGACAGTAT 230231

RESULT 13
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 LOCUS AF424783 42722 bp DNA linear PHG 10-JUN-2002
 DEFINITION Staphylococcus aureus phage phi 13, complete genome.
 ACCESSION AF424783
 VERSION AF424783.1 GI:18920591
 KEYWORDS
 SOURCE Staphylococcus aureus phage phi 13
 ORGANISM Staphylococcus aureus phage phi 13
 REFERENCE Viruses; deDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
 1 (bases 1 to 42722)
 AUTHORS Iandolo,J.J., Morrell,V., Grolicher,K.H., Qian,Y., Tian,R.,
 Kenton,S., Dorman,A., Ji,H., Lin,S., Loh,P., Qi,S., Zhu,H. and
 Roe,B.A.
 TITLE Comparative analysis of the genomes of the temperate bacteriophages
 phi11, phi12 and phi13 of Staphylococcus aureus 8325
 JOURNAL Gene 289 (1-2), 109-118 (2002)
 MEDLINE 22032962
 PUBMED 12036589
 REFERENCE 2 (bases 1 to 42722)
 Iandolo,J.J., Morrell,V., Roe,B., Qian,Y., Dorman,A., Tian,R.,
 Lin,S. and Ji,H.
 TITLE Direct Submission
 JOURNAL Submitted (26-SEP-2001) Microbiology and Immunology, Univ. of
 Oklahoma Health Sciences Center, 940 S.L. Young Blvd, Oklahoma City,
 OK 73190, USA

FEATURES
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 location/Qualifiers
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 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 6585 ATGACGACATTATATAAGCTAAGTACGAGTA 6620

RESULT 14
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LOCUS AP004828 272850 bp DNA linear BCT 20-DEC-2002
DEFINITION Staphylococcus aureus subsp. aureus MW2 DNA, complete genome,
 strain:MW2, section 7/10.
ACCESSION AP004828 BA000033
VERSION AP004828.1 GI:21204850
KEYWORDS
SOURCE Staphylococcus aureus subsp. aureus MW2
ORGANISM Staphylococcus aureus subsp. aureus MW2
REFERENCE 1
AUTHORS Baba,T., Takeuchi,F., Kuroda,M., Yuzawa,H., Aoki,K., Oguchi,A.,
 Nagai,Y., Iwama,N., Amano,K., Naima,T., Kuroda,H., Oki,L.,
 Yamamoto,K. and Hiramatsu,K.
 Genome and virulence determinants of high virulence
 community-acquired MRSA
JOURNAL Lancet 359 (9320), 1819-1827 (2002)
MEDLINE 22040717
PUBMED 12044378
REFERENCE 2 (bases 1 to 272850)
AUTHORS Director-General, Biotechnology Center, Aoki,K., Oguchi,A.,
 Nagai,Y., Amano,K., Iwama,N., Baba,T., Kuroda,M., Hiramatsu,K. and
 Kikuchi,H.
TITLE Direct Submision
JOURNAL Submitted (06-MAR-2002) Director-General, Biotechnology Center,
 National Institute of Technology and Evaluation, Biotechnology
 Center, 2Chome 49-10 Nishihara, Shibuya-Ku, Tokyo 151-0066, Japan
 (E-mail:biotech.go.jp, URL:http://www.bio.nite.go.jp/,
 Tel:81-3-3481-1933, Fax:81-3-3481-8424)
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RESULT 15
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sequence, section 7/9.
ACCESSION
AP003364 BA000017
VERSION
AP003364.2 GI:14247707
KEYWORDS
Staphylococcus aureus subsp. aureus Mu50
ORGANISM
Staphylococcus aureus subsp. aureus Mu50
Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE
AUTHORS
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Kuruda,M., Ohta,T., Uchiyama,I., Baba,T., Yuzawa,H., Kobayashi,I.,
Cui,L., Oguchi,A., Aoki,K., Nagai,Y., Lien,J., Ito,T., Kanamori,M.,
Matsumaru,H., Maruyama,A., Murakami,H., Hosoyama,A.,
Mizutani-Uji,Y., Takahashi,N.K., Sawano,T., Inoue,R., Kaito,C.,
Sekizawa,K., Hirakawa,H., Kuhara,S., Goto,S., Yabuzaki,J.,
Kanehisa,M., Yamashita,A., Oshima,K., Furuya,K., Yoshino,C.,
Shiba,T., Hattori,M., Ogasawara,N., Hayashi,H. and Hiratsuka,K.
TITLE
Whole genome sequencing of methicillin-resistant Staphylococcus
aureus
JOURNAL
Lancet 357 (9264), 1225-1240 (2001)
MEDLINE
21311952
PUBMED
11418146
REFERENCE
2 (bases 1 to 348650)
AUTHORS
Ohta,T.
TITLE
Direct Submision
COMMENT
Submitted (28-FEB-2001) Tooshiko Ohta, University of Tsukuba College
of Medical Technology and Nursing, Department of Medical
Technology/ 1-1-1 Ten-nodori, Tsukuba, Ibaraki 305-8577, Japan
(E-mail:tooshiko@tsukuba.ac.jp, Tel:81-298-53-3454,
Fax:81-298-53-3454)
On May 29, 2001 this sequence version replaced gi:13873637.
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Query Match 22.2%; Score 36; DB 1; Length 348650;
Best Local Similarity 100.0%; Pred.No.3.2e-08;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGCACTTTAAAGCTACCTAGTACGACGTA 36
DB 40698 ATGAGCACTTTAAAGCTACCTAGTACGACGTA 40663

Search completed: October 15, 2004, 03:31:40
Job time : 897.824 secs

OM nucleotide - nucleotide search, using om model

Run on: October 14, 2004, 18:55:29 ; Search time 108.072 Seconds
(without alignments)
6368.040 Million cell updates/sec

Title: US-09-407-804A-7

Perfect score: 162

Sequence: 1 atgagcaacattataaag.....aatgcttttcaagaactaa 162

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

- 1: N_Geneseq_29Jan04:*
- 2: geneseqn1980s:*
- 3: geneseqn1990s:*
- 4: geneseqn2000s:*
- 5: geneseqn2001as:*
- 6: geneseqn2002as:*
- 7: geneseqn2003as:*
- 8: geneseqn2003bs:*
- 9: geneseqn2003cs:*
- 10: geneseqn2004s:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	162	100.0	162	3	AAA68251 Bacterioph
2	162	100.0	41708	3	AAA68247 Bacterioph
3	162	100.0	41708	4	AAc86106 Complete
4	74	45.7	159	7	ABr14900 Pathogen
5	67	41.4	159	7	ACF73074 Staphyloc
6	67	41.4	1408	2	AAV74851 Staphyloc
7	65	40.1	43095	3	AAA68254 Bacterioph

8	55	34.0	43576	3	AAA68609	AAA68609 Bacterioph
9	26	16.0	2049	2	AAV74602	AAV74602 Staphyloc
10	23	14.2	25	3	AAA68911	AAA68911 Bacterioph
11	21	13.0	25	3	AAA68846	AAA68846 Bacterioph
12	19	11.7	4895	9	ADD18757	ADD18757 Human dls
13	19	11.7	4983	4	AAE44629	AAE44629 Bovine em
14	18	11.1	365	6	ABR73359	ABR73359 Bovine em
15	18	11.1	365	6	ABR73269	ABR73269 Bovine em
16	18	11.1	599	5	ABV51104	ABV51104 Human pro
17	18	11.1	625	5	ABV52273	ABV52273 Human pro
18	17	10.5	464	4	AAI88984	AAI88984 Human pol
19	17	10.5	1379	3	AAc59134	AAc59134 Human sec
20	17	10.5	2175	4	AB124603	AB124603 Drosophill
21	17	10.5	2815	4	AAK91396	AAK91396 Human dfg
22	17	10.5	2815	6	ABs99941	ABs99941 Genomic D
23	17	10.5	2815	9	ADB93094	ADB93094 Human col
24	17	10.5	2851	4	AAK91397	AAK91397 Human dfg
25	17	10.5	2851	4	AAK91395	AAK91395 Human col
26	17	10.5	2851	4	AAI57765	AAI57765 Human col
27	17	10.5	2851	4	AAI57763	AAI57763 Human col
28	17	10.5	2851	4	AAI57765	AAI57765 Human col
29	17	10.5	2851	6	ABs99940	ABs99940 Genomic D
30	17	10.5	2851	6	ABs99942	ABs99942 Genomic D
31	17	10.5	2851	9	ADB93093	ADB93093 Human col
32	17	10.5	2851	9	ADB93095	ADB93095 Human col
33	17	10.5	4690	4	AB124602	AB124602 Drosophill
34	17	10.5	6477	7	ADA69607	ADA69607 Rice gene
35	17	10.5	32768	2	AAK20515	AAK20515 Polynucle
36	17	10.5	54355	8	ADA02753	ADA02753 Mouse Mor
37	17	10.5	54355	9	ADB72491	ADB72491 Mouse Mor
38	17	10.5	54355	9	ADB85233	ADB85233 Mouse Mor
39	17	10.5	72149	9	ADB81173	ADB81173 ML-236b s
40	17	10.5	96596	8	ADA02504	ADA02504 Human BAC
41	17	10.5	96596	9	ADB72242	ADB72242 Human BAC
42	16	9.9	25	3	AAA68671	AAA68671 Bacterioph
43	16	9.9	176	3	AACT2838	AACT2838 Single nu
44	16	9.9	240	5	ABV25110	ABV25110 Human pro
45	16	9.9	277	5	ABV07959	ABV07959 Human pro
46	16	9.9	320	6	AB181329	AB181329 Human ova
47	16	9.9	335	5	ABV37882	ABV37882 Human pro
48	16	9.9	400	2	AAV77246	AAV77246 Staphyloc
49	16	9.9	495	4	AAH12739	AAH12739 Human cDN
50	16	9.9	565	9	ADD34087	ADD34087 Mouse mit
51	16	9.9	592	4	AAI17525	AAI17525 Probe #74
52	16	9.9	592	4	ABs62456	ABs62456 Human foe
53	16	9.9	592	4	AAI42434	AAI42434 Probe #11
54	16	9.9	592	4	ABs29789	ABs29789 Probe #82
55	16	9.9	592	4	AAK36670	AAK36670 Human bon
56	16	9.9	592	4	AAK10804	AAK10804 Human bra
57	16	9.9	592	6	ABs36328	ABs36328 Human liv
58	16	9.9	592	6	ABs10673	ABs10673 Human gen
59	16	9.9	597	5	ABV55060	ABV55060 Human pro
60	16	9.9	799	6	ABK75454	ABK75454 Bacillus
61	16	9.9	1189	4	AB126168	AB126168 Drosophill
62	16	9.9	1210	6	ABK65324	ABK65324 Arabidops
63	16	9.9	1210	7	AAV47726	AAV47726 Arabidops
64	16	9.9	1210	9	ADB31836	ADB31836 DNA encod

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c 66	16	9.9	1896	7	ACF73128	AcF73128 Stephyloc	c 123	15	9.3	186	6	ABS22398	AbS22398 Human gen
c 67	16	9.9	2212	4	AAK17132	AaH17132 Human cDN	c 124	15	9.3	196	4	AAK45376	AAK45376 Human bon
c 68	16	9.9	2295	4	AA502396	Aa502396 Human sec	c 125	15	9.3	196	4	ABS45056	AbS45056 Human liv
c 69	16	9.9	2298	6	ABV78091	AbV78091 Hypoxia-r	c 126	15	9.3	196	6	ABS19637	AbS19637 Human gen
c 70	16	9.9	2298	9	AA058485	Aa058485 Human GAT	c 127	15	9.3	199	3	AAAC02763	AAc02763 Human gen
c 71	16	9.9	2349	6	ABT07280	AbT07280 Chironomu	c 128	15	9.3	226	3	AAAC30940	AAc30940 Human sec
c 72	16	9.9	2496	6	ABK35358	AbK35358 Human cDN	c 129	15	9.3	243	3	AAAC30458	AAc30458 Human sec
c 73	16	9.9	2863	4	ABN08949	AbN08949 Human GAB	c 130	15	9.3	252	4	AAK54931	AAK54931 Human hae
c 74	16	9.9	3050	4	ABL21870	AbL21870 Drosophill	c 131	15	9.3	276	7	ABX84956	ABx84956 Corri ear-
c 75	16	9.9	3307	4	AAK62353	AAK62353 Human imm	c 132	15	9.3	294	6	ABL72956	ABl72956 Corri tass
c 76	16	9.9	3397	4	ABL26422	AbL26422 Drosophill	c 133	15	9.3	320	5	ABV68083	ABv68083 Human pro
c 77	16	9.9	3357	3	AAA47423	AaA47423 Sequence	c 134	15	9.3	357	1	AAAS50368	AAAS50368 Human pro
c 78	16	9.9	3889	4	ABL26168	AbL26168 Drosophill	c 135	15	9.3	363	4	AAAS3693	AAAS3693 DNA fragm
c 79	16	9.9	4317	4	AAH57574	AaH57574 Human bra	c 136	15	9.3	363	7	ACB34892	ACb34892 Prokaryot
c 80	16	9.9	4433	7	ABT19691	AbT19691 Aspergill	c 137	15	9.3	366	8	ACH42642	ACH42642 Human foe
c 81	16	9.9	4504	7	ABT17877	AbT17877 Aspergill	c 138	15	9.3	383	5	ABV07672	ABv07672 Human pro
c 82	16	9.9	4956	4	ABL09357	AbL09357 Drosophill	c 139	15	9.3	391	8	ACH16289	ACH16289 Human edu
c 83	16	9.9	5469	6	ABQ99271	AbQ99271 Human cod	c 140	15	9.3	396	7	ABX52082	ABx52082 Bovine ES
c 84	16	9.9	5561	3	AAA34842	AaA34842 Human ade	c 141	15	9.3	398	4	AAAL01930	AAAL01930 Human rep
c 85	16	9.9	5561	3	AAE20864	AaE20864 Human low	c 142	15	9.3	398	4	ABL97223	ABl97223 Human tes
c 86	16	9.9	5561	3	ABE29658	AbE29658 Human nuc	c 143	15	9.3	401	4	ABA72549	ABa72549 Human foe
c 87	16	9.9	6744	7	ABX14056	AbX14056 cDNA enco	c 144	15	9.3	401	4	AAI52962	AAI52962 Probe #21
c 88	16	9.9	6956	7	ACCT2031	AccT2031 BCU0720 g	c 145	15	9.3	401	4	AAK47126	AAK47126 Human bon
c 89	16	9.9	7116	4	ABL26196	AbL26196 Drosophill	c 146	15	9.3	401	4	AAK20873	AAK20873 Human bra
c 90	16	9.9	10470	2	AAV74331	AaV74331 Stephyloc	c 147	15	9.3	401	4	ABS46884	ABs46884 Human liv
c 91	16	9.9	15561	4	AAE25341	AaE25341 Nucleotid	c 148	15	9.3	401	6	AAAS21353	AAAS21353 Human gen
c 92	16	9.9	15117	4	AAH84829	AaH84829 Human imm	c 149	15	9.3	402	5	AAAS38813	AAAS38813 Novel hum
c 93	16	9.9	22421	3	AAA34844	AaA34844 Human ade	c 150	15	9.3	402	5	AAAS73759	AAAS73759 Human gen
c 94	16	9.9	22421	3	AAE20966	AaE20966 Human low	c 151	15	9.3	402	5	ADC31885	ADC31885 DNA enco
c 95	16	9.9	22421	7	ABE29660	AbE29660 Human nuc	c 152	15	9.3	408	7	ABX39009	ABx39009 Bovine ES
c 96	16	9.9	32127	4	AAI99255	AaI99255 Human exc	c 153	15	9.3	421	5	ABV10980	ABv10980 Human pro
c 97	16	9.9	32127	5	AAI63605	AaI63605 Human kid	c 154	15	9.3	423	2	AAK14444	AAK14444 H. pylori
c 98	16	9.9	32167	7	AAU56075	AaU56075 Human SNL	c 155	15	9.3	433	3	AAAC26430	AAAC26430 Human sec
c 99	16	9.9	32767	9	AD802437	Ad802437 Human SNL	c 156	15	9.3	443	5	AAV37601	AAV37601 Human pro
c 100	16	9.9	32767	9	AD872176	Ad872176 Human SNL	c 157	15	9.3	447	2	AAAT83757	AAAT83757 Human sec
c 101	16	9.9	32767	9	AD882920	Ad882920 Human SNL	c 158	15	9.3	451	8	ACH14509	ACH14509 Human adu
c 102	16	9.9	35633	4	ABL09356	AbL09356 Drosophill	c 159	15	9.3	457	4	AAK32324	AAK32324 Human bon
c 103	16	9.9	43576	3	AAA68609	AaA68609 Bacteriop	c 160	15	9.3	457	6	ABS32030	ABs32030 Human liv
c 104	16	9.9	72215	4	AAK86832	AaK86832 Human imm	c 161	15	9.3	457	6	ACH24536	ACH24536 Human adu
c 105	16	9.9	110000	2	AAV58840_1	AAV58840_1 Continuation (2 of	c 162	15	9.3	467	8	AAAC24536	AAAC24536 Human adu
c 106	16	9.9	110000	2	AAV21209_10	AAV21209_10 Continuation (11 of	c 163	15	9.3	471	2	AAAC32978	AAAC32978 S. aureus
c 107	16	9.9	110000	6	ABK08336_03	ABK08336_03 Continuation (13 of	c 164	15	9.3	488	6	ABN75368	ABN75368 Human ORF
c 108	16	9.9	110000	6	ABA03041_12	ABA03041_12 Continuation (13 of	c 165	15	9.3	508	2	AAK30869	AAK30869 Streptoco
c 109	16	9.9	334462	9	ADC24763	AdC24763 Human wll	c 166	15	9.3	512	6	ABN61185	ABN61185 Human can
c 110	16	9.9	335199	9	ADC24703	AdC24703 Human wll	c 167	15	9.3	528	5	AAAS3765	AAAS3765 Human cDN
c 111	15	9.3	29	2	AAI11651	AaI11651 HePepes st	c 168	15	9.3	540	5	ABV08906	ABv08906 Human pro
c 112	15	9.3	33	6	AAI43838	AaI43838 Human cit	c 169	15	9.3	549	3	AAAC93947	AAAC93947 Cat flea
c 113	15	9.3	41	6	AAI43840	AaI43840 Human cit	c 170	15	9.3	552	4	ABA60008	ABa60008 Human foe
c 114	15	9.3	156	7	ACA54965	AaA54965 Stephyloc	c 171	15	9.3	552	4	AAI39881	AAI39881 Probe #85
c 115	15	9.3	156	7	ACA16693	AaC16693 Prokaryot	c 172	15	9.3	552	4	AAK34158	AAK34158 Human bon
c 116	15	9.3	186	4	AAI26290	AaI26290 Probe #16	c 173	15	9.3	552	4	AAK08279	AAK08279 Human bra
c 117	15	9.3	186	4	ABV74032	AbV74032 Human foe	c 174	15	9.3	552	4	ABS33954	ABS33954 Human liv
c 118	15	9.3	186	4	AAI54481	AaI54481 Probe #23	c 175	15	9.3	552	6	ABSO8919	ABSO8919 Human gen
c 119	15	9.3	186	4	ABA39093	AbA39093 Probe #17	c 176	15	9.3	555	2	AAAT98705	AAAT98705 DNA enco
c 120	15	9.3	186	4	AAK48653	AaK48653 Human bon	c 177	15	9.3	555	2	AAK58477	AAK58477 Human imm
c 121	15	9.3	186	4	AAK22485	AaK22485 Human bra	c 178	15	9.3	556	5	AAV77296	AAV77296 DNA enco

c 179	15	9.3	564	8	ADA29537	AdA29537 DNA encod
c 180	15	9.3	580	6	ABK33576	AbK33576 Human eos
c 181	15	9.3	585	5	AA582260	AA582260 DNA encod
c 182	15	9.3	590	6	ABN65863	ABn65863 Human can
c 183	15	9.3	591	4	AA117113	AA117113 Probe #70
c 184	15	9.3	591	4	ABA61534	ABa61534 Human foe
c 185	15	9.3	591	4	AA141443	AA141443 Probe #10
c 186	15	9.3	591	4	ABA29243	ABa29243 Probe #77
c 187	15	9.3	591	4	AAK35728	AAK35728 Human bon
c 188	15	9.3	591	4	AAK09834	AAK09834 Human bra
c 189	15	9.3	591	4	AB535446	AB535446 Human liv
c 190	15	9.3	591	6	AB509996	AB509996 Human gen
c 191	15	9.3	599	4	AAK72878	AAK72878 Human imm
c 192	15	9.3	599	4	AAK72880	AAK72880 Human imm
c 193	15	9.3	599	4	AAK72879	AAK72879 Human imm
c 194	15	9.3	603	4	AAK57096	AAK57096 Human imm
c 195	15	9.3	605	6	ABK62139	ABK62139 Rat seque
c 196	15	9.3	605	9	ADB55108	ADB55108 Tox1city-
c 197	15	9.3	605	9	ADB49636	ADB49636 Primary r
c 198	15	9.3	637	6	ABQ31795	ABq31795 Oligonuc1
c 199	15	9.3	637	6	ABQ31794	ABq31794 Oligonuc1
c 200	15	9.3	645	5	ABV58266	ABV58266 Human pro
c 201	15	9.3	654	5	AA573760	AA573760 DNA encod
c 202	15	9.3	662	3	AAA10744	AAA10744 Fragment
c 203	15	9.3	663	4	AAH07307	AAH07307 Human cDN
c 204	15	9.3	672	7	ABQ82869	ABq82869 Human lun
c 205	15	9.3	678	6	ABN69374	ABn69374 Streptoco
c 206	15	9.3	681	6	AB212468	AB212468 Arabidops
c 207	15	9.3	703	4	AAH07260	AAH07260 Human cDN
c 208	15	9.3	708	6	ABO69482	ABO69482 Listeria
c 209	15	9.3	708	9	ADD34749	ADD34749 Mouse mit
c 210	15	9.3	713	7	ABZ51801	ABz51801 Aspergill1
c 211	15	9.3	719	5	ABV23482	ABv23482 Human pro
c 212	15	9.3	719	5	ABV29340	ABv29340 Human pro
c 213	15	9.3	720	7	ACA29150	ACA29150 Prokaryot
c 214	15	9.3	729	2	AAK99516	AAK99516 Nucleic a
c 215	15	9.3	777	3	ACA44445	ACA44445 Arabidops
c 216	15	9.3	808	4	AAH04147	AAH04147 Human cDN
c 217	15	9.3	822	4	ABU09121	ABu09121 Drosoph11
c 218	15	9.3	822	6	ABO68312	ABo68312 Listeria
c 219	15	9.3	834	4	ACF74010	ACF74010 Stephyloc
c 220	15	9.3	851	6	ABK66888	ABK66888 Helicobac
c 221	15	9.3	855	6	ABO67710	ABo67710 Listeria
c 222	15	9.3	873	6	ABO81541	ABo81541 Gene up-r
c 223	15	9.3	915	7	ABK07572	ABK07572 S. pneumo
c 224	15	9.3	948	8	ACD06180	ACD06180 Human cDN
c 225	15	9.3	961	2	AAK14562	AAK14562 H. pylori
c 226	15	9.3	963	7	ACA21513	ACA21513 Prokaryot
c 227	15	9.3	992	2	AAV41892	AAV41892 Alternati
c 228	15	9.3	1000	2	AAV27350	AAV27350 Streptoco
c 229	15	9.3	1000	6	ABO84818	ABo84818 S. pneumo
c 230	15	9.3	1000	9	ADC45134	ADC45134 S. pneumo
c 231	15	9.3	1002	5	AA568799	AA568799 DNA encod
c 232	15	9.3	1005	7	ABK07806	ABK07806 S. pneumo
c 233	15	9.3	1006	4	AA137573	AA137573 Human mus
c 234	15	9.3	1006	7	ABK60561	ABK60561 cDNA enc
c 235	15	9.3	1008	4	AA551981	AA551981 Stephyloc
c 236	15	9.3	1008	6	ABN70591	ABn70591 Streptoco
c 237	15	9.3	1008	6	ABN71389	ABn71389 Streptoco
c 238	15	9.3	1008	7	ACF73799	ACF73799 Stephyloc
c 239	15	9.3	1011	4	AA554805	AA554805 Stephyloc
c 240	15	9.3	1011	6	ABA91332	ABa91332 Streptoco
c 241	15	9.3	1011	6	ABA91332	ABa91332 Streptoco
c 242	15	9.3	1011	6	ABA91328	ABa91328 Streptoco
c 243	15	9.3	1011	6	ABA91328	ABa91328 Streptoco
c 244	15	9.3	1011	6	ABA91331	ABa91331 Streptoco
c 245	15	9.3	1011	6	ABA91248	ABa91248 Streptoco
c 246	15	9.3	1011	6	ABA91251	ABa91251 Streptoco
c 247	15	9.3	1011	6	ABA91252	ABa91252 Streptoco
c 248	15	9.3	1011	7	ACA19943	ACA19943 Prokaryot
c 249	15	9.3	1011	7	ACA50325	ACA50325 Prokaryot
c 250	15	9.3	1011	6	ACN46200	ACN46200 Bovine em
c 251	15	9.3	1012	7	AAV74774	AAV74774 Bovine em
c 252	15	9.3	1018	3	AA559581	AA559581 Human sec
c 253	15	9.3	1020	7	ACA47671	ACA47671 Prokaryot
c 254	15	9.3	1035	6	ABN69737	ABn69737 Streptoco
c 255	15	9.3	1035	8	ACD06179	ACD06179 Human cDN
c 256	15	9.3	1053	6	ABQ70392	ABq70392 Listeria
c 257	15	9.3	1068	7	ACF67989	ACF67989 Phototrab
c 258	15	9.3	1079	2	AAV41891	AAV41891 Alternati
c 259	15	9.3	1080	4	AA555858	AA555858 Streptoco
c 260	15	9.3	1080	4	AA555434	AA555434 Streptoco
c 261	15	9.3	1080	7	ACA50132	ACA50132 Prokaryot
c 262	15	9.3	1083	7	ACA22586	ACA22586 Prokaryot
c 263	15	9.3	1088	2	AAV41890	AAV41890 Nucleotid
c 264	15	9.3	1122	7	ACF72673	ACF72673 Stephyloc
c 265	15	9.3	1125	2	AAO70705	AAO70705 Plasmid r
c 266	15	9.3	1125	4	AA666140	AA666140 Streptoco
c 267	15	9.3	1164	7	ADA89862	ADA89862 Stephyloc
c 268	15	9.3	1164	7	ADA89858	ADA89858 Stephyloc
c 269	15	9.3	1182	6	ABZ14118	ABz14118 Arabidops
c 270	15	9.3	1221	2	AAZ96375	AAZ96375 S. pneumo
c 271	15	9.3	1230	6	ABN67067	ABn67067 Streptoco
c 272	15	9.3	1272	7	ACA54186	ACA54186 Prokaryot
c 273	15	9.3	1275	6	ABQ68879	ABQ68879 Listeria
c 274	15	9.3	1288	5	AA688104	AA688104 Human FLE
c 275	15	9.3	1296	9	ADC93798	ADC93798 E. faeciu
c 276	15	9.3	1339	6	AB217389	AB217389 Arabidops
c 277	15	9.3	1341	6	ABQ70500	ABQ70500 Listeria
c 278	15	9.3	1344	3	AA637617	AA637617 Arabidops
c 279	15	9.3	1347	6	ABA91327	ABa91327 Streptoco
c 280	15	9.3	1353	7	ACA36751	ACA36751 Prokaryot
c 281	15	9.3	1355	5	AA577302	AA577302 DNA encod
c 282	15	9.3	1383	7	ACA22605	ACA22605 Prokaryot
c 283	15	9.3	1389	6	AA143835	AA143835 Human cit
c 284	15	9.3	1394	3	AA654934	AA654934 Arabidops
c 285	15	9.3	1396	3	AA635657	AA635657 Arabidops
c 286	15	9.3	1422	4	AA551752	AA551752 Stephyloc
c 287	15	9.3	1422	7	ACF74255	ACF74255 Stephyloc
c 288	15	9.3	1425	4	AA554921	AA554921 Stephyloc
c 289	15	9.3	1425	7	ACA20267	ACA20267 Prokaryot
c 290	15	9.3	1425	7	ACA28992	ACA28992 Prokaryot
c 291	15	9.3	1435	1	AAV70101	AAV70101 Sequence
c 292	15	9.3	1497	9	ADC08302	ADC08302 Rice DNA

c 293	15	9.3	1526	6	ABO68969	Abg68969	listeria
c 294	15	9.3	1549	7	ABX70791	Abx70791	Novel hum
c 295	15	9.3	1582	9	ADCO7895	Adc07895	Rice DNA
c 296	15	9.3	1660	4	AAf32054	Aaf32054	Carnation
c 297	15	9.3	1660	6	ABK88372	Abk88372	Carnation
c 298	15	9.3	1660	5	AA880734	Aa880734	DNA encod
c 299	15	9.3	1671	4	AAH99737	Aah99737	Human pro
c 300	15	9.3	1672	6	ABH94904	Abh94904	Human nov
c 301	15	9.3	1689	7	ABH13416	Abh13416	Breast sp
c 302	15	9.3	1737	4	AAAC84891	Aaac84891	Human SEC
c 303	15	9.3	1743	6	ABK53362	Abk53362	Human cDN
c 304	15	9.3	1745	7	ADA52935	Ada52935	Human cod
c 305	15	9.3	1760	4	AAH17483	Aah17483	Mouse sec
c 306	15	9.3	1762	3	AAH26385	Aah26385	Human sec
c 307	15	9.3	1763	3	AAH26452	Aah26452	Human sec
c 308	15	9.3	1769	2	AAH21170	Aah21170	Malize elo
c 309	15	9.3	1795	7	ACD19480	Acid19480	cDNA enco
c 310	15	9.3	1812	3	ADG78456	Adg78456	Human PRO
c 311	15	9.3	1812	6	ABH90612	Abh90612	Human pol
c 312	15	9.3	1815	2	AAH52238	Aah52238	Protein P
313	15	9.3	1815	4	AAE72296	Aae72296	Human PRO
314	15	9.3	1815	4	AAH45934	Aah45934	Human DNA
315	15	9.3	1815	7	ABX78537	Abx78537	Human PRO
316	15	9.3	1815	7	ACA59008	Aca59008	Human PRO
317	15	9.3	1815	7	ACA75509	Aca75509	Novel hum
318	15	9.3	1815	7	ACA70989	AcA70989	Human sec
319	15	9.3	1815	7	ACB87517	AcB87517	Human sec
320	15	9.3	1815	7	ACCB6903	AcCB6903	Human sec
321	15	9.3	1815	7	ACD04076	AcD04076	Human sec
322	15	9.3	1815	7	ACA69407	Aca69407	cDNA enco
323	15	9.3	1815	7	ACA90252	AcA90252	Novel hum
324	15	9.3	1815	7	ACA58405	Aca58405	cDNA enco
325	15	9.3	1815	7	ACCB9359	AcCB9359	Human sec
326	15	9.3	1815	7	ACA98150	AcA98150	Novel hum
327	15	9.3	1815	7	ACA93792	AcA93792	Human sec
328	15	9.3	1815	7	ACD15185	AcD15185	Human sec
329	15	9.3	1815	7	ACD08772	AcD08772	Human sec
330	15	9.3	1815	7	ACCB6692	AcCB6692	Human sec
331	15	9.3	1815	7	ACF15413	AcF15413	Human sec
332	15	9.3	1815	7	ACA72780	AcA72780	Human PRO
333	15	9.3	1815	7	ACD02952	AcD02952	Novel hum
334	15	9.3	1815	7	ACD01167	AcD01167	Novel hum
335	15	9.3	1815	7	ACA91959	Aca91959	Novel hum
336	15	9.3	1815	7	ACA60112	Aca60112	Human cDN
337	15	9.3	1815	7	ACA89384	AcA89384	cDNA enco
338	15	9.3	1815	7	ACA73394	AcA73394	Human sec
339	15	9.3	1815	7	ACA05709	Aca05709	Human sec
340	15	9.3	1815	7	ACA66543	Aca66543	cDNA enco
341	15	9.3	1815	7	ACD07512	AcD07512	Novel hum
342	15	9.3	1815	7	ACF20118	AcF20118	Human sec
343	15	9.3	1815	7	ACF19504	AcF19504	Human sec
344	15	9.3	1815	7	ACD21792	AcD21792	Human sec
345	15	9.3	1815	7	ACF12957	AcF12957	Human sec
346	15	9.3	1815	7	ACD25060	AcD25060	Human sec
347	15	9.3	1815	7	ACF00109	AcF00109	Human sec
348	15	9.3	1815	7	ACA72166	Aca72166	Novel hum
349	15	9.3	1815	7	ACD04690	AcD04690	Novel hum
350	15	9.3	1815	7	ACD18151	AcD18151	Human sec
351	15	9.3	1815	7	ACD08158	AcD08158	Human sec
352	15	9.3	1815	7	ABX71560	Abx71560	Human cDN
353	15	9.3	1815	7	ACB88592	AcB88592	Novel hum
354	15	9.3	1815	7	ACA70034	AcA70034	Human sec
355	15	9.3	1815	7	ACD12256	AcD12256	Human sec
356	15	9.3	1815	7	ACF74171	AcF74171	Human sec
357	15	9.3	1815	7	ACD15799	AcD15799	Human sec
358	15	9.3	1815	7	ACD25367	AcD25367	Novel hum
359	15	9.3	1815	7	ACD17844	AcD17844	Human sec
360	15	9.3	1815	7	ACCB8131	AcCB8131	Human sec
361	15	9.3	1815	7	ACD1485	AcD1485	Human sec
362	15	9.3	1815	7	ACD18552	AcD18552	Human sec
363	15	9.3	1815	7	ACH06892	ACH06892	Human sec
364	15	9.3	1815	7	ABX98162	Abx98162	Human cDN
365	15	9.3	1815	7	ACD13913	AcD13913	Human PRO
366	15	9.3	1815	7	ACD09693	AcD09693	Human PRO
367	15	9.3	1815	7	ACCB8438	AcCB8438	Human sec
368	15	9.3	1815	7	ABX7550	Abx7550	Human cDN
369	15	9.3	1815	7	ABX7550	Abx7550	Human cDN
370	15	9.3	1815	7	ABX97753	Abx97753	Human PRO
371	15	9.3	1815	7	ACA97229	Aca97229	Novel hum
372	15	9.3	1815	7	ACA57692	AcA57692	Human PRO
373	15	9.3	1815	7	ACD14220	AcD14220	Human PRO
374	15	9.3	1815	7	ACC91003	AcC91003	Human sec
375	15	9.3	1815	7	ACCB8745	AcCB8745	Human sec
376	15	9.3	1815	7	ACD06942	AcD06942	Human PRO
377	15	9.3	1815	7	ACA67393	AcA67393	Human PRO
378	15	9.3	1815	7	ACCB1448	AcCB1448	Human sec
379	15	9.3	1815	7	ACCB9052	AcCB9052	Human sec
380	15	9.3	1815	7	ACCB6408	AcCB6408	Human sec
381	15	9.3	1815	7	ACCB9666	AcCB9666	Human sec
382	15	9.3	1815	7	ACC92845	AcC92845	Human sec
383	15	9.3	1815	7	ACA72473	AcA72473	Human PRO
384	15	9.3	1815	7	ACB88991	AcB88991	Human sec
385	15	9.3	1815	7	ACA68921	AcA68921	Human sec
386	15	9.3	1815	7	ACA96870	AcA96870	Human sec
387	15	9.3	1815	7	ACA90866	AcA90866	Novel hum
388	15	9.3	1815	7	ACA70648	AcA70648	Human sec
389	15	9.3	1815	7	ACA95158	AcA95158	Novel hum
390	15	9.3	1815	7	ACCB6101	AcCB6101	Human sec
391	15	9.3	1815	7	ACCB9973	AcCB9973	Human sec
392	15	9.3	1815	7	ACD12581	AcD12581	Human sec
393	15	9.3	1815	7	ACF19811	AcF19811	Human sec
394	15	9.3	1815	7	ABX76755	Abx76755	Human sec
395	15	9.3	1815	7	ABX96129	Abx96129	Human PRO
396	15	9.3	1815	7	ACA73087	AcA73087	Novel hum
397	15	9.3	1815	7	ACA05450	Aca05450	cDNA enco
398	15	9.3	1815	7	ACA68630	Aca68630	Novel hum
399	15	9.3	1815	7	ACA74474	AcA74474	cDNA enco
400	15	9.3	1815	7	ACA70341	AcA70341	Human sec
401	15	9.3	1815	7	ACD14527	AcD14527	Human PRO
402	15	9.3	1815	7	ACD20117	AcD20117	Human PRO
403	15	9.3	1815	7	ACA68199	AcA68199	Novel hum
404	15	9.3	1815	7	ABX98664	Abx98664	Novel hum
405	15	9.3	1815	7	ACCB1141	AcCB1141	Human sec

406	15	9.3	1815	7	ACA95465	Ac95465	Novel	hum	463	15	9.3	1815	8	ACF41106	AcF41106	Human	sec
407	15	9.3	1815	7	ACD04383	AcD04383	Novel	hum	464	15	9.3	1815	8	ACF15720	AcF15720	Human	sec
408	15	9.3	1815	7	ACC87824	AcC87824	Human	sec	465	15	9.3	1815	8	ACF16027	AcF16027	Human	sec
409	15	9.3	1815	7	ACF12486	AcF12486	Human	sec	466	15	9.3	1815	8	ACD31854	AcD31854	Human	sec
410	15	9.3	1815	7	ACA96201	AcA96201	Human	PRO	467	15	9.3	1815	8	ACF18662	AcF18662	Human	sec
411	15	9.3	1815	7	ACA64975	AcA64975	Human	PRO	468	15	9.3	1815	8	ACF09109	AcF09109	Human	sec
412	15	9.3	1815	7	ACA73701	AcA73701	Human	sec	469	15	9.3	1815	8	ACF78230	AcF78230	Human	sec
413	15	9.3	1815	7	ACA74113	AcA74113	Novel	hum	470	15	9.3	1815	8	ACF51829	AcF51829	Human	sec
414	15	9.3	1815	7	ACA6508	AcA6508	Human	PRO	471	15	9.3	1815	8	ACF26316	AcF26316	Human	sec
415	15	9.3	1815	7	ACD10614	AcD10614	cDNA	enco	472	15	9.3	1815	8	ACF24109	AcF24109	Human	sec
416	15	9.3	1815	7	ACC91310	AcC91310	Human	sec	473	15	9.3	1815	8	ACF63420	AcF63420	Human	sec
417	15	9.3	1815	7	ACD02645	AcD02645	cDNA	enco	474	15	9.3	1815	8	ACF50294	AcF50294	Human	sec
418	15	9.3	1815	7	ACC87210	AcC87210	Human	sec	475	15	9.3	1815	8	ACF07765	AcF07765	Human	sec
419	15	9.3	1815	7	ACC85794	AcC85794	Human	sec	476	15	9.3	1815	8	ACF13571	AcF13571	Human	sec
420	15	9.3	1815	7	ACA65282	AcA65282	Human	PRO	477	15	9.3	1815	8	ACD41497	AcD41497	Human	sec
421	15	9.3	1815	7	ACA94099	AcA94099	Human	sec	478	15	9.3	1815	8	ACF31910	AcF31910	Human	sec
422	15	9.3	1815	7	ACA97843	AcA97843	Human	PRO	479	15	9.3	1815	8	ACF23188	AcF23188	Human	sec
423	15	9.3	1815	7	ACA91345	AcA91345	Novel	hum	480	15	9.3	1815	8	ACF31878	AcF31878	Human	sec
424	15	9.3	1815	7	ACA90559	AcA90559	Novel	hum	481	15	9.3	1815	8	ACD45400	AcD45400	Human	sec
425	15	9.3	1815	7	ACD16106	AcD16106	Human	sec	482	15	9.3	1815	8	ACF53057	AcF53057	Human	sec
426	15	9.3	1815	7	ACD17267	AcD17267	Human	sec	483	15	9.3	1815	8	ACF27237	AcF27237	Human	sec
427	15	9.3	1815	7	ACC91924	AcC91924	Human	sec	484	15	9.3	1815	8	ACF45075	AcF45075	Human	sec
428	15	9.3	1815	7	ACA74781	AcA74781	cDNA	enco	485	15	9.3	1815	8	ACF29693	AcF29693	Human	sec
429	15	9.3	1815	7	ACA91652	AcA91652	Human	PRO	486	15	9.3	1815	8	ACD89769	AcD89769	Human	sec
430	15	9.3	1815	7	ACA71296	AcA71296	Human	sec	487	15	9.3	1815	8	ACD84550	AcD84550	Human	sec
431	15	9.3	1815	7	ACC90696	AcC90696	Human	sec	488	15	9.3	1815	8	ACD98710	AcD98710	Human	PRO
432	15	9.3	1815	7	ACA65706	AcA65706	cDNA	enco	489	15	9.3	1815	8	ACF77002	AcF77002	Human	sec
433	15	9.3	1815	7	ACA54920	AcA54920	Novel	hum	490	15	9.3	1815	8	ACF76695	AcF76695	Human	sec
434	15	9.3	1815	7	ACA94851	AcA94851	cDNA	enco	491	15	9.3	1815	8	ACF49680	AcF49680	Human	sec
435	15	9.3	1815	7	ACD16413	AcD16413	Human	sec	492	15	9.3	1815	8	ACD09386	AcD09386	Human	sec
436	15	9.3	1815	7	ABD15492	AbD15492	Human	sec	493	15	9.3	1815	8	ACD08465	AcD08465	Human	sec
437	15	9.3	1815	7	ABX16595	AbX16595	Human	CDN	494	15	9.3	1815	8	ACD08465	AcD08465	Human	sec
438	15	9.3	1815	7	ACA97536	AcA97536	Human	PRO	495	15	9.3	1815	8	ACF12179	AcF12179	Human	sec
439	15	9.3	1815	7	ACA98985	AcA98985	Novel	hum	496	15	9.3	1815	8	ACC94687	AcC94687	Human	sec
440	15	9.3	1815	7	ACC91617	AcC91617	Human	sec	497	15	9.3	1815	8	ACD22406	AcD22406	Human	sec
441	15	9.3	1815	7	ACD11028	AcD11028	Novel	hum	498	15	9.3	1815	8	ACF51106	AcF51106	Human	sec
442	15	9.3	1815	7	ACD14878	AcD14878	Human	sec	499	15	9.3	1815	8	ACC97201	AcC97201	Human	sec
443	15	9.3	1815	7	ACD19755	AcD19755	Human	sec	500	15	9.3	1815	8	ADL18197	AdL18197	Human	sec
444	15	9.3	1815	7	ACD11642	AcD11642	Human	sec	501	15	9.3	1815	8	ACD66902	AcD66902	Human	CDN
445	15	9.3	1815	7	ACC95771	AcC95771	Human	sec	502	15	9.3	1815	8	ACC92231	AcC92231	Human	sec
446	15	9.3	1815	7	ACF16034	AcF16034	Human	sec	503	15	9.3	1815	8	ACF13878	AcF13878	Human	sec
447	15	9.3	1815	7	ACF02452	AcF02452	Human	sec	504	15	9.3	1815	8	ACF14185	AcF14185	Human	sec
448	15	9.3	1815	7	ACF02759	AcF02759	Human	sec	505	15	9.3	1815	8	ACF09416	AcF09416	Human	sec
449	15	9.3	1815	7	ACF21346	AcF21346	Human	sec	506	15	9.3	1815	8	ACD45707	AcD45707	Human	sec
450	15	9.3	1815	7	ACF10030	AcF10030	Human	sec	507	15	9.3	1815	8	ACD47856	AcD47856	Human	sec
451	15	9.3	1815	7	ACF77923	AcF77923	Human	sec	508	15	9.3	1815	8	ACD87927	AcD87927	Human	sec
452	15	9.3	1815	7	ACD46628	AcD46628	Human	sec	509	15	9.3	1815	8	ACF25395	AcF25395	Human	sec
453	15	9.3	1815	7	ACD49391	AcD49391	Human	sec	510	15	9.3	1815	8	ACF29079	AcF29079	Human	sec
454	15	9.3	1815	7	ACF28158	AcF28158	Human	sec	511	15	9.3	1815	8	ACD84857	AcD84857	Human	sec
455	15	9.3	1815	7	ACD88848	AcD88848	Human	sec	512	15	9.3	1815	8	ACD89336	AcD89336	Human	PRO
456	15	9.3	1815	7	ACD84243	AcD84243	Human	PRO	513	15	9.3	1815	8	ACD87927	AcD87927	Human	sec
457	15	9.3	1815	7	ACD99017	AcD99017	cDNA	enco	514	15	9.3	1815	8	ACF30614	AcF30614	Human	sec
458	15	9.3	1815	7	ADA77771	AdA77771	Human	sec	515	15	9.3	1815	8	ACF32217	AcF32217	Human	sec
459	15	9.3	1815	7	ACF48759	AcF48759	Human	sec	516	15	9.3	1815	8	ACH11877	AcH11877	CDN	enco
460	15	9.3	1815	7	ADB29341	AdB29341	Human	sec	517	15	9.3	1815	8	ACH12184	AcH12184	CDN	enco
461	15	9.3	1815	7	ACD09079	AcD09079	Human	sec	518	15	9.3	1815	8	ACD40576	AcD40576	Human	sec
462	15	9.3	1815	7	ACF11872	AcF11872	Human	sec	519	15	9.3	1815	8	ACF18048	AcF18048	Human	sec

520	15	9.3	1815	8	ACF08495	Acf08495	Human	sec	577	15	9.3	1815	8	ACF21039	Acf21039	Human	sec
521	15	9.3	1815	8	ACF31296	Acf31296	Human	sec	578	15	9.3	1815	8	ACF20732	Acf20732	Human	sec
522	15	9.3	1815	8	ACF52136	Acf52136	Human	sec	579	15	9.3	1815	8	ACD47549	Acad47549	Human	sec
523	15	9.3	1815	8	ACD50005	Acad50005	Human	sec	580	15	9.3	1815	8	ACF47531	Acf47531	Human	sec
524	15	9.3	1815	8	ACF38708	Acf38708	Human	sec	581	15	9.3	1815	8	ACF53364	Acf53364	Human	sec
525	15	9.3	1815	8	ACF26623	Acf26623	Human	sec	582	15	9.3	1815	8	ACD86399	Acad86399	Human	sec
526	15	9.3	1815	8	ACF24723	Acf24723	Human	sec	583	15	9.3	1815	8	ACH04947	ACH04947	Human	sec
527	15	9.3	1815	8	ACF46303	Acf46303	Human	sec	584	15	9.3	1815	8	ACF44444	Acf44444	Human	sec
528	15	9.3	1815	8	ACF27851	Acf27851	Human	sec	585	15	9.3	1815	8	AD442317	Ad442317	Human	sec
529	15	9.3	1815	8	ACD89155	Acad89155	Human	sec	586	15	9.3	1815	8	AD481290	Ad481290	Human	sec
530	15	9.3	1815	8	ACF63727	Acf63727	Human	sec	587	15	9.3	1815	8	ACD22099	Acad22099	Human	sec
531	15	9.3	1815	8	ACF60367	Acf60367	Human	sec	588	15	9.3	1815	8	ACD24446	Acad24446	Human	sec
532	15	9.3	1815	8	ACH12491	ACH12491	cDNA	encc	589	15	9.3	1815	8	ACD39649	Acad39649	Human	sec
533	15	9.3	1815	8	ACH09914	ACH09914	Human	sec	590	15	9.3	1815	8	ACD39956	Acad39956	cDNA	encc
534	15	9.3	1815	8	ACH03769	ACH03769	Human	sec	591	15	9.3	1815	8	ACF13264	Acf13264	Human	sec
535	15	9.3	1815	8	ACD10307	Acad10307	Human	sec	592	15	9.3	1815	8	ACF03066	Acf03066	Human	sec
536	15	9.3	1815	8	ACD11949	Acad11949	Human	sec	593	15	9.3	1815	8	ACD23241	Acad23241	Human	sec
537	15	9.3	1815	8	ACD83063	Acad83063	Human	PRO	594	15	9.3	1815	8	ACF78537	Acf78537	Human	PRO
538	15	9.3	1815	8	ACF42334	Acf42334	Human	sec	595	15	9.3	1815	8	ACH11238	ACH11238	Human	sec
539	15	9.3	1815	8	ADA16172	Ada16172	Human	sec	596	15	9.3	1815	8	ACF50601	Acf50601	Human	sec
540	15	9.3	1815	8	ACH18355	ACH18355	Human	sec	597	15	9.3	1815	8	ACF34096	Acf34096	Human	sec
541	15	9.3	1815	8	ACF02145	Acf02145	Human	sec	598	15	9.3	1815	8	ACD46321	Acad46321	Human	sec
542	15	9.3	1815	8	ACF21653	Acf21653	Human	sec	599	15	9.3	1815	8	ACD48163	Acad48163	Human	sec
543	15	9.3	1815	8	ACF10337	Acf10337	Human	sec	600	15	9.3	1815	8	ACF27544	Acf27544	Human	sec
544	15	9.3	1815	8	ACF33789	Acf33789	Human	sec	601	15	9.3	1815	8	ACD24416	Acad24416	Human	sec
545	15	9.3	1815	8	ACF44751	Acf44751	Human	sec	602	15	9.3	1815	8	ACD85471	Acad85471	Human	sec
546	15	9.3	1815	8	ACD90383	Acad90383	Human	sec	603	15	9.3	1815	8	ACD90076	Acad90076	Human	sec
547	15	9.3	1815	8	ACD90996	Acad90996	Human	sec	604	15	9.3	1815	8	ACD83629	Acad83629	Human	PRO
548	15	9.3	1815	8	ACF30307	Acf30307	Human	sec	605	15	9.3	1815	8	ACH07151	ACH07151	Human	sec
549	15	9.3	1815	8	ACD87006	Acad87006	Human	sec	606	15	9.3	1815	8	ACH07438	ACH07438	Human	sec
550	15	9.3	1815	8	ACF60060	Acf60060	Human	sec	607	15	9.3	1815	8	ACH07458	ACH07458	Human	sec
551	15	9.3	1815	8	ACF46610	Acf46610	Human	sec	608	15	9.3	1815	8	ACH08072	ACH08072	Human	sec
552	15	9.3	1815	8	ACF73467	Acf73467	Human	sec	609	15	9.3	1815	8	ACH11263	ACH11263	cDNA	encc
553	15	9.3	1815	8	ADA79563	Ada79563	Human	sec	610	15	9.3	1815	8	ACH11570	ACH11570	cDNA	encc
554	15	9.3	1815	8	ACF17127	Acf17127	Human	sec	611	15	9.3	1815	8	ACH10221	ACH10221	Human	sec
555	15	9.3	1815	8	ACF22881	Acf22881	Human	sec	612	15	9.3	1815	8	ACF01224	Acf01224	Human	sec
556	15	9.3	1815	8	ACF07881	Acf07881	Human	sec	613	15	9.3	1815	8	ACF40799	Acf40799	Human	sec
557	15	9.3	1815	8	ACF08188	Acf08188	Human	sec	614	15	9.3	1815	8	ACD24139	Acad24139	Human	sec
558	15	9.3	1815	8	ACF40492	Acf40492	Human	sec	615	15	9.3	1815	8	ACD31240	Acad31240	Human	sec
559	15	9.3	1815	8	ACF53671	Acf53671	Human	sec	616	15	9.3	1815	8	ACF17741	Acf17741	Human	sec
560	15	9.3	1815	8	ACD46935	Acad46935	Human	sec	617	15	9.3	1815	8	ACF32524	Acf32524	Human	sec
561	15	9.3	1815	8	ACF47838	Acf47838	Human	sec	618	15	9.3	1815	8	ACF40185	Acf40185	Human	sec
562	15	9.3	1815	8	ACF47838	Acf47838	Human	sec	619	15	9.3	1815	8	ACF48145	Acf48145	Human	sec
563	15	9.3	1815	8	ACF45996	Acf45996	Human	sec	620	15	9.3	1815	8	ACF38094	Acf38094	Human	sec
564	15	9.3	1815	8	ACD86085	Acad86085	Human	sec	621	15	9.3	1815	8	ACF25030	Acf25030	Human	sec
565	15	9.3	1815	8	ACF52443	Acf52443	Human	sec	622	15	9.3	1815	8	ACF26930	Acf26930	Human	sec
566	15	9.3	1815	8	ACF52750	Acf52750	Human	sec	623	15	9.3	1815	8	ACF29386	Acf29386	Human	sec
567	15	9.3	1815	8	ACF64743	Acf64743	Human	sec	624	15	9.3	1815	8	ACD87620	Acad87620	Human	sec
568	15	9.3	1815	8	ACF76388	Acf76388	Human	sec	625	15	9.3	1815	8	ACF76081	Acf76081	Human	sec
569	15	9.3	1815	8	ACF61288	Acf61288	Human	sec	626	15	9.3	1815	8	ACF49373	Acf49373	Human	sec
570	15	9.3	1815	8	ACF61595	Acf61595	Human	sec	627	15	9.3	1815	8	ACF49830	Acf49830	Human	sec
571	15	9.3	1815	8	ACD30626	Acad30626	Human	sec	628	15	9.3	1815	8	ACH06175	ACH06175	cDNA	encc
572	15	9.3	1815	8	ACD31547	Acad31547	Human	sec	629	15	9.3	1815	8	ACH06482	ACH06482	cDNA	encc
573	15	9.3	1815	8	ACD32468	Acad32468	Human	sec	630	15	9.3	1815	8	AD483088	Ad483088	Human	sec
574	15	9.3	1815	8	ACF17434	Acf17434	Human	sec	631	15	9.3	1815	8	ACF29258	Acf29258	Human	sec
575	15	9.3	1815	8	ACF07267	Acf07267	Human	sec	632	15	9.3	1815	8	ACF93152	Acf93152	Human	sec
576	15	9.3	1815	8	ACF20425	Acf20425	Human	sec	633	15	9.3	1815	8	ACF19197	Acf19197	Human	sec

634	15	9.3	1815	8	ACD12888	Adc12888	Human	sec	691	15	9.3	1815	8	ADA1893	Ada1893	Human	sec
635	15	9.3	1815	8	ACF06346	AcF06346	Human	sec	692	15	9.3	1815	8	ACC90280	Acc90280	Human	sec
636	15	9.3	1815	8	ACC94380	Acc94380	Human	sec	693	15	9.3	1815	8	ACF10644	AcF10644	Human	sec
637	15	9.3	1815	8	ACC97808	Acc97808	Human	sec	694	15	9.3	1815	8	ACC93459	Acc93459	Human	sec
638	15	9.3	1815	8	ACC94073	Acc94073	Human	sec	695	15	9.3	1815	8	ACC96078	Acc96078	Human	sec
639	15	9.3	1815	8	ACF42027	AcF42027	Human	sec	696	15	9.3	1815	8	ACD22574	AcD22574	Human	sec
640	15	9.3	1815	8	ACD30933	AcD30933	Human	sec	697	15	9.3	1815	8	ADN17240	Adn17240	Human	sec
641	15	9.3	1815	8	ACD42962	AcD42962	cDNA	encc	698	15	9.3	1815	8	ACF01838	AcF01838	Human	sec
642	15	9.3	1815	8	ACD43269	AcD43269	cDNA	encc	699	15	9.3	1815	8	ACF21960	AcF21960	Human	sec
643	15	9.3	1815	8	ACF14799	AcF14799	Human	sec	700	15	9.3	1815	8	ACF08802	AcF08802	Human	sec
644	15	9.3	1815	8	ACF01531	AcF01531	Human	sec	701	15	9.3	1815	8	ACF33138	AcF33138	Human	sec
645	15	9.3	1815	8	ACF31603	AcF31603	Human	sec	702	15	9.3	1815	8	ACF33138	AcF33138	Human	sec
646	15	9.3	1815	8	ACD67280	AcD67280	cDNA	encc	703	15	9.3	1815	8	ACF34592	AcF34592	Human	sec
647	15	9.3	1815	8	ACD48470	AcD48470	Human	sec	704	15	9.3	1815	8	ACF48452	AcF48452	Human	sec
648	15	9.3	1815	8	ACD48777	AcD48777	Human	sec	705	15	9.3	1815	8	ACD47242	AcD47242	Human	sec
649	15	9.3	1815	8	ACF51215	AcF51215	Human	sec	706	15	9.3	1815	8	ACD49084	AcD49084	Human	sec
650	15	9.3	1815	8	ACF53978	AcF53978	Human	sec	707	15	9.3	1815	8	ACF37787	AcF37787	Human	sec
651	15	9.3	1815	8	ACF25702	AcF25702	Human	sec	708	15	9.3	1815	8	ACF33000	AcF33000	Human	sec
652	15	9.3	1815	8	ACF39015	AcF39015	Human	sec	709	15	9.3	1815	8	ACD87313	AcD87313	Human	sec
653	15	9.3	1815	8	ACF28772	AcF28772	Human	sec	710	15	9.3	1815	8	ACF61902	AcF61902	Human	sec
654	15	9.3	1815	8	ACD90689	AcD90689	Human	sec	711	15	9.3	1815	8	ACF61902	AcF61902	Human	sec
655	15	9.3	1815	8	ACD86392	AcD86392	Human	sec	712	15	9.3	1815	8	ACH10835	Ach10835	Human	sec
656	15	9.3	1815	8	ACH05254	Ach05254	cDNA	encc	713	15	9.3	1815	8	ADA42743	Ada42743	Human	sec
657	15	9.3	1815	8	ACF65050	AcF65050	Human	sec	714	15	9.3	1815	8	ACD10000	AcD10000	Human	sec
658	15	9.3	1815	8	ADB20131	AdB20131	Human	sec	715	15	9.3	1815	8	ACD16725	AcD16725	cDNA	encc
659	15	9.3	1815	8	ACF43523	AcF43523	Human	sec	716	15	9.3	1815	8	ACC99022	Acc99022	Human	sec
660	15	9.3	1815	8	ACH08993	Ach08993	Human	sec	717	15	9.3	1815	8	ACF00416	AcF00416	Human	sec
661	15	9.3	1815	8	ACH09300	Ach09300	Human	sec	718	15	9.3	1815	8	ACD40883	AcD40883	Human	sec
662	15	9.3	1815	8	ADA78383	Ada78383	Human	sec	719	15	9.3	1815	8	ACF14492	AcF14492	Human	sec
663	15	9.3	1815	8	ACF09723	AcF09723	Human	sec	720	15	9.3	1815	8	ACF22267	AcF22267	Human	sec
664	15	9.3	1815	8	ACF50908	AcF50908	Human	sec	721	15	9.3	1815	8	ACF78844	AcF78844	Human	sec
665	15	9.3	1815	8	ACF23802	AcF23802	Human	sec	722	15	9.3	1815	8	ACF11565	AcF11565	Human	sec
666	15	9.3	1815	8	ACH8234	Ach8234	Human	sec	723	15	9.3	1815	8	ACF35122	AcF35122	Human	sec
667	15	9.3	1815	8	ACH09607	Ach09607	Human	sec	724	15	9.3	1815	8	ACF33445	AcF33445	Human	sec
668	15	9.3	1815	8	ACH10528	Ach10528	Human	sec	725	15	9.3	1815	8	ACD49698	AcD49698	Human	sec
669	15	9.3	1815	8	ACD11335	AcD11335	Human	sec	726	15	9.3	1815	8	ACF37480	AcF37480	Human	sec
670	15	9.3	1815	8	ACC96385	Acc96385	Human	sec	727	15	9.3	1815	8	ACD28465	AcD28465	Human	sec
671	15	9.3	1815	8	ACC98415	Acc98415	Human	sec	728	15	9.3	1815	8	ACD88541	AcD88541	Human	sec
672	15	9.3	1815	8	ADA16596	Ada16596	Human	sec	729	15	9.3	1815	8	ACF75160	AcF75160	Human	sec
673	15	9.3	1815	8	ACF41720	AcF41720	Human	sec	730	15	9.3	1815	8	ACF60981	AcF60981	Human	sec
674	15	9.3	1815	8	ACF16641	AcF16641	Human	sec	731	15	9.3	1815	8	ACF44137	AcF44137	Human	sec
675	15	9.3	1815	8	ADA13025	Ada13025	Human	sec	732	15	9.3	1815	8	ACH08379	Ach08379	Human	sec
676	15	9.3	1815	8	ACD32161	AcD32161	Human	sec	733	15	9.3	1815	8	ACC93766	Acc93766	Human	sec
677	15	9.3	1815	8	ACD30319	AcD30319	Human	sec	734	15	9.3	1815	8	ACD20871	AcD20871	Human	sec
678	15	9.3	1815	8	ACD41190	AcD41190	Human	sec	735	15	9.3	1815	8	ACF06653	AcF06653	Human	sec
679	15	9.3	1815	8	ACF07574	AcF07574	Human	sec	736	15	9.3	1815	8	ACD20564	AcD20564	Human	sec
680	15	9.3	1815	8	ACF30989	AcF30989	Human	sec	737	15	9.3	1815	8	ACD22713	AcD22713	Human	sec
681	15	9.3	1815	8	ACF77309	AcF77309	Human	sec	738	15	9.3	1815	8	ACF41413	AcF41413	Human	sec
682	15	9.3	1815	8	ACF10951	AcF10951	Human	sec	739	15	9.3	1815	8	ACF06960	AcF06960	Human	sec
683	15	9.3	1815	8	ACF32831	AcF32831	Human	sec	740	15	9.3	1815	8	ACD23603	AcD23603	Human	sec
684	15	9.3	1815	8	ACF26009	AcF26009	Human	sec	741	15	9.3	1815	8	ACF77616	AcF77616	Human	sec
685	15	9.3	1815	8	ACD83322	AcD83322	Human	PRO	742	15	9.3	1815	8	ACD46014	AcD46014	Human	sec
686	15	9.3	1815	8	ACF23495	AcF23495	Human	sec	743	15	9.3	1815	8	ACF46917	AcF46917	Human	sec
687	15	9.3	1815	8	ACF42909	AcF42909	Human	sec	744	15	9.3	1815	8	ACF54285	AcF54285	Human	sec
688	15	9.3	1815	8	ACF43216	AcF43216	Human	sec	745	15	9.3	1815	8	ACF45689	AcF45689	Human	sec
689	15	9.3	1815	8	ACH05868	Ach05868	cDNA	encc	746	15	9.3	1815	8	ACF45382	AcF45382	Human	sec
690	15	9.3	1815	8	ACH08686	Ach08686	Human	sec	747	15	9.3	1815	8	ACF38401	AcF38401	Human	sec
														ACD89462	AcD89462	Human	sec

748	15	9.3	1815	8	ACD85164	AcD85164 Human sec	805	15	9.3	2082	2	AAI05901	AAc05901 Human IL-
749	15	9.3	1815	8	ACD85778	AcD85778 Human sec	806	15	9.3	2088	2	AAQ14479	AAq14479 Truncated
750	15	9.3	1815	8	ACF75774	AcF75774 Human sec	807	15	9.3	2151	6	ABE12355	ABe12355 Arabidops
751	15	9.3	1815	8	ACF60674	AcF60674 Human sec	808	15	9.3	2179	5	AA576333	AA576333 DNA encod
752	15	9.3	1815	8	ACI05561	AcI05561 cDNA emco	809	15	9.3	2292	6	AB189940	AB189940 Human pol
753	15	9.3	1815	8	ADA82454	AdA82454 Human sec	810	15	9.3	2297	3	AAE21718	AAE21718 Human bre
754	15	9.3	1815	8	ACF55820	AcF55820 Human sec	811	15	9.3	2394	4	AAH16440	AAH16440 Human cDN
755	15	9.3	1815	8	ACF55206	AcF55206 Human sec	812	15	9.3	2478	7	AD53202	Ad53202 Human cod
756	15	9.3	1815	9	ADB77662	AdB77662 Human sec	813	15	9.3	2490	9	ADC30181	AdC30181 Human nov
757	15	9.3	1815	9	ADB874798	AdB874798 Human sec	814	15	9.3	2499	3	AAZ95233	AAZ95233 Human pho
758	15	9.3	1815	9	ACF56127	AcF56127 Human sec	815	15	9.3	2499	3	AAZ95234	AAZ95234 Human pho
759	15	9.3	1815	9	ACF56434	AcF56434 Human sec	816	15	9.3	2499	3	AAZ95963	AAZ95963 Human cGM
760	15	9.3	1815	9	ACF55513	AcF55513 Human sec	817	15	9.3	2499	3	AAZ95963	AAZ95963 Human cGM
761	15	9.3	1815	9	ACF54899	AcF54899 Human sec	818	15	9.3	2503	4	AB103136	AB103136 Drosophi11
762	15	9.3	1815	9	ADC28444	AdC28444 Human sec	819	15	9.3	2533	4	AA169959	AA169959 Human rib
763	15	9.3	1815	9	ADC28444	AdC28444 Human sec	820	15	9.3	2604	6	ABA96980	ABa96980 Human pro
764	15	9.3	1815	9	ADC40158	AdC40158 Human sec	821	15	9.3	2637	2	AAQ29614	AAQ29614 Marek's d
765	15	9.3	1815	9	ADC40158	AdC40158 Human sec	822	15	9.3	2645	2	AAQ79715	AAQ79715 Cyclic gu
766	15	9.3	1815	9	ADC18986	AdC18986 Human sec	823	15	9.3	2645	2	AAV62158	AAV62158 HSV-2 str
767	15	9.3	1815	9	ADC42482	AdC42482 Human sec	824	15	9.3	2645	2	AAV93933	AAV93933 Human cGM
768	15	9.3	1815	9	ADC29337	AdC29337 Human sec	825	15	9.3	2645	8	ACD26123	AcD26123 cDNA emco
769	15	9.3	1815	9	ADC28868	AdC28868 Human sec	826	15	9.3	2666	7	AAZ21437	AAZ21437 Prokaryot
770	15	9.3	1815	9	ADC40753	AdC40753 Human sec	827	15	9.3	2688	3	AAA12375	AAa12375 Mutine em
771	15	9.3	1815	9	ADC19410	AdC19410 Human sec	828	15	9.3	2704	2	AAV22792	AAV22792 Class II S
772	15	9.3	1815	9	ADC33858	AdC33858 Human sec	829	15	9.3	2706	7	ACC46813	ACc46813 cDNA for
773	15	9.3	1815	9	ADC12928	AdC12928 Human sec	830	15	9.3	2706	7	ADB58184	AdB58184 Toxicity-
774	15	9.3	1815	9	ADC12280	AdC12280 Human sec	831	15	9.3	2707	8	ADA20928	AdA20928 Mouse BAX
775	15	9.3	1815	9	ADDO5492	AdD05492 Human sec	832	15	9.3	2709	7	ABT20996	ABt20996 Aspergill11
776	15	9.3	1815	9	ADDO4935	AdD04935 Human sec	833	15	9.3	2712	1	AAH71303	AAH71303 Herpes SI
777	15	9.3	1815	9	ADDO3941	AdD03941 Human sec	834	15	9.3	2724	1	AAH71399	AAH71399 Herpes SI
778	15	9.3	1815	9	ADDO3517	AdD03517 Human sec	835	15	9.3	2724	1	AAH18868	AAH18868 Human ner
779	15	9.3	1815	9	ADDE34769	AdE34769 Human sec	836	15	9.3	2724	5	AAH50517	AAH50517 Sequence
780	15	9.3	1815	10	ADE79214	AdE79214 Human sec	837	15	9.3	2749	2	AAQ32649	AAQ32649 S recepto
781	15	9.3	1815	10	ADE79638	AdE79638 Human sec	838	15	9.3	2769	3	AAA08533	AAa08533 Pseudocl
782	15	9.3	1815	10	ADE79314	AdE79314 Human sec	839	15	9.3	2859	6	ABE32071	ABe32071 Human cDN
783	15	9.3	1815	10	ADE74156	AdE74156 Human sec	840	15	9.3	2859	6	ABE32071	ABe32071 Human gen
784	15	9.3	1815	10	ADE79849	AdE79849 Human sec	841	15	9.3	2881	4	AB109120	AB109120 Drosophi11
785	15	9.3	1815	10	ADE74768	AdE74768 Human sec	842	15	9.3	2881	4	AB109120	AB109120 Drosophi11
786	15	9.3	1818	9	ADBE62516	AdB62516 Human cDN	843	15	9.3	2881	4	AB109120	AB109120 Drosophi11
787	15	9.3	1839	4	AAU08059	AAu08059 Human ext	844	15	9.3	2925	2	AAO14455	AAO14455 HSV-2 str
788	15	9.3	1885	5	AA169952	AA169952 Human 2-h	845	15	9.3	2925	2	AAO14455	AAO14455 HSV-2 str
789	15	9.3	1911	7	ACD19479	AcD19479 cDNA emco	846	15	9.3	2929	7	ABT20398	ABt20398 HSV surfa
790	15	9.3	1933	8	ACD26113	AcD26113 Human cDN	847	15	9.3	2929	7	ABT18582	ABt18582 Aspergill11
791	15	9.3	1982	2	AAQ79705	AAq79705 Cyclic gu	848	15	9.3	2936	3	AAO30837	AAO30837 Arabidops
792	15	9.3	1982	2	AAV09066	AAV09066 Bovine ph	849	15	9.3	2957	3	AAO30837	AAO30837 Arabidops
793	15	9.3	1982	2	AAV93983	AAV93983 Human cGB	850	15	9.3	2994	2	AAV36086	AAV36086 cDNA emco
794	15	9.3	2000	6	ABE16487	ABe16487 Arabidops	851	15	9.3	2994	2	AAV36086	AAV36086 cDNA emco
795	15	9.3	2000	6	ABE16379	ABe16379 Arabidops	852	15	9.3	3001	3	AAH51786	AAH51786 Chromosom
796	15	9.3	2000	6	ABE215017	ABe215017 Arabidops	853	15	9.3	3004	9	ADD93577	ADd93577 Arabidops
797	15	9.3	2000	7	ADM68829	AdM68829 Arabidops	854	15	9.3	3013	4	AAE44626	AAE44626 Novel pro
798	15	9.3	2002	4	AAH14767	AAH14767 Human cDN	855	15	9.3	3021	4	AAE44626	AAE44626 Novel pro
799	15	9.3	2005	3	AAAS7382	AAAS7382 cDNA emco	856	15	9.3	3034	3	AAZ29224	AAZ29224 Human I k
800	15	9.3	2060	2	AAQ79704	AAQ79704 Cyclic gu	857	15	9.3	3037	9	ADB58358	ADb58358 Toxicity-
801	15	9.3	2060	2	AAV09065	AAV09065 Bovine ph	858	15	9.3	3051	9	ADC27060	AdC27060 Human deu
802	15	9.3	2060	2	AAV09065	AAV09065 Bovine ph	859	15	9.3	3051	9	ADC27060	AdC27060 Human deu
803	15	9.3	2067	7	ADA52883	AdA52883 Human cod	860	15	9.3	3057	4	AAO84394	AAO84394 Human TAN
804	15	9.3	2067	7	ADA52883	AdA52883 Human cod	861	15	9.3	3057	4	AAO84377	AAO84377 Human TAN

862	15	9.3	3057	4	AAc84395	919	15	9.3	5737	7	ABZ96657	ABZ96657 Human nuc
863	15	9.3	3057	4	AAc84393	920	15	9.3	5839	2	AAV46335	AAV46335 Hydra hea
864	15	9.3	3072	6	ABK66731	c 921	15	9.3	5848	6	AA594835	AA594835 Human DNA
865	15	9.3	3098	1	AAAG60195	c 922	15	9.3	5869	7	ABX08745	ABX08745 Angiogene
c 866	15	9.3	3157	2	AAQ13316	c 923	15	9.3	5894	4	AAH57511	AAH57511 Human Kid
c 867	15	9.3	3313	6	ABK72883	c 924	15	9.3	6048	2	AAV74439	AAV74439 Strephylot
c 868	15	9.3	3372	4	AAQ14494	c 925	15	9.3	6105	4	ABJ09402	ABJ09402 Drosophill
c 869	15	9.3	3381	2	AAAI4957	c 926	15	9.3	6127	6	ABJ33614	ABJ33614 Human Imm
c 870	15	9.3	3382	2	AAQ62300	c 927	15	9.3	6529	2	AAV41889	AAV41889 Nucleotid
871	15	9.3	3390	5	AAE75054	c 928	15	9.3	6749	4	AAE28594	AAE28594 Drosophill
872	15	9.3	3461	1	AAAT70681	c 929	15	9.3	6854	2	AAV52333	AAV52333 Streptoco
873	15	9.3	3465	2	AAQ14478	c 930	15	9.3	7267	4	AAK69457	AAK69457 Human Imm
874	15	9.3	3471	1	AAAT93650	c 931	15	9.3	7468	9	ADE53840	ADE53840 Human pro
875	15	9.3	3472	1	AAAT80907	c 932	15	9.3	7571	2	AAV52135	AAV52135 Streptoco
876	15	9.3	3472	2	AAQ48496	c 933	15	9.3	7808	8	ACQ19234	ACQ19234 E. coli 0
877	15	9.3	3472	2	AAQ48497	c 934	15	9.3	7818	9	ACQ19335	ACQ19335 Enterohae
878	15	9.3	3473	2	AAAT93651	c 935	15	9.3	11050	2	AAV74407	AAV74407 Strephylot
879	15	9.3	3474	1	AAAT80908	c 936	15	9.3	12701	9	ADD46676	ADD46676 Human gen
c 880	15	9.3	3489	4	AAI07139	c 937	15	9.3	16768	4	ABJ15650	ABJ15650 Drosophill
c 881	15	9.3	3556	6	AAE75055	c 938	15	9.3	16825	4	ABK42608	ABK42608 Connectiv
c 882	15	9.3	3590	5	ADQ18507	c 939	15	9.3	16825	8	ADB60764	ADB60764 Connectiv
883	15	9.3	3642	1	AAAS0364	c 940	15	9.3	17841	4	ABJ04868	ABJ04868 Drosophill
884	15	9.3	3771	3	AAAI0741	c 941	15	9.3	21129	4	AA536234	AA536234 Human car
c 885	15	9.3	3774	9	ADE57960	c 942	15	9.3	21129	9	ADE46928	ADE46928 Human car
c 886	15	9.3	3774	9	ADK83401	c 943	15	9.3	23636	7	ACC48894	ACC48894 Rhodococ
c 887	15	9.3	3774	9	ADK57956	c 944	15	9.3	26464	4	AAK81246	AAK81246 Human Imm
888	15	9.3	3780	6	ABZ31833	c 945	15	9.3	26639	9	ADE35685	ADE35685 Mouse mCG
c 889	15	9.3	3932	4	ABJ09146	c 946	15	9.3	26642	8	ADA03059	ADA03059 Mouse Kcn
890	15	9.3	3996	1	AAAS0516	c 947	15	9.3	26642	8	ADA66343	ADA66343 Mouse Kcn
891	15	9.3	4066	6	ABV76591	c 948	15	9.3	28642	2	ABM72797	ABM72797 Mouse Kcn
c 892	15	9.3	4249	6	ABJ61770	c 949	15	9.3	28690	6	AAK13075	AAK13075 Enterococ
c 893	15	9.3	4249	6	ADK89105	c 950	15	9.3	28690	6	AB598870	AB598870 Enterococ
c 894	15	9.3	4273	9	ABD47493	c 951	15	9.3	31814	7	AAD47150	AAD47150 Human Ras
895	15	9.3	4360	4	ABE24698	c 952	15	9.3	32195	5	AA532232	AA532232 Novel hum
896	15	9.3	4605	4	ABJ14308	c 953	15	9.3	32195	6	AB567535	AB567535 Human DNA
897	15	9.3	4738	9	ADD18755	c 954	15	9.3	33206	6	ABN95882	ABN95882 Gene #238
c 898	15	9.3	4741	4	AAI07140	c 955	15	9.3	35776	4	AAK68321	AAK68321 Human Imm
899	15	9.3	4779	6	ABZ78009	c 956	15	9.3	37322	6	ABJ61996	ABJ61996 Colton ade
900	15	9.3	4790	7	ABK49963	c 957	15	9.3	62782	8	AAJ58281	AAJ58281 Human tum
c 901	15	9.3	4862	9	ADK58780	c 958	15	9.3	62782	8	AAJ58281	AAJ58281 Human tum
c 902	15	9.3	4862	9	ADK58780	c 959	15	9.3	63020	6	ABO67197	ABO67197 Continuation (12 o
c 903	15	9.3	4862	9	ADK58780	c 960	15	9.3	66479	6	ABO80567	ABO80567 Mutant hu
904	15	9.3	4895	7	ABK63018	c 961	15	9.3	66479	6	ABO80566	ABO80566 Mutant hu
c 905	15	9.3	4809	7	ACCT2016	c 962	15	9.3	66479	6	ABQ80565	ABQ80565 Mutant hu
c 906	15	9.3	4911	9	ADK53715	c 963	15	9.3	66479	6	ABQ80565	ABQ80565 Mutant hu
907	15	9.3	4928	7	ABT17988	c 964	15	9.3	87977	8	ADA02639	ADA02639 Mouse Znf
908	15	9.3	4929	7	ABT19802	c 965	15	9.3	87977	8	ADK72377	ADK72377 Mouse Znf
c 909	15	9.3	4992	9	ADD69642	c 966	15	9.3	90541	6	AB552847	AB552847 Human SR
910	15	9.3	5211	7	ACC47334	c 967	15	9.3	90583	7	ACD13447	ACD13447 Human DNA
911	15	9.3	5290	6	ABZ76452	c 968	15	9.3	96593	9	ADK85347	ADK85347 Mouse Bln
912	15	9.3	5448	2	AAV65229	c 969	15	9.3	96594	8	ADA02888	ADA02888 Human Bln
c 913	15	9.3	5535	4	AAV90649	c 970	15	9.3	96594	8	ADK72626	ADK72626 Human Bln
c 914	15	9.3	5576	7	ACC48897	c 971	15	9.3	96595	8	ADA03068	ADA03068 Human PPP
915	15	9.3	5737	2	AAQ58034	c 972	15	9.3	96595	8	ADK72806	ADK72806 Human PPP
916	15	9.3	5737	2	AAQ58034	c 973	15	9.3	96596	8	ADA66352	ADA66352 Human PPP
917	15	9.3	5737	2	AAQ58034	c 974	15	9.3	99500	6	AAJ41740	AAJ41740 Human REC
918	15	9.3	5737	3	AAE20963	c 975	15	9.3	105184	6	ABK24122	ABK24122 Bacterial

c 976	15	9.3 106286	6	ABSS5320_4	Continuation (5 of
c 977	15	9.3 110000	2	AAV21209_08	Continuation (9 of
c 978	15	9.3 110000	2	AAV21209_09	Continuation (10 o
c 979	15	9.3 110000	2	AAV21209_14	Continuation (15 o
c 980	15	9.3 110000	2	AAK20248_05	Continuation (6 of
c 981	15	9.3 110000	4	AAK95240_00	Continuation (10 o
c 982	15	9.3 110000	4	AAK95240_09	Continuation (10 o
c 983	15	9.3 110000	4	AAK96733_00	Continuation (10 o
c 984	15	9.3 110000	4	AAK96733_09	Continuation (10 o
c 985	15	9.3 110000	6	ABN71527_07	Continuation (8 of
c 986	15	9.3 110000	6	ABN71527_09	Continuation (11 o
c 987	15	9.3 110000	6	ABN71527_10	Continuation (11 o
c 988	15	9.3 110000	6	ABN71527_10	Continuation (11 o
c 989	15	9.3 110000	6	ABN71527_17	Continuation (18 o
c 990	15	9.3 110000	6	ABSS5320_1	Continuation (2 of
c 991	15	9.3 110000	6	ABT00010_00	Continuation (10 o
c 992	15	9.3 110000	6	ABT00010_09	Continuation (8 of
c 993	15	9.3 110000	6	ABK08336_07	Continuation (12 o
c 994	15	9.3 110000	6	ABG69245_11	Continuation (13 o
c 995	15	9.3 110000	6	ABG69245_12	Continuation (11 o
c 996	15	9.3 110000	6	ABG67197_10	Continuation (11 o
c 997	15	9.3 110000	6	ABT01503_00	Continuation (10 o
c 998	15	9.3 110000	6	ABT01503_09	Continuation (25 o
c 999	15	9.3 110000	6	ABA03041_24	Continuation (16 o
c 1000	15	9.3 110000	7	ABSS6454_15	Continuation (16 o

ALIGNMENTS

RESULT 1
AAA68231
ID AAA68231 standard; DNA; 162 BP.
XX
AC AAA68231;
XX
DT 15-SEP-2003 (revised)
DT 06-AUG-2003 (revised)
DT 27-OCT-2000 (first entry)
XX
DE Bacteriophage 77 77ORF102 nucleotide sequence.
XX
KW Bacteriophage; antimicrobial; genome; identification; antibacterial;
KW bacterial growth inhibition; bacterial infection; ds.
OS Staphylococcus aureus; bacteriophage 77.
XX
PN WO200032825-A2.
XX
PD 08-JUN-2000.
XX
PF 03-DEC-1999; 99WC-1B002040.
XX
PR 03-DEC-1998; 98US-0110992P.
PR 03-JUN-1999; 99US-00326144.
PR 28-SEP-1999; 99US-00407804.
PR 30-SEP-1999; 99US-0157218P.

PR 01-DEC-1999; 99US-0168777P.
PR 02-DEC-1999; 99US-00454252.
XX
XX (PHAG-) PHAGE TECH INC.
XX
XX Pelletier J, Gros P, Dubow M;
XX WPI; 2000-412361/35.
XX P-PSDB; AAB16526.
DR
PT Identifying a bacteriophage coding region for treating bacterial
PT infections comprises identifying a nucleic acid encoding a product that
PT inhibits bacteria when a bacteriophage infects a bacterium.
XX
XX Disclosure; Page 159; 456pp; English.
XX
XX The present invention describes a method for identifying a bacteriophage
XX coding region encoding a product active on an essential bacterial target.
XX The method comprises identifying a nucleic acid sequence encoding a gene
XX product that provides a bacteria-inhibiting function when an
XX uncharacterised bacteriophage infects a pathogenic bacterium. The
XX compound active on a target of a bacteriophage inhibitor protein in a
XX bacteria is used to treat or prevent a bacterial infection in an animal.
XX AA68243 to AB69442 and AB16523 to AB16954 represent bacteriophage
XX nucleotide and protein sequences which are used in the exemplification of
XX the present invention. (Updated on 06-AUG-2003 to correct 05 field.)
XX (Updated on 15-SEP-2003 to standardise 05 field)
SQ
SQ Sequence 162 BP; 52 A; 32 C; 27 G; 51 T; 0 U; 0 other;

Query Match 100.0%; Score 162; DB 3; Length 162;
Best Local Similarity 100.0%; Pred. No. 4e-74;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGCACTTTAAAAAGTACGTAGTATGATGCTGACAGTCTAGCGATT 60
DB 1 ATGAGCACTTTAAAAAGTACGTAGTATGATGCTGACAGTCTAGCGATT 60
QY 61 GTACTTATGCCGTTTCTATCTTCACTGACATGATGCTGATGCGGATGCGAGTATC 120
DB 61 GTACTTATGCCGTTTCTATCTTCACTGACATGATGCTGATGCGGATGCGAGTATC 120
QY 121 GCAACATCATGTACTACAAAGATGCTTTTCAAGATTA 162
DB 121 GCAACATCATGTACTACAAAGATGCTTTTCAAGATTA 162

RESULT 2
AAA68247
ID AAA68247 standard; DNA; 41708 BP.
XX
XX AAA68247;
XX
AC
XX
DT 15-SEP-2003 (revised)
DT 06-AUG-2003 (revised)
DT 27-OCT-2000 (first entry)
XX

XX (CHIR-) CHIRON SPA.
 XX
 XX Malignant V, Mora M, Scarselli M;
 XX WPI; 2003-120766/11.
 DR P-PSDB; ABM71514.
 XX
 PT New Staphylococcus aureus protein, useful as a vaccine for treating or
 PT preventing Staphylococcal infection, specifically an infection caused by
 PT S. aureus, e.g. sepsis.
 XX
 PS Claim 6; SEQ ID NO 1507; 49pp; English.
 XX
 CC The invention relates to novel genes and encoded proteins from
 CC Staphylococcus aureus. A composition comprising the S. aureus protein, a
 CC nucleic acid encoding the protein, or an antibody to the protein, is
 CC useful as a pharmaceutical, particularly as a vaccine for treating or
 CC preventing infection due to Staphylococcus bacteria, specifically an
 CC infection caused by S. aureus. The composition is particularly useful for
 CC treating or preventing sepsis in a patient. The composition can also be
 CC used for diagnostics. The protein is also used in an assay for enzymatic
 CC studies and as a target for antibiotics. This sequence represents one of
 CC the novel S. aureus genes of the invention
 XX
 SQ Sequence 159 BP; 51 A; 30 C; 26 G; 52 T; 0 U; 0 Other;
 Query Match 41.4%; Score 67; DB 7; Length 159;
 Best Local Similarity 100.0%; Pred. No. 8-26-25;
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 TATGCTTACAGCTTAGCGATTGACTTATGCCGTTCTATCTTCACTACAGCATGCT 97
 DB 38 TATGCTTACAGCTTAGCGATTGACTTATGCCGTTCTATCTTCACTACAGCATGCT 97
 QY 98 CAATGC 104
 DB 98 CAATGC 104
 RESULT 6
 ID AAV74851/c
 ID AAV74851 standard; DNA; 1408 BP.
 XX
 AC AAV74851;
 XX
 DT 16-MAR-1999 (first entry)
 XX
 DE Staphylococcus aureus contig SEQ ID #540.
 XX
 KW Computer readable medium; vaccine; S. aureus infection; immunodetection;
 KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KW skin infection; surgical wound infection; scalded skin syndrome;
 KW toxic shock syndrome; ds.
 XX
 OS Staphylococcus aureus.
 XX

EH Key Location/Qualifiers
 FT misc_feature 1081..1140
 FT /'tag' a
 FT /note= "these bases represent a line of missing text in
 FT the sequence listing in the specification. They are
 FT included to maintain the nucleotide numbering given in
 FT the specification for this DNA sequence"
 XX
 PN EP786519-A2.
 XX
 PD 30-JUL-1997.
 XX
 PF 07-JAN-1997; 97EP-00100117.
 XX
 PR 05-JAN-1996; 96US-0009861P.
 XX
 PA (HUMAN) HUMAN GENOME SCI INC.
 XX
 PI Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
 DR WPI; 1997-374922/35.
 XX
 PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -
 PT stored on computer readable medium and used in the production of anti-
 PT S. aureus vaccines.
 XX
 PS Claim 1; Page 1475-1476; 3271pp; English.
 XX
 CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences
 CC of the invention. The DNA sequences are recorded on a computer readable
 CC medium, preferably selected from a floppy or hard disk, random access
 CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
 CC the S. aureus DNA sequences allows putative functions to be assigned so
 CC that protein-encoding or regulatory regions of commercial, therapeutic or
 CC industrial importance can be obtained. Specifically, sequences which are
 CC likely to encode antigens have been identified and these polypeptides can
 CC be used in a vaccine composition against S. aureus infection. The
 CC polypeptides can also be used in a kit for the immunodetection of
 CC S. aureus in a sample. S. aureus is implicated in numerous human diseases,
 CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
 CC skin and surgical wound infections, scalded skin syndrome, toxic shock
 CC syndrome, etc. Organisms transformed with the DNA sequences can be used
 CC for recombinant production of the polypeptides. The new DNA sequences
 CC (and their fragments) are useful as primers or probes for isolating
 CC homologues of any of the S. aureus DNA sequences contained on the computer
 CC readable medium
 XX
 SQ Sequence 1408 BP; 332 A; 250 C; 218 G; 543 T; 0 U; 65 Other;
 Query Match 41.4%; Score 67; DB 2; Length 1408;
 Best Local Similarity 100.0%; Pred. No. 8e-25;
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 TATGCTTACAGCTTAGCGATTGACTTATGCCGTTCTATCTTCACTACAGCATGCT 97
 DB 302 TATGCTTACAGCTTAGCGATTGACTTATGCCGTTCTATCTTCACTACAGCATGCT 243

QY 98 CAATTGC 104
| | | | |
Db 242 CAATTGC 236

RESULT 7

AAA68254
ID AAA68254 standard; DNA; 43095 BP.

AAA68254;

DT 06-AUG-2003 (revised)
DT 27-OCT-2000 (first entry)

DE Bacteriophage 3a complete genome sequence.

KW Bacteriophage; antimicrobial; genome; identification; antibacterial;
bacterial growth inhibition; bacterial infection; ds.

OS Staphylococcus phage 3a.

PN W0200032825-A2.

PD 08-JUN-2000.

PF 03-DEC-1999; 99WO-1B002040.

PR 03-DEC-1998; 98US-0110992P.

PR 03-JUN-1999; 99US-00326144.

PR 28-SEP-1999; 99US-00407804.

PR 30-SEP-1999; 99US-0157218P.

PR 01-DEC-1999; 99US-0168777P.

PR 02-DEC-1999; 99US-00434252.

PA (PHAG-) PHAGETECH INC.

PI Polletier J, Gros P, Dubow M;

WP1; 2000-412361/35.

PT Identifying a bacteriophage coding region for treating bacterial

PT infections comprises identifying a nucleic acid encoding a product that

PT inhibits bacteria when a bacteriophage infects a bacterium.

PS Disclosure; Page 175-183; 456pp; English.

XX The present invention describes a method for identifying a bacteriophage

XX coding region encoding a product active on an essential bacterial target.

XX The method comprises identifying a nucleic acid sequence encoding a gene

XX product that provides a bacteria-inhibiting function when an

XX uncharacterised bacteriophage infects a pathogenic bacterium. The

XX compound active on a target of a bacteriophage inhibitor protein in a

XX bacterium is used to treat or prevent a bacterial infection in an animal.

XX AAA68243 to AAA69442 and AAB16523 to AAB16954 represent bacteriophage

XX nucleotide and protein sequences which are used in the exemplification of

XX the present invention. (Updated on 06-AUG-2003 to correct OS field.)

XX

SQ Sequence 43095 BP; 16332 A; 5908 C; 8513 G; 12342 T; 0 U; 0 Other;

Query Match 40.1%; Score 65; DB 3; Length 43095;

Best Local Similarity 100.0%; Pred.No. 8.2e-24;

Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGCGTTTCTACTTCACTACAGCATGGTCATTCGGGATTCGCAAGTATCGCAACA 126

Db 29508 ATGCGTTTCTACTTCACTACAGCATGGTCATTCGGGATTCGCAAGTATCGCAACA 29567

QY 127 TTCAT 131
| | | | |

Db 29568 TTCAT 29572

AAA68609
ID AAA68609 standard; DNA; 43576 BP.

AAA68609;

DT 15-SEP-2003 (revised)

DT 06-AUG-2003 (revised)

DT 27-OCT-2000 (first entry)

DE Bacteriophage 96 complete genome sequence.

KW Bacteriophage; antimicrobial; genome; identification; antibacterial;

KW bacterial growth inhibition; bacterial infection; ds.

OS Staphylococcus aureus; bacteriophage 96.

PN W0200032825-A2.

PD 08-JUN-2000.

PF 03-DEC-1999; 99WO-1B002040.

PR 03-DEC-1998; 98US-0110992P.

PR 03-JUN-1999; 99US-00326144.

PR 28-SEP-1999; 99US-00407804.

PR 30-SEP-1999; 99US-0157218P.

PR 01-DEC-1999; 99US-0168777P.

PR 02-DEC-1999; 99US-00434252.

PA (PHAG-) PHAGETECH INC.

PI Polletier J, Gros P, Dubow M;

WP1; 2000-412361/35.

PT Identifying a bacteriophage coding region for treating bacterial

PT infections comprises identifying a nucleic acid encoding a product that

PT inhibits bacteria when a bacteriophage infects a bacterium.

PS Disclosure; Page 190-198; 456pp; English.

XX

XX

XX

XX

XX

CC The present invention describes a method for identifying a bacteriophage
 CC coding region encoding a product active on an essential bacterial target.
 CC The method comprises identifying a nucleic acid sequence encoding a gene
 CC product that provides a bacteria-inhibiting function when an
 CC uncharacterized bacteriophage infects a pathogenic bacterium. The
 CC compound active on a target of a bacteriophage inhibitor protein in a
 CC bacteria is used to treat or prevent a bacterial infection in an animal.
 CC AAA68243 to AAA69442 and AAB16523 to AAB16954 represent bacteriophage
 CC nucleotide and protein sequences which are used in the exemplification of
 CC the present invention. (Updated on 06-AUG-2003 to correct OS field.)
 CC (Updated on 15-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 43576 BP; 16057 A; 6485 C; 8769 G; 12265 T; 0 U; 0 Other;
 Query Match 34.0%; Score 55; DB 3; Length 43576;
 Best Local Similarity 100.0%; Pred. No. 1.3e-18;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 TATGCTTACAGCTGATGCGATTTGACTTATGCCCTTCTATCTTCACTACAGC 92
 DB 4475 TATGCTTACAGCTGATGCGATTTGACTTATGCCCTTCTATCTTCACTACAGC 4529
 RESULT 9
 AAV74602
 ID AAV74602 standard; DNA; 2049 BP.
 AC AAV74602;
 XX
 DT 16-MAR-1999 (first entry)
 XX
 DE Staphylococcus aureus contig SEQ ID #291.
 XX
 KW Computer readable medium; vaccine; S.aureus infection; immunodetection;
 KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KW skin infection; surgical wound infection; scalded skin syndrome;
 KW toxic shock syndrome; ds.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1681..1740
 FT /tag= a
 FT /note= "these bases represent a line of missing text in
 FT the sequence listing in the specification. They are
 FT included to maintain the nucleotide numbering given in
 FT the specification for this DNA sequence"
 XX
 PN EP786519-A2.
 XX
 PD 30-JUL-1997.
 XX
 PF 07-JAN-1997; 97EP-00100117.
 XX
 PR 05-JAN-1996; 96US-0009861P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.

XX
 P1 Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
 XX WPI; 1997-374922/35.
 DR
 XX
 PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -
 PT stored on computer readable medium and used in the production of anti-
 PT S.aureus vaccines.
 PS
 XX
 PS Claim 1; Page 1117-1118; 3271pp; English.
 XX
 CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences
 CC of the invention. The DNA sequences are recorded on a computer readable
 CC medium, preferably selected from a floppy or hard disk, random access
 CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
 CC the S.aureus DNA sequences allows putative functions to be assigned so
 CC that protein-encoding or regulatory regions of commercial, therapeutic or
 CC industrial importance can be obtained. Specifically, sequences which are
 CC likely to encode antigens have been identified and these polypeptides can
 CC be used in a vaccine composition against S.aureus infection. The
 CC polypeptides can also be used in a kit for the immunodetection of
 CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,
 CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
 CC skin and surgical wound infections, scalded skin syndrome, toxic shock
 CC syndrome, etc. Organisms transformed with the DNA sequences can be used
 CC for recombinant production of the polypeptides. The new DNA sequences
 CC (and their fragments) are useful as primers or probes for isolating
 CC homologues of any of the S.aureus DNA sequences contained on the computer
 CC readable medium
 XX
 SQ Sequence 2049 BP; 768 A; 272 C; 382 G; 562 T; 0 U; 65 Other;
 Query Match 16.0%; Score 26; DB 2; Length 2049;
 Best Local Similarity 100.0%; Pred. No. 0.0015;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 79 TACTTCACTACAGCATGTCATTC 104
 DB 713 TACTTCACTACAGCATGTCATTC 738
 RESULT 10
 AAA68911
 ID AAA68911 standard; DNA; 25 BP.
 AC AAA68911;
 XX
 DT 15-SEP-2003 (revised)
 DT 06-AUG-2003 (revised)
 DT 27-OCT-2000 (first entry)
 XX
 DE Bacteriophage 96 ORF RBS sequence 96ORF303.
 XX
 KW Bacteriophage; antimicrobial; genome; identification; antibacterial;
 KW bacterial growth inhibition; PCR primer; RBS; ribosome binding site;
 KW bacterial infection; ss.
 XX

05 Staphylococcus aureus; bacteriophage 96.
XX
XX W0200032825-A2.
FN
XX 08-JUN-2000.
PD
XX 03-DEC-1999; 99WO-1B002040.
PF
XX 03-DEC-1998; 98US-0110992P.
PR 03-JUN-1999; 99US-00326144.
PR 28-SEP-1999; 99US-00407804.
PR 30-SEP-1999; 99US-0157218P.
PR 01-DEC-1999; 99US-0168777P.
PR 02-DEC-1999; 99US-00454252.
XX
XX (PHAG-) PHAGETECH INC.
XX
XX Pelletier J, Gros P, Dubow M;
PI
XX WPI; 2000-412361/35.
DR
XX
XX Identifying a bacteriophage coding region for treating bacterial
PT infections comprises identifying a nucleic acid encoding a product that
PT inhibits bacteria when a bacteriophage infects a bacterium.
XX
XX Disclosure; Page 203; 456pp; English.
PS
XX
XX The present invention describes a method for identifying a bacteriophage
CC coding region encoding a product active on an essential bacterial target.
CC The method comprises identifying a nucleic acid sequence encoding a gene
CC product that provides a bacteria-inhibiting function when an
CC uncharacterized bacteriophage infects a pathogenic bacterium. The
CC compound active on a target of a bacteriophage inhibitor protein in a
CC bacteria is used to treat or prevent a bacterial infection in an animal.
CC AA66243 to AA69442 and AB16523 to AB16954 represent bacteriophage
CC nucleotide and protein sequences which are used in the exemplification of
CC the present invention. (Updated on 06-AUG-2003 to correct OS field.)
CC (Updated on 15-SEP-2003 to standardise OS field)
XX
SQ Sequence 25 BP; 10 A; 5 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 14.2%; Score 23; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 ATAAAGCTACTAGTAGCACTA 36
DB 1 ATAAAGCTACTAGTAGCACTA 23
RESULT 11
AAA68846
ID AAA68846 standard; DNA; 23 BP.
XX
AC AAA68846;
XX
DT 15-SEP-2003 (revised)

DT 06-AUG-2003 (revised)
DT 27-OCT-2000 (first entry)
XX
XX Bacteriophage 96 ORF RBS sequence 96ORF237.
DE
XX
XX Bacteriophage; antimicrobial; genome; identification; antibacterial;
KW bacterial growth inhibition; PCR primer; RBS; ribosome binding site;
KW bacterial infection; ss.
XX
XX Staphylococcus aureus; bacteriophage 96.
OS
XX W0200032825-A2.
XX
XX 08-JUN-2000.
PD
XX
XX 03-DEC-1999; 99WO-1B002040.
PF
XX
XX 03-DEC-1998; 98US-0110992P.
PR 03-JUN-1999; 99US-00326144.
PR 28-SEP-1999; 99US-00407804.
PR 30-SEP-1999; 99US-0157218P.
PR 01-DEC-1999; 99US-0168777P.
PR 02-DEC-1999; 99US-00454252.
XX
XX (PHAG-) PHAGETECH INC.
XX
XX Pelletier J, Gros P, Dubow M;
PI
XX WPI; 2000-412361/35.
DR
XX
XX Identifying a bacteriophage coding region for treating bacterial
PT infections comprises identifying a nucleic acid encoding a product that
PT inhibits bacteria when a bacteriophage infects a bacterium.
XX
XX Disclosure; Page 202; 456pp; English.
PS
XX
XX The present invention describes a method for identifying a bacteriophage
CC coding region encoding a product active on an essential bacterial target.
CC The method comprises identifying a nucleic acid sequence encoding a gene
CC product that provides a bacteria-inhibiting function when an
CC uncharacterized bacteriophage infects a pathogenic bacterium. The
CC compound active on a target of a bacteriophage inhibitor protein in a
CC bacteria is used to treat or prevent a bacterial infection in an animal.
CC AA66243 to AA69442 and AB16523 to AB16954 represent bacteriophage
CC nucleotide and protein sequences which are used in the exemplification of
CC the present invention. (Updated on 06-AUG-2003 to correct OS field.)
CC (Updated on 15-SEP-2003 to standardise OS field)
XX
SQ Sequence 25 BP; 6 A; 6 C; 5 G; 8 T; 0 U; 0 Other;
Query Match 13.0%; Score 21; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 TATGCTCAGCTTACGCA 58
DB 5 TATGCTCAGCTTACGCA 25

RESULT 12
 ID ADD18757/c
 AC ADD18757 standard; DNA; 4895 BP.
 XX
 AC ADD18757;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Human disease related protein DNA sequence SeqID188.
 XX
 KW human; disease state; cytostatic; antiinflammatory; ophthalmological;
 KW antiatherosclerotic; vlnnary; gene therapy;
 KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
 KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;
 KW glucose transportation; catecholamine synthesis; iron transport;
 KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
 KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
 KW inflammatory condition; wound healing; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2003018621-A2.
 XX
 PD 06-MAR-2003.
 XX
 PF 23-AUG-2002; 2002WO-GB003892.
 XX
 PR 23-AUG-2001; 2001GB-00020558.
 XX
 PR 03-OCT-2001; 2001GB-00024037.
 XX
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.
 XX
 PI Kingman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;
 XX
 DR WPI; 2003-290046/28.
 XX
 DR P-PSDB; ADD18756.
 XX
 PT Now substantially purified polypeptide, useful for diagnosing or treating
 PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
 PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
 PT wound healing.
 XX
 PS Claim 27; SEQ ID NO 188; 424bp; English.
 XX
 CC This invention relates to novel human genes and gene product which are
 CC implicated in certain disease states. Compounds which modulate the
 CC proteins of the invention may have cytostatic, antiinflammatory,
 CC ophthalmological, antiatherosclerotic or vlnnary activities. The
 CC sequences of the invention may be useful for gene therapy. The invention
 CC may be useful for diagnosing or treating a hypoxia-regulated condition,
 CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,
 CC erythropoiesis, or the biological response to hypoxia conditions
 CC including processes such as glycolysis, gluconeogenesis, glucose
 CC transportation, catecholamine synthesis, iron transport or nitric oxide
 CC synthesis. The disease includes cancer, ischemic conditions, reperfusion

CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,
 CC inflammatory conditions or wound healing. The present sequence is that of
 CC a disease related protein encoding DNA sequence of the invention.
 XX
 SQ Sequence 4895 BP; 1597 A; 754 C; 916 G; 1628 T; 0 U; 0 Other;
 CC
 Query Match 11.7%; Score 19; DB 9; Length 4895;
 Best Local Similarity 100.0%; Pred. No. 6.4;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 QY 4 AGCACATTATAAAGCT 22
 DB 3016 AGCACATTATAAAGCT 2998
 CC
 RESULT 13
 ID AAF44629/c
 AC AAF44629 standard; cDNA; 4983 BP.
 XX
 AC AAF44629;
 XX
 DT 27-MAR-2001 (first entry)
 XX
 DE Novel protein kinase cDN, SEQ ID NO: 8.
 XX
 KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
 KW immunosuppressive; cardiac; renal; antiinflammatory; antisthmatic;
 KW dermatological; antidiabetic; antifertility; gene therapy; vaccine;
 KW immune disorder; cardiovascular disease; neurodegenerative disease;
 KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
 KW inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200073469-A2.
 XX
 PD 07-DEC-2000.
 XX
 PF 26-MAY-2000; 2000WO-US014842.
 XX
 PR 28-MAY-1999; 99US-0136503P.
 XX
 PA (SUGE-) SUGEN INC.
 XX
 PI Ploewman GD, Martinez R, Whyte D, Sudersanam S;
 XX
 DR WPI; 2001-032161/04.
 XX
 DR P-PSDB; AAB65603.
 XX
 PT Nucleic acids encoding kinase polypeptides, useful for diagnosing and
 PT treating immune-related diseases and disorders, cardiovascular disease,
 PT neurodegenerative diseases and/or cancers.
 XX
 PS Example 1; Fig 2; 310pp; English.
 XX
 CC The present sequence encodes a novel protein kinase. The nucleic acids
 CC and the protein kinases they encode may be used in the treatment and

CC diagnosis of diseases associated with inappropriate kinase expression
 CC such as immune-related diseases and disorders, cardiovascular disease,
 CC neurodegenerative diseases and/or cancers. The nucleic acids and
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays. The kinase polypeptides may be used as antigens in the production
 CC of antibodies of kinase expression and activity. Anti-kinase antibodies
 CC and kinase antagonists may also be used to down regulate kinase
 CC expression and activity. Diseases related to kinase expression and
 CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
 CC disorders, complications of organ transplantation, myocardial infarction,
 CC immune disorders, cardiomyopathies, strokes, renal failure, oxidative-
 CC stress related disorders, chronic inflammatory bowel disease, chronic
 CC inflammatory polyic disease, multiple sclerosis, asthma, osteoarthritis,
 CC psoriasis, rhabdits, autoimmunity, diabetes, cancers and reproductive
 CC disorders

SQ Sequence 4983 BP; 1607 A; 782 C; 954 G; 1640 T; 0 U; 0 Other;

Query Match 11.7%; Score 19; DB 4; Length 4983;
 Best Local Similarity 100.0%; Pred. No. 6.4;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 AGCAACATTATATAAAGCT 22
 DB 3103 AGCAACATTATATAAAGCT 3085
 |||||

RESULT 14
 AEN73359
 ID AEN73359 standard; cDNA; 365 BP.
 XX
 AC AEN73359;
 XX
 DT 03-JUL-2002 (first entry)
 XX
 DE Bovine embryonic germ (EG) cell cDNA EST 000203a CONTIG 45.
 XX
 KW Bovine; Bos taurus; EST; expressed sequence tag; totipotency;
 KW development; gene; ss.
 XX
 OS Bos taurus.
 OS
 PN WO200194550-A2.
 PN
 PD 13-DEC-2001.
 PD
 XX 07-JUN-2001; 2001WO-US018576.
 PF
 XX 07-JUN-2000; 2000US-0209874P.
 PR
 XX 06-JUN-2001; 2001US-00876143.
 XX
 PA (INF1-) INFIGEN INC.
 XX
 PI Ellertsen KJ, Pfister-Gonskow M, Childs L;
 XX
 DR WPI; 2002-351289/38.
 XX

PT An expressed sequence tag (EST), the expression of which, or its
 PT complementary sequence, in a cell identifies the cell as a
 PT developmentally competent or incompetent cell.
 XX
 PS Example 16; Page 157; 584pp; English.

CC The present invention describes an expressed sequence tag (EST), where
 CC the EST is an isolated, enriched, or purified nucleic acid sequence
 CC representing all or part of a gene, the expression of which, or its
 CC complementary sequence, in a cell identifies the cell as a
 CC developmentally competent or incompetent cell. Molecules which induce
 CC developmental competence in a cell line are useful for inducing
 CC totipotency in one or more cells. Molecules which induce developmental
 CC incompetence in a cell line are useful for preventing a full term
 CC pregnancy in an animal and inhibiting totipotency. The molecules are also
 CC useful for treating a disease in an animal by inducing development of one
 CC or more cells of the animal into a specific cell type. The present
 CC sequence represents a bovine EST which is given in the exemplification of
 CC the present invention

SQ Sequence 365 BP; 101 A; 52 C; 68 G; 143 T; 0 U; 1 Other;

Query Match 11.1%; Score 18; DB 6; Length 365;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TGAGCAACATTATATAAA 19
 DB 170 TGAGCAACATTATATAAA 187
 |||||

RESULT 15
 AEN73269
 ID AEN73269 standard; cDNA; 365 BP.
 XX
 AC AEN73269;
 XX
 DT 03-JUL-2002 (first entry)
 XX
 DE Bovine embryonic germ (EG) cell cDNA EST 000203a CONTIG 45.
 XX
 KW Bovine; Bos taurus; EST; expressed sequence tag; totipotency;
 KW development; gene; ss.
 XX
 OS Bos taurus.
 OS
 PN WO200194550-A2.
 PN
 PD 13-DEC-2001.
 PD
 XX 07-JUN-2001; 2001WO-US018576.
 PF
 XX 07-JUN-2000; 2000US-0209874P.
 PR
 XX 06-JUN-2001; 2001US-00876143.
 XX
 PA (INF1-) INFIGEN INC.
 XX

OM nucleic - nucleic search, using SW model

Run on: October 14, 2004, 22:42:59 ; Search time 757.155 Seconds
(without alignments)
6389,277 Million cell updates/sec

Title: US-09-407-804X-7

Perfect score: 162

Sequence: 1 atgagcacattataaaag.....aatgctttccaagaataa 162

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

EST:*

1: em_estda:*
2: em_estnu:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hcc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hcc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcm:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pin:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mem:*
23: em_gss_nus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_png:*
27: em_gss_vrt:*

PI Ellertsen KJ, Pfister-Genskow M, Childs L;
XX WPI, 2002-351289/38.
XX
XX An expressed sequence tag (EST), the expression of which, or its
XX
XX complementary sequence, in a cell identifies the cell as a
XX
XX developmentally competent or incompetent cell.

XX Example 16, Page 139, 584pp; English.

XX The present invention describes an expressed sequence tag (EST), where
XX the EST is an isolated, enriched, or purified nucleic acid sequence
XX representing all or part of a gene, the expression of which, or its
XX complementary sequence, in a cell identifies the cell as a
XX developmentally competent or incompetent cell. Molecules which induce
XX developmental competence in a cell line are useful for inducing
XX totipotency in one or more cells. Molecules which induce developmental
XX incompetence in a cell line are useful for preventing a full term
XX pregnancy in an animal and inhibiting totipotency. The molecules are also
XX useful for treating a disease in an animal by inducing development of one
XX or more cells of the animal into a specific cell type. The present
XX sequence represents a bovine EST which is given in the exemplification of
XX the present invention

XX Sequence 365 BP; 101 A; 52 C; 68 G; 143 T; 0 U; 1 Other;

Query Match 11.1%; Score 18; DB 6; Length 365;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGAGCAACATTATATAA 19
DB 170 TGAGCAACATTATATAA 187

Search completed: October 15, 2004, 00:17:05
Job time : 144.072 secs

28: gp_ges1:*
29: gp_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	12.3	673	28	AA083798 CpG0636A
2	19	11.7	151	29	CS578291 OST21462
3	19	11.7	203	14	NS4725 Yz10M07.r1
4	19	11.7	276	9	AA370794 EST82486
5	19	11.7	304	9	AA626426 ad49e07.r
6	19	11.7	307	9	AI193401 qe5Bp04.x
7	19	11.7	411	10	AA993583 RC3-BN003
8	19	11.7	522	13	BX669118 BX669118
9	19	11.7	563	10	BX813366 RC3-BN003
10	19	11.7	568	9	AV713963 AV713963
11	19	11.7	576	10	AA993702 RC3-BN003
12	19	11.7	591	9	AL600769 DFE26313C
13	19	11.7	623	10	AA957241 EST368311
14	19	11.7	628	10	AA957243 EST368313
15	19	11.7	664	12	BG528724 60258184
16	19	11.7	673	13	BX073823 BX073823
17	19	11.7	684	13	CA044602 ssa1p1mb5
18	19	11.7	695	10	AA963975 EST376048
19	19	11.7	741	13	BX073824 BX073824
20	19	11.7	749	14	CD101799 AGNCOURT
21	19	11.7	762	13	BX104583 BX104583
22	19	11.7	764	13	BX083417 BX083417
23	19	11.7	785	13	BX083416 BX083416
24	19	11.7	786	13	BX873875 BX873875
25	19	11.7	788	10	BF254557 HVSMEF000
26	19	11.7	788	13	BU744406 CH1#001_H
27	19	11.7	832	14	CB310205 AGNCOURT
28	19	11.7	843	13	BQ432932 AGNCOURT
29	19	11.7	888	13	BX745780 BX745780
30	19	11.7	920	13	BQ892400 AGNCOURT
31	19	11.7	976	12	BG429709 602493714
32	19	11.7	3062	11	BC014782 Homo sapi
33	18	11.1	229	9	AI235862 EST232424
34	18	11.1	280	10	BB342911 BB342911
35	18	11.1	307	10	BB342911 BB342911
36	18	11.1	344	9	AJ539901 AJ539901
37	18	11.1	438	9	AL805128 AL805128
38	18	11.1	450	10	AA636634 B149803.M
39	18	11.1	454	9	AJ497350 AJ497350
40	18	11.1	496	10	BF604820 270997 MA
41	18	11.1	517	28	AA510134 nbh00094J
42	18	11.1	524	13	BQ458119 kof6c05.y
43	18	11.1	530	9	AL776006 AL776006
44	18	11.1	552	28	AJ798690 HS_5270_A
45	18	11.1	588	10	AA177700 RC1-CT019

103	c	121	17	10.5	506	28	B2184427	B2184427	CH230-465	c	160	17	10.5	671	28	BH016955	BH016955	TDCR70TH
104	c	122	17	10.5	515	10	BF232047	BF232047	dd98b03.x	c	161	17	10.5	675	10	BF025209	BF025209	dF98d08.x
105	c	123	17	10.5	517	28	AQ260984	AQ260984	CITBI-El-	c	162	17	10.5	678	13	BQ511092	BQ511092	EST618507
106	c	124	17	10.5	521	29	CE519620	CE519620	tlgr-gss-	c	163	17	10.5	679	14	CB044177	CB044177	NISC_gcc02
107	c	125	17	10.5	526	12	B1563669	B1563669	RH3436.5	c	164	17	10.5	685	14	CD815699	CD815699	BN15_-027D
108	c	126	17	10.5	532	29	BM262108	BM262108	dag40h01.	c	165	17	10.5	696	12	BQ443510	BQ443510	Bj443510
109	c	127	17	10.5	532	29	AC222664	AC222664	Lotus cor	c	166	17	10.5	711	12	BG888775	BG888775	EST514626
110	c	128	17	10.5	538	10	AW917383	AW917383	EST346867	c	167	17	10.5	717	10	BF611888	BF611888	d699e05.y
111	c	129	17	10.5	543	13	BK282869	BK282869	BX282869	c	168	17	10.5	717	28	CC153009	CC153009	CSU-K34.1
112	c	130	17	10.5	544	14	CF358004	CF358004	rm98c08.y	c	169	17	10.5	717	29	CG096235	CG096235	PUI7171B
113	c	131	17	10.5	555	12	BG555581	BG555581	dF03e11.x	c	170	17	10.5	724	29	CE123318	CE123318	tlgr-gss-
114	c	132	17	10.5	557	12	B1446646	B1446646	dae78h07.	c	171	17	10.5	728	14	CD819044	CD819044	BN20_047L
115	c	133	17	10.5	559	29	CE193474	CE193474	tlgr-gss-	c	172	17	10.5	729	14	CA509002	CA509002	UI-R-F50-
116	c	134	17	10.5	565	10	BE441742	BE441742	925009B01	c	173	17	10.5	730	14	CD833681	CD833681	BN45_001D
117	c	135	17	10.5	565	12	BM002957	BM002957	1031107F0	c	174	17	10.5	732	10	BF231587	BF231587	daeB6-02.x
118	c	136	17	10.5	567	10	AW931215	AW931215	EST357058	c	175	17	10.5	743	29	CG047336	CG047336	PUIJDI94TB
119	c	137	17	10.5	570	12	BG600823	BG600823	EST505718	c	176	17	10.5	754	29	CG415356	CG415356	ZMBB6-002
120	c	138	17	10.5	574	13	BU648461	BU648461	1112080D0	c	177	17	10.5	759	12	BQ047754	BQ047754	EST596872
121	c	139	17	10.5	576	12	B1350279	B1350279	dae65h07.	c	178	17	10.5	767	12	BM408310	BM408310	EST5982637
122	c	140	17	10.5	581	14	BM383994	BM383994	UI-R-DM1-	c	179	17	10.5	768	14	CD833966	CD833966	BN45_040C
123	c	141	17	10.5	588	14	CA945909	CA945909	UI-R-F50-	c	180	17	10.5	769	12	BG437931	BG437931	602489685
124	c	142	17	10.5	588	28	A2197761	A2197761	SP_1036_A	c	181	17	10.5	772	29	CG234107	CG234107	OGC516TV
125	c	143	17	10.5	589	28	BH112159	BH112159	RPCL-24-3	c	182	17	10.5	774	29	CG039307	CG039307	PUIB0157B
126	c	144	17	10.5	590	12	BH106854	BH106854	EST556390	c	183	17	10.5	775	28	CC198298	CC198298	ZMBB6-031
127	c	145	17	10.5	596	10	AW981577	AW981577	PC14C06_P	c	184	17	10.5	780	29	CC834357	CC834357	NDL_119J2
128	c	146	17	10.5	600	13	BU904521	BU904521	AGENCOURT	c	185	17	10.5	791	14	CD815682	CD815682	BN15_027C
129	c	147	17	10.5	609	12	AW215836	AW215836	uo99h09.x	c	186	17	10.5	791	29	CC525221	CC525221	CH240_399
130	c	148	17	10.5	609	12	B1446959	B1446959	dae91c08.	c	187	17	10.5	796	28	BZ608215	BZ608215	WHACAL3TF
131	c	149	17	10.5	610	14	CD293543	CD293543	SCFPU336.	c	188	17	10.5	801	12	BG128412	BG128412	EST474058
132	c	150	17	10.5	616	14	CF358053	CF358053	rm98g12.y	c	189	17	10.5	806	12	BP122340	BP122340	BP122340
133	c	151	17	10.5	619	12	B1878237	B1878237	963122H10	c	190	17	10.5	809	28	BZ272365	BZ272365	CH230-263
134	c	152	17	10.5	627	14	CA731358	CA731358	wJpLc.pK0	c	191	17	10.5	830	9	AV400830	AV400830	AV400830
135	c	153	17	10.5	627	14	CF358064	CF358064	rm99a01.y	c	192	17	10.5	835	14	CB199253	CB199253	AGENCOURT
136	c	154	17	10.5	630	29	BX137310	BX137310	DanLo ref	c	193	17	10.5	840	14	CD337729	CD337729	AGENCOURT
137	c	155	17	10.5	631	10	AW187417	AW187417	BNTGHI140	c	194	17	10.5	841	29	CC530277	CC530277	CH240_406
138	c	156	17	10.5	633	12	BQ416595	BQ416595	BU416595	c	195	17	10.5	853	28	BH163374	BH163374	ENTTM64TF
139	c	157	17	10.5	636	29	CE628613	CE628613	tlgr-gss-	c	196	17	10.5	855	29	CC594584	CC594584	OGHVI9TH
140	c	158	17	10.5	637	13	CA039998	CA039998	ssalshc50	c	197	17	10.5	855	29	CG444577	CG444577	OGHVI9TH
141	c	159	17	10.5	641	14	CD834236	CD834236	BN45_041A	c	198	17	10.5	864	28	B2148143	B2148143	CH230-406
142	c	160	17	10.5	643	29	CE761914	CE761914	tlgr-gss-	c	199	17	10.5	879	29	CG101857	CG101857	PUIJDI04TB
143	c	161	17	10.5	646	10	AWB06167	AWB06167	MRI-UM010	c	200	17	10.5	880	29	CG444585	CG444585	OGHVI9TV
144	c	162	17	10.5	646	14	CD829126	CD829126	BN40_041C	c	201	17	10.5	882	14	CB197889	CB197889	AGENCOURT
145	c	163	17	10.5	648	12	BG592490	BG592490	EST491168	c	202	17	10.5	883	14	CD256565	CD256565	AGENCOURT
146	c	164	17	10.5	650	10	AW907036	AW907036	EST343068	c	203	17	10.5	886	29	CC484850	CC484850	CH240_314
147	c	165	17	10.5	650	9	AV336688	AV336688	AV336688	c	204	17	10.5	887	28	CC095939	CC095939	CSU-K34.1
148	c	166	17	10.5	653	13	BX869160	BX869160	BM409160	c	205	17	10.5	892	14	CK268012	CK268012	EST714090
149	c	167	17	10.5	653	14	CD828880	CD828880	BN40_040E	c	206	17	10.5	901	14	CB561106	CB561106	AGENCOURT
150	c	168	17	10.5	659	28	BH074563	BH074563	RPCL-24-2	c	207	17	10.5	907	29	CG765366	CG765366	TCB43_2_C
151	c	169	17	10.5	660	14	CF358027	CF358027	rm98e09.y	c	208	17	10.5	908	13	BU214454	BU214454	603108563
152	c	170	17	10.5	662	12	B1447009	B1447009	dae92c07.	c	209	17	10.5	910	14	CB984261	CB984261	AGENCOURT
153	c	171	17	10.5	663	29	BK221062	BK221062	DanLo ref	c	210	17	10.5	929	14	CB560981	CB560981	AGENCOURT
154	c	172	17	10.5	668	29	CE745740	CE745740	tlgr-gss-	c	211	17	10.5	930	29	CD517912	CD517912	AGENCOURT
155	c	173	17	10.5	668	29	AC057950	AC057950	Pan tcoyl	c	212	17	10.5	936	29	CD838802	CD838802	ZMBB6-049
156	c	174	17	10.5	669	9	AT768217	AT768217	w982e11.x	c	213	17	10.5	968	29	CG063792	CG063792	PUMCY197D
157	c	175	17	10.5	671	10	BF863192	BF863192	963041H04	c	214	17	10.5	984	28	CC265194	CC265194	CH261-37A
158	c	176	17	10.5						c	215	17	10.5	984	28	CC265194	CC265194	
159	c	177	17	10.5						c	216	17	10.5	997	29	CG457228	CG457228	PURXJ07TD

c	217	17	10.5	1034	28	BH157253	BH157253	ENTRHO3TF	c	274	16	9.9	378	28	B96541	B96541	T30G197R	TA
c	218	17	10.5	1070	28	BE2607705	BE2607705	WHADJ32TR	c	275	16	9.9	379	29	A1019049	A1019049	ub18c06.r	
c	219	17	10.5	1110	28	CC291185	CC291185	CH261-34I	c	276	16	9.9	383	29	AG2304077	AG2304077	Lotus	cor
c	220	17	10.5	1144	28	CC294442	CC294442	CH261-63I	c	277	16	9.9	384	14	R33779	R33779	YB82007.r	fl
c	221	17	10.5	1153	29	CC753656	CC753656	P048-4-CI	c	278	16	9.9	385	14	BV046240	BV046240	YB82007	fl
c	222	17	10.5	1191	29	AG039728	AG039728	Par. trogl	c	279	16	9.9	388	10	AM478171	AM478171	18B64	MAH
c	223	17	10.5	1303	10	AM914571	AM914571	EST345875	c	280	16	9.9	388	12	BG439838	BG439838	da627909.r	
c	224	17	10.5	1518	28	CC185828	CC185828	CH261-17E	c	281	16	9.9	395	28	CC102196	CC102196	CSU-K34.1	
c	225	16	9.9	116	28	BZ378781	BZ378781	SAUK_1119	c	282	16	9.9	396	13	BY701432	BY701432	AG-ND-17707	
c	226	16	9.9	126	10	AM176573	AM176573	RC3-CT007	c	283	16	9.9	401	28	BH399296	BH399296	AG-ND-17707	
c	227	16	9.9	126	28	AZ819734	AZ819734	2M0091G03	c	284	16	9.9	402	10	AM978069	AM978069	EST390187	
c	228	16	9.9	168	29	AG205814	AG205814	Oryza sat	c	285	16	9.9	402	14	R16121	R16121	YAS111.r	82
c	229	16	9.9	176	9	AA750246	AA750246	ISCA0139	c	286	16	9.9	404	10	BC075015	BC075015	pa22f03.y	
c	230	16	9.9	195	9	AA750239	AA750239	ISCA0131	c	287	16	9.9	406	10	AM626986	AM626986	pa22f03.y	
c	231	16	9.9	197	28	AZ848927	AZ848927	2M0150G10	c	288	16	9.9	406	10	BF566104	BF566104	UT-R-BT1-1	
c	232	16	9.9	198	14	CO961678	CO961678	SDX_224 G	c	289	16	9.9	407	9	AA585635	AA585635	SW309CA36	
c	233	16	9.9	198	14	CO966727	CO966727	SDX_13 Ge	c	290	16	9.9	407	29	CE695663	CE695663	t18r-gss-	
c	234	16	9.9	208	9	AA557261	AA557261	MBAS1M1B4	c	291	16	9.9	408	14	CB188998	CB188998	kz27f06.y	
c	235	16	9.9	222	9	AA151682	AA151682	LD419662.5	c	292	16	9.9	408	28	AZ924920	AZ924920	4906.fld55	
c	236	16	9.9	249	14	CM000202	CM000202	S345T_B03	c	293	16	9.9	409	29	CG686738	CG686738	ZMBB0C014	
c	237	16	9.9	250	10	AM409395	AM409395	sa19b5.sa	c	294	16	9.9	411	9	AA119853	AA119853	mp92a09.r	
c	238	16	9.9	250	28	BZ896399	BZ896399	CH240_14G	c	295	16	9.9	411	14	CF528923	CF528923	UT-1-BC1P	
c	239	16	9.9	251	9	AV150344	AV150344	AV150344	c	296	16	9.9	414	14	N71833	N71833	yz30c10.r	
c	240	16	9.9	258	13	BU791214	BU791214	PN158_Pop	c	297	16	9.9	418	10	BB704473	BB704473	BE7004473	
c	241	16	9.9	260	10	AM409231	AM409231	Fbd_P4_Fe	c	298	16	9.9						

c 331	16	9.9	480	14	CA873992	CA873992 K0929A05-	388	16	9.9	561	13	BX48885	BX48885 BX48885
c 332	16	9.9	481	29	CE178598	CE178598 t1gr-gsa-	c 389	16	9.9	561	29	CG990071	CG990071 CH240.148
c 333	16	9.9	483	12	BG553261	BG553261 dac23h09.	c 390	16	9.9	562	10	AM494096	AM494096 UI-M-BH3-
c 334	16	9.9	484	28	AZ632981	AZ632981 1M0487K22	c 391	16	9.9	564	28	AZ061798	AZ061798 RPTC-23-4
c 335	16	9.9	487	14	CB929887	CB929887 r169d03.y	c 392	16	9.9	566	12	BM893671	BM893671 118bbl0.x
c 336	16	9.9	488	9	AA170152	AA170152 m8bhl1.r	c 393	16	9.9	567	28	AQ176792	AQ176792 HS_3213.A
c 337	16	9.9	490	10	BE212504	BE212504 IPB1n012	c 394	16	9.9	569	9	AU043928	AU043928 AU043928
c 338	16	9.9	493	29	CE063030	CE063030 t1gr-gsa-	c 395	16	9.9	571	14	CF038515	CF038515 QCH24410.
c 339	16	9.9	495	9	AU157133	AU157133 AU157133	c 396	16	9.9	573	12	B1234171	B1234171 RE29827.5
c 340	16	9.9	496	10	BE629288	BE629288 uubbl1.y	c 397	16	9.9	576	28	AZ792847	AZ792847 2M0045B07
c 341	16	9.9	504	10	BE687130	BE687130 u06b08.y	c 398	16	9.9	577	12	BM485847	BM485847 pmlc-p0
c 342	16	9.9	505	13	BU445873	BU445873 603764244	c 399	16	9.9	580	12	BG212511	BG212511 R5732098
c 343	16	9.9	506	14	CA547648	CA547648 K0149604	c 400	16	9.9	581	29	CE513203	CE513203 t1gr-gsa-
c 344	16	9.9	508	28	AO598820	AO598820 HS_5348.A	c 401	16	9.9	583	10	AM187106	AM187106 BNLGH1952
c 345	16	9.9	509	28	AO557391	AO557391 HS_2081.A	c 402	16	9.9	584	29	CE181601	CE181601 t1gr-gsa-
c 346	16	9.9	510	28	AZ447929	AZ447929 1M0245N15	c 403	16	9.9	586	28	AZ071742	AZ071742 RPTC-23-4
c 347	16	9.9	511	28	BH383582	BH383582 AG-ND-175	c 404	16	9.9	587	28	B23361	B23361 F88ZTR 10F
c 348	16	9.9	513	12	BM902423	BM902423 rc35p04.y	c 405	16	9.9	587	29	CE634172	CE634172 t1gr-gsa-
c 349	16	9.9	515	28	AO401929	AO401929 HS_5045.A	c 406	16	9.9	588	10	BE775871	BE775871 MA3-0001U
c 350	16	9.9	516	12	BG521314	BG521314 p647e03.y	c 407	16	9.9	588	14	CD075410	CD075410 SD03976.5
c 351	16	9.9	520	9	AV712276	AV712276 AV712276	c 408	16	9.9	590	14	CA397750	CA397750 c85c01.y
c 352	16	9.9	520	14	CD483518	CD483518 atc01-14m	c 409	16	9.9	592	29	CG846339	CG846339 CG846339
c 353	16	9.9	521	13	BQ542151	BQ542151 P939h11.y	c 410	16	9.9	593	9	AA060977	AA060977 m18eg07.r
c 354	16	9.9	522	14	CF048856	CF048856 QC14c02.y	c 411	16	9.9	593	12	BM350788	BM350788 P1C1_56.F
c 355	16	9.9	522	14	CF048856	CF048856 QC14c02.y	c 412	16	9.9	593	29	CE425669	CE425669 t1gr-gsa-
c 356	16	9.9	529	29	CE784950	CE784950 t1gr-gsa-	c 413	16	9.9	594	28	AZ763102	AZ763102 1M0558K20
c 357	16	9.9	530	28	CC336918	CC336918 OGJAE19TV	c 414	16	9.9	596	13	BX103371	BX103371 BX103371
c 358	16	9.9	533	28	AO822194	AO822194 HS_5494.A	c 415	16	9.9	597	10	BG071624	BG071624 H3101C08-
c 359	16	9.9	534	29	CNS00USF	AO822194 HS_5494.A	c 416	16	9.9	597	28	AZ030184	AZ030184 RPTC-23-3
c 360	16	9.9	537	14	CB533975	CB533975 767275.MA	c 417	16	9.9	599	12	BM876941	BM876941 1h73d08.x
c 361	16	9.9	539	9	AL823328	AL823328 AL923328	c 418	16	9.9	599	28	BM403628	BM403628 AG-ND-138
c 362	16	9.9	540	10	BF499749	BF499749 AT14388.5	c 419	16	9.9	600	29	DR12E135	DR12E135 Dantlo ref
c 363	16	9.9	540	28	AQ788523	AQ788523 HS_2088.B	c 420	16	9.9	602	14	CF545349	CF545349 1ae7fa03.
c 364	16	9.9	540	29	CE852968	CE852968 t1gr-gsa-	c 421	16	9.9	603	12	B1636086	B1636086 SD17654.5
c 365	16	9.9	541	14	CB395924	CB395924 OSTR16358	c 422	16	9.9	604	9	AA540077	AA540077 606008E05
c 366	16	9.9	541	14	CB395924	CB395924 OSTR16358	c 423	16	9.9	606	13	BU320640	BU320640 603466696
c 367	16	9.9	542	9	AL520380	AL520380 LD40523.3	c 424	16	9.9	607	13	BX555119	BX555119 BX555119
c 368	16	9.9	543	14	CF794572	CF794572 B90100.MA	c 425	16	9.9	607	29	AG212146	AG212146 OY72a 98C
c 369	16	9.9	543	10	AM812203	AM812203 RC4-ST01.7	c 426	16	9.9	608	10	BG067978	BG067978 H306D05-
c 370	16	9.9	545	14	CD562175	CD562175 B0443F08-	c 427	16	9.9	609	9	AI692185	AI692185 m437f12.x
c 371	16	9.9	547	10	BE667228	BE667228 151477.MA	c 428	16	9.9	610	29	CE000811	CE000811 t1gr-gsa-
c 372	16	9.9	549	13	BQ085247	BQ085247 1h73d08.y	c 429	16	9.9	611	13	BU986819	BU986819 HFI2P24r
c 373	16	9.9	550	28	AZ054344	AZ054344 RPTC-23-4	c 430	16	9.9	611	14	CD563461	CD563461 B046A04-
c 374	16	9.9	550	29	CE023655	CE023655 t1gr-gsa-	c 431	16	9.9	612	28	BM877417	BM877417 h37h02.g
c 375	16	9.9	551	12	BM257782	BM257782 521636.MA	c 432	16	9.9	613	9	AL602935	AL602935 DKF2P686E
c 376	16	9.9	551	14	CB373904	CB373904 r660f06.y	c 433	16	9.9	614	10	BE775477	BE775477 MY-01-D-0
c 377	16	9.9	551	29	CE206231	CE206231 t1gr-gsa-	c 434	16	9.9	615	28	AZ397894	AZ397894 1M0163N05
c 378	16	9.9	551	29	CE206231	CE206231 t1gr-gsa-	c 435	16	9.9	616	12	BG616700	BG616700 602614913
c 379	16	9.9	551	29	CE206231	CE206231 t1gr-gsa-	c 436	16	9.9	617	10	BB161636	BB161636 BB161636
c 380	16	9.9	551	29	CE206231	CE206231 t1gr-gsa-	c 437	16	9.9	618	14	CB429326	CB429326 605134.MA
c 381	16	9.9	552	12	B1813367	B1813367 PFSSTgeal	c 438	16	9.9	619	29	CE531186	CE531186 t1gr-gsa-
c 382	16	9.9	553	28	AQ766761	AQ766761 HS_2101.A	c 439	16	9.9	620	13	BX555119	BX555119 BX555119
c 383	16	9.9	554	14	CF788428	CF788428 860377.MA	c 440	16	9.9	621	28	AZ397894	AZ397894 1M0163N05
c 384	16	9.9	555	10	BF693832	BF693832 602082382	c 441	16	9.9	622	12	BG616700	BG616700 602614913
c 385	16	9.9	556	10	BB756027	BB756027 BB756027	c 442	16	9.9	623	10	BB161636	BB161636 BB161636
c 386	16	9.9	556	14	CB532876	CB532876 757360.MA	c 443	16	9.9	624	14	CB429326	CB429326 605134.MA
c 387	16	9.9	558	12	BG538080	BG538080 RH122_66-	c 444	16	9.9	625	29	CE531186	CE531186 t1gr-gsa-

445	c	445	16	9.9	619	29	CE825113	t1gr-gsa-	502	16	664	14	CF789214	CF789214	866466	MA
446	c	446	16	9.9	620	29	CE559277	CE559277	503	16	664	14	CF810779	CF810779	CA521F	CD
447	c	447	16	9.9	622	10	AM535071	AM535071	504	16	664	28	AQ157286	AQ157286	Nbhd	009A
448	c	448	16	9.9	622	10	BU439174	604142919	505	16	664	28	CC086559	CC086559	CSU	-K33-
449	c	449	16	9.9	622	14	CA211066	CA211066	506	16	665	14	CF623971	CF623971	zmmw05	-O
450	c	450	16	9.9	622	14	CK098124	CK098124	507	16	667	14	CA223731	CA223731	SCdFfLIC	
451	c	451	16	9.9	623	9	AA949183	AA949183	508	16	667	14	CF253453	CF253453	advn12B	-C
452	c	452	16	9.9	623	9	AI338630	AI338630	509	16	668	28	AZ568861	AZ568861	252PVE12	
453	c	453	16	9.9	624	28	A2994273	2M0279X09	510	16	668	28	AQ250794	AQ250794	T1BP17	-T7
454	c	454	16	9.9	624	29	AG226080	Lotus cor	511	16	671	28	BZ601681	BZ601681	WHAF35TR	
455	c	455	16	9.9	626	12	BK639623	170006875	512	16	671	28	BZ941013	BZ941013	CH240	91C
456	c	456	16	9.9	626	28	BH515668	BH515668	513	16	672	28	BH702051	BH702051	BOMLPR3TR	
457	c	457	16	9.9	627	14	CB455966	CB455966	514	16	673	29	CG153573	CG153573	PUEFEL4TB	
458	c	458	16	9.9	627	28	BH319373	BH319373	515	16	674	9	AVB821927	AVB821927	AVB821927	
459	c	459	16	9.9	628	28	AB897310	AB897310	516	16	675	14	CB455280	CB455280	712414	NA
460	c	460	16	9.9	628	29	CC857793	CC857793	517	16	675	29	AG049167	AG049167	Pan trngl	
461	c	461	16	9.9	629	14	CA365723	CA365723	518	16	676	28	AZ659169	AZ659169	1M0516E21	
462	c	462	16	9.9	630	9	AI405818	AI405818	519	16	676	29	CE719078	CE719078	CE719078	
463	c	463	16	9.9	631	10	BB629376	BB629376	520	16	677	29	CNS05AJJ	CNS05AJJ	t1gr-gsa-	
464	c	464	16	9.9	634	29	CE277247	t1gr-gsa-	521	16	678	28	AZ575158	AZ575158	TeBtaodon	
465	c	465	16	9.9	636	13	BK099019	BK099019	522	16	678	28	BH178932	BH178932	338PVA11	
466	c	466	16	9.9	636	14	CB538309	CB538309	523	16	679	29	CNS07LAU	CNS07LAU	T7 end of	
467	c	467	16	9.9	637	10	AW791396	D00514-F	524	16	679	29	1BAF029G09	1BAF029G09	1A691686	
468	c	468	16	9.9	638	28	A2987216	A2987216	525	16	680	10	BE325920	BE325920	NFO43B11S	
469	c	469	16	9.9	639	10	BG067505	BG067505	526	16	681	14	CK003897	CK003897	AGNOCOURT	
470	c	470	16	9.9	639	13	BO517268	BO517268	527	16	684	14	CF200052	CF200052	BB653687	
471	c	471	16	9.9	640	12	BZ626946	BZ626946	528	16	684	14	CF200052	CF200052	BB653687	
472	c	472	16	9.9	640	29	CC860672	NDL.18J3	529	16	687	28	AZ968036	AZ968036	EST5167	T
473	c	473	16	9.9	641	28	A2401200	A2401200	530	16	688	29	CE223207	CE223207	t1gr-gsa-	
474	c	474	16	9.9	642	12	B1231463	B1231463	531	16	689	9	AU129220	AU129220	AU129220	
475	c	475	16	9.9	642	29	CE359090	CE359090	532	16	692	12	BH341247	BH341247	MEST332-D	
476	c	476	16	9.9	643	10	BH183510	BH183510	533	16	692	28	BH999290	BH999290	oeh12e09	
477	c	477	16	9.9	643	13	BX717850	BX717850	534	16	693	13	EX845303	EX845303	BX845303	
478	c	478	16	9.9	643	13	BH723970	BH723970	535	16	693	28	AZ952120	AZ952120	2M0216017	
479	c	479	16	9.9	646	14	CA359249	CA359249	536	16	695	28	A2987599	A2987599	CMK1078.5	
480	c	480	16	9.9	646	14	CA352422	CA352422	537	16	695	28	AZ9670416	AZ9670416	BMO270A16	
481	c	481	16	9.9	647	28	AQ200875	AQ200875	538	16	695	28	BH421862	BH421862	BOGYPO7TR	
482	c	482	16	9.9	648	28	AB955759	AB955759	539	16	695	28	BZ010906	BZ010906	oeh61h05	
483	c	483	16	9.9	651	28	BZ334376	BZ334376	540	16	699	14	CA384766	CA384766	CH230-352	
484	c	484	16	9.9	651	29	CC065596	CC065596	541	16	699	14	CA384766	CA384766	6654927	NC
485	c	485	16	9.9	652	29	AG243390	AG243390	542	16	700	13	BQ190789	BQ190789	Ud141F08	
486	c	486	16	9.9	653	28	BZ373337	BZ373337	543	16	703	13	BUT68129	BUT68129	UI-R-DZO	
487	c	487	16	9.9	653	28	A2401025	A2401025	544	16	703	13	CE464734	CE464734	t1gr-gsa-	
488	c	488	16	9.9	655	28	BZ892684	BZ892684	545	16	703	13	BUT68129	BUT68129	STBGB11	
489	c	489	16	9.9	656	29	CE275976	CE275976	546	16	706	28	AQ345539	AQ345539	UI-R-FFO	
490	c	490	16	9.9	657	14	CF787473	CF787473	547	16	710	9	A1200883	A1200883	qf68a10.x	
491	c	491	16	9.9	657	14	CF788067	CF788067	548	16	711	14	CB428754	CB428754	604501	MA
492	c	492	16	9.9	657	28	BZ343375	BZ343375	549	16	715	28	BH403106	BH403106	AG-ND-155	
493	c	493	16	9.9	658	28	A2420339	A2420339	550	16	716	12	EM606494	EM606494	170006870	
494	c	494	16	9.9	660	10	BH168452	BH168452	551	16	717	28	BZ768072	BZ768072	PUEF162TD	
495	c	495	16	9.9	660	12	BH993569	BH993569	552	16	720	28	BZ891966	BZ891966	hml1_0140	
496	c	496	16	9.9	660	13	BH138813	BH138813	553	16	721	14	CB427237	CB427237	602805	MA
497	c	497	16	9.9	660	13	BY741957	BY741957	554	16	722	14	BUT68004	BUT68004	STBEB12	
498	c	498	16	9.9	660	29	CC590740	CC590740	555	16	722	14	CA447176	CA447176	UI-H-EIO-	
499	c	499	16	9.9	662	9	AI405617	AI405617	556	16	722	14	CA447176	CA447176	UI-H-EIO-	
500	c	500	16	9.9	662	9	AI405617	AI405617	557	16	722	14	CA447176	CA447176	UI-H-EIO-	
501	c	501	16	9.9	664	12	BZ293160	BZ293160	558	16	722	14	CA447176	CA447176	UI-H-EIO-	

c 559	16	9.9	722	29	CG949817	CG949817	MEHMB1TR	c 616	16	9.9	795	28	BH389992	BH389992	AG-ND-138
c 560	16	9.9	722	29	BK233518	BK233518	Danlo ref	c 617	16	9.9	796	9	AUI37771	AUI37771	AUI37771
c 561	16	9.9	726	13	BU249040	BU249040	603784017	c 618	16	9.9	797	28	BH335464	BH335464	BH335464
c 562	16	9.9	727	13	BK883341	BK883341	BK883341	c 619	16	9.9	798	13	BU333177	BU333177	BU333177
c 563	16	9.9	727	28	BH485224	BH485224	BH485224	c 620	16	9.9	798	29	CE425788	CE425788	CE425788
c 564	16	9.9	727	29	CG641738	CG641738	OGFVY6TV	c 621	16	9.9	799	28	BH021670	BH021670	BH021670
c 565	16	9.9	728	28	BH583083	BH583083	BOGLA80TF	c 622	16	9.9	801	29	BK185384	BK185384	BK185384
c 566	16	9.9	730	12	BH359737	BH359737	GA_Ea002	c 623	16	9.9	802	14	CAJ18126	CAJ18126	CAJ18126
c 567	16	9.9	731	28	BH402292	BH402292	AG-ND-173	c 624	16	9.9	803	29	BK243830	BK243830	BK243830
c 568	16	9.9	731	29	CG707343	CG707343	OGLEA66TH	c 625	16	9.9	804	29	BK167767	BK167767	BK167767
c 569	16	9.9	736	14	CK024960	CK024960	AGENCOCURT	c 626	16	9.9	807	13	CAJ51038	CAJ51038	CAJ51038
c 570	16	9.9	736	28	BZ247285	BZ247285	CH230-314	c 627	16	9.9	809	13	BU247028	BU247028	BU247028
c 571	16	9.9	738	28	BZ267545	BZ267545	CH230-509	c 628	16	9.9	809	28	BH581997	BH581997	BH581997
c 572	16	9.9	740	13	BK308145	BK308145	BK308145	c 629	16	9.9	811	14	CB987011	CB987011	CB987011
c 573	16	9.9	740	14	CF440304	CF440304	EST676849	c 630	16	9.9	812	14	CB643080	CB643080	CB643080
c 574	16	9.9	740	28	A0579380	A0579380	rbdb0084E	c 631	16	9.9	813	14	CB652581	CB652581	CB652581
c 575	16	9.9	741	28	CC128947	CC128947	NDL_24H7.	c 632	16	9.9	814	13	BU381144	BU381144	BU381144
c 576	16	9.9	742	28	BZ442381	BZ442381	BONQ028TF	c 633	16	9.9	815	29	CC702332	CC702332	CC702332
c 577	16	9.9	742	29	CG961933	CG961933	MBSGES2TF	c 634	16	9.9	816	13	BK854332	BK854332	BK854332
c 578	16	9.9	743	29	CG304722	CG304722	t1gr-gss-	c 635	16	9.9	816	28	BZ444844	BZ444844	BZ444844
c 579	16	9.9	745	13	BU631677	BU631677	UI-H-FL0-	c 636	16	9.9	818	28	BZ427573	BZ427573	BZ427573
c 580	16	9.9	745	13	BW017012	BW017012	BW017012	c 637	16	9.9	818	29	CC753721	CC753721	CC753721
c 581	16	9.9	748	29	AG095742	AG095742	Pan treq1	c 638	16	9.9	819	9	AA439751	AA439751	AA439751
c 582	16	9.9	748	29	AG095742	AG095742	Pan treq1	c 639	16	9.9	819	14	CB628438	CB628438	CB628438
c 583	16	9.9	754	14	CK111978	CK111978	V060F12_P	c 640	16	9.9	824	14	CB678408	CB678408	CB678408
c 584	16	9.9	756	29	BK215180	BK215180	Danlo ref	c 641	16	9.9	825	28	AY080049	AY080049	AY080049
c 585	16	9.9	758	12	B1333881	B1333881	B1333881	c 642	16	9.9	826	14	CF451006	CF451006	CF451006
c 586	16	9.9	758	28	BZ481949	BZ481949	BONBF64TR	c 643	16	9.9	829	13	BF997432	BF997432	BF997432
c 587	16	9.9	758	29	CG944722	CG944722	MBSF65TR	c 644	16	9.9	830	14	B0930760	B0930760	B0930760
c 588	16	9.9	759	29	CG870064	CG870064	NDL_52114	c 645	16	9.9	830	28	BZ612705	BZ612705	BZ612705
c 589	16	9.9	762	28	AG857071	AG857071	rbdb0004J	c 646	16	9.9	833	14	CF436537	CF436537	CF436537
c 590	16	9.9	764	29	CC542550	CC542550	CH240_423	c 647	16	9.9	835	28	BZ259663	BZ259663	BZ259663
c 591	16	9.9	765	29	CC738960	CC738960	PUIAC35TD	c 648	16	9.9	836	29	CG173131	CG173131	CG173131
c 592	16	9.9	766	13	BU631648	BU631648	UI-H-FL0-	c 649	16	9.9	837	29	CC587519	CC587519	CC587519
c 593	16	9.9	768	13	BU928780	BU928780	AGENCOCURT	c 650	16	9.9	841	29	CC955594	CC955594	CC955594
c 594	16	9.9	770	10	BE738201	BE738201	601572625	c 651	16	9.9	842	14	CB625678	CB625678	CB625678
c 595	16	9.9	770	28	BE978517	BE978517	PUGGSA5TD	c 652	16	9.9	844	29	CG108421	CG108421	CG108421
c 596	16	9.9	772	28	BZ416431	BZ416431	1f67d07.g	c 653	16	9.9	845	29	AG035722	AG035722	AG035722
c 597	16	9.9	776	28	BZ150589	BZ150589	CH230-395	c 654	16	9.9	847	14	CF253967	CF253967	CF253967
c 598	16	9.9	776	29	CG151708	CG151708	PURQ662TB	c 655	16	9.9	847	28	AZ128532	AZ128532	AZ128532
c 599	16	9.9	778	28	AZ828358	AZ828358	2M0107B05	c 656	16	9.9	847	14	CF253967	CF253967	CF253967
c 600	16	9.9	780	13	BU630464	BU630464	UI-H-FL0-	c 657	16	9.9	847	28	AQ576217	AQ576217	AQ576217
c 601	16	9.9	780	14	CF483412	CF483412	POL1_22.D	c 658	16	9.9	855	29	CC602805	CC602805	CC602805
c 602	16	9.9	781	29	BK222679	BK222679	Danlo ref	c 659	16	9.9	856	12	BG916179	BG916179	BG916179
c 603	16	9.9	783	29	CC859732	CC859732	NDL_111M2	c 660	16	9.9	858	29	PT005A23R	PT005A23R	PT005A23R
c 604	16	9.9	783	29	CG669492	CG669492	t1gr-gss-	c 661	16	9.9	860	29	CG946918	CG946918	CG946918
c 605	16	9.9	784	28	BH199999	BH199999	Sml-55B18	c 662	16	9.9	860	29	CG958977	CG958977	CG958977
c 606	16	9.9	785	29	CG923947	CG923947	t072e24ba	c 663	16	9.9	863	29	CG963364	CG963364	CG963364
c 607	16	9.9	786	12	BG185998	BG185998	RST4954.A	c 664	16	9.9	864	14	CF589353	CF589353	CF589353
c 608	16	9.9	786	12	BG208101	BG208101	RST27591	c 665	16	9.9	866	28	BH682706	BH682706	BH682706
c 609	16	9.9	788	28	BH699188	BH699188	BOMAT35TF	c 666	16	9.9	876	29	CG767005	CG767005	CG767005
c 610	16	9.9	789	28	BZ422320	BZ422320	1d52c09.b	c 667	16	9.9	877	29	CG173133	CG173133	CG173133
c 611	16	9.9	790	13	BQ438031	BQ438031	AGENCOCURT	c 668	16	9.9	878	12	BW801605	BW801605	BW801605
c 612	16	9.9	792	29	CC923973	CC923973	t072h02ba	c 669	16	9.9	879	13	BU909786	BU909786	BU909786
c 613	16	9.9	793	28	CC128692	CC128692	NDL_32F18	c 670	16	9.9	880	10	BE573888	BE573888	BE573888
c 614	16	9.9	794	13	BU751446	BU751446	CH4#002.B	c 671	16	9.9	881	10	BF625057	BF625057	BF625057
c 615	16	9.9	795	14	CG301791	CG301791	AGENCOCURT	c 672	16	9.9	891	10	BF625057	BF625057	BF625057

673	16	9.9	882	28	B2563263	B2563263	pac2-164	c 720	16	9.9	991	12	BM470743	BM470743	AGENCOURT
674	16	9.9	882	28	B267444	B267444	PUGC96TB	731	16	9.9	995	28	CC188842	CC188842	CC188842
675	16	9.9	882	29	CG31617	CG31617	OGIAR28TH	732	16	9.9	997	10	BF105334	BF105334	BF105334
676	16	9.9	883	14	CF619324	CF619324	AGENCOURT	733	16	9.9	999	28	BE799407	BE799407	BE799407
677	16	9.9	885	29	CG153374	CG153374	PUIFEI4TD	c 734	16	9.9	1002	12	BM465904	BM465904	BM465904
678	16	9.9	889	28	B2152441	B2152441	CH230-300	735	16	9.9	1004	9	AA142280	AA142280	AA142280
679	16	9.9	891	13	BU218483	BU218483	603105678	c 736	16	9.9	1004	14	CD081586	CD081586	CD081586
680	16	9.9	891	29	CG362146	CG362146	OGIDE90TH	c 737	16	9.9	1004	29	CG462023	CG462023	CG462023
681	16	9.9	893	28	AQ745410	AQ745410	HS_2276_A	c 738	16	9.9	1011	28	CC191499	CC191499	CC191499
682	16	9.9	894	29	CG31626	CG31626	OGIAR28TV	739	16	9.9	1011	28	CC257436	CC257436	CC257436
683	16	9.9	894	29	CG946014	CG946014	MBECG81TR	740	16	9.9	1014	28	CC253070	CC253070	CC253070
684	16	9.9	895	14	CF375319	CF375319	EX371377	741	16	9.9	1017	28	CC271663	CC271663	CC271663
685	16	9.9	896	13	BK371377	BK371377	AGENCOURT	c 742	16	9.9	1034	28	BM692631	BM692631	BM692631
686	16	9.9	898	29	CG970696	CG970696	MBEED27R	743	16	9.9	1038	28	CC245241	CC245241	CC245241
687	16	9.9	903	29	CG362154	CG362154	OGIDE90TV	744	16	9.9	1042	29	ONS05EVH	ONS05EVH	ONS05EVH
688	16	9.9	904	13	BK716763	BK716763	AL22888	745	16	9.9	1047	12	BG873533	BG873533	BG873533
689	16	9.9	904	29	CNS03021	CNS03021	Tetradon	c 746	16	9.9	1050	28	CC240612	CC240612	CC240612
690	16	9.9	909	12	B1523195	B1523195	603175292	c 747	16	9.9	1063	10	BE548664	BE548664	BE548664
691	16	9.9	910	12	BG420928	BG420928	602451139	748	16	9.9	1072	14	CF594645	CF594645	CF594645
692	16	9.9	910	28	BH138789	BH138789	ENTND15TR	749	16	9.9	1082	28	CC238259	CC238259	CC238259
693	16	9.9	914	12	B1690101	B1690101	603310579	750	16	9.9	1101	29	CNS00221	CNS00221	CNS00221
694	16	9.9	914	13	BU517782	BU517782	AGENCOURT	c 751	16	9.9	1106	28	AQ446181	AQ446181	AQ446181
695	16	9.9	915	29	CG151709	CG151709	PURFG62TD	752	16	9.9	1108	28	CC262998	CC262998	CC262998
696	16	9.9	916	29	CG436376	CG436376	OGVGF48TV	753	16	9.9	1125	28	CC185298	CC185298	CC185298
697	16	9.9	919	28	CC130183	CC130183	NDL_18816	754	16	9.9	1129	10	BE905413	BE905413	BE905413
698	16	9.9	921	13	BK773762	BK773762	EX773762	c 755	16	9.9	1136	28	A2916351	A2916351	A2916351
699	16	9.9	923	29	CG131415	CG131415	PUDJ84TD	756	16	9.9	1139	12	BM467431	BM467431	BM467431
700	16	9.9	924	12	BM423230	BM423230	PLATE3_HO	c 757	16	9.9	1168	28	CC298383	CC298383	CC298383
701	16	9.9	925	28	CC125527	CC125527	NDL_34P9_	c 758	16	9.9	1173	12	BM51289	BM51289	BM51289
702	16	9.9	931	13	BK410931	BK410931	EX410931	759	16	9.9	1175	28	CC256247	CC256247	CC256247
703	16	9.9	933	28	BH137941	BH137941	ENTOKO9TF	c 760	16	9.9	1201	13	BK335869	BK335869	BK335869
704	16	9.9	934	13	BU148598	BU148598	AGENCOURT	c 761	16	9.9	1216	28	CC235126	CC235126	CC235126
705	16	9.9	935	29	CNS042CH	CNS042CH	Tetradon	c 762	16	9.9	1224	12	BM802570	BM802570	BM802570
706	16	9.9	936	28	B237678	B237678	CH230-382	763	16	9.9	1272	13	BU598573	BU598573	BU598573
707	16	9.9	937	29	CG392166	CG392166	FGHCRC-GT-	764	16	9.9	1294	12	BM463932	BM463932	BM463932
708	16	9.9	939	13	BO959509	BO959509	AGENCOURT	765	16	9.9	1324	12	BM913824	BM913824	BM913824
709	16	9.9	939	28	CC108498	CC108498	NDL_32K16	c 766	16	9.9	1333	13	BO065958	BO065958	BO065958
710	16	9.9	940	29	CG057912	CG057912	PUDGN14TD	c 767	16	9.9	1486	28	CC287785	CC287785	CC287785
711	16	9.9	942	13	BU916451	BU916451	AGENCOURT	c 768	16	9.9	1510	28	CC194715	CC194715	CC194715
712	16	9.9	944	13	BU511146	BU511146	AGENCOURT	769	16	9.9	1533	28	CC286541	CC286541	CC286541
713	16	9.9	945	28	CC126815	CC126815	NDL_76B2_	770	16	9.9	1545	29	AV413932	AV413932	AV413932
714	16	9.9	945	29	CG957595	CG957595	MBEGP67TR	771	16	9.9	1562	29	AV413931	AV413931	AV413931
715	16	9.9	951	29	CNS020MD	CNS020MD	Tetradon	772	16	9.9	1652	12	BG847977	BG847977	BG847977
716	16	9.9	954	12	BT453051	BT453051	603170023	c 773	16	9.9	2416	11	AK037904	AK037904	AK037904
717	16	9.9	957	28	CC389388	CC389388	PURH139TD	774	16	9.9	3378	11	AK045737	AK045737	AK045737
718	16	9.9	958	29	CG34429	CG34429	OGW6114TV	775	16	9.9	4488	11	BC051291	BC051291	BC051291
719	16	9.9	962	28	CC004068	CC004068	PUDG250TD	c 776	16	9.9	123	10	BM384173	BM384173	BM384173
720	16	9.9	965	12	BG180043	BG180043	602329604	777	15	9.3	125	13	BM029376	BM029376	BM029376
721	16	9.9	965	13	BO963710	BO963710	AGENCOURT	778	15	9.3	130	13	BO097827	BO097827	BO097827
722	16	9.9	967	13	BU520154	BU520154	CSU-K33F-	779	15	9.3	132	14	CF384710	CF384710	CF384710
723	16	9.9	970	28	CC066430	CC066430	PURFR79TD	780	15	9.3	133	13	BO557397	BO557397	BO557397
724	16	9.9	970	28	BZ799408	BZ799408	PURFR79TD	781	15	9.3	138	29	BM094377	BM094377	BM094377
725	16	9.9	974	28	BZ477598	BZ477598	BONK49TF	c 782	15	9.3	140	13	BM094377	BM094377	BM094377
726	16	9.9	980	28	BZ477598	BZ477598	BONK49TF	c 783	15	9.3	143	28	BM893664	BM893664	BM893664
727	16	9.9	981	12	BG105901	BG105901	602290078	784	15	9.3	153	9	AV346340	AV346340	AV346340
728	16	9.9	983	29	CNS010CW	CNS010CW	Anopheles	c 785	15	9.3	155	14	CA851790	CA851790	CA851790
729	16	9.9	986	28	BH721819	BH721819	BONNEB6TF	786	15	9.3	155	14	CA851790	CA851790	CA851790

787	15	9.3	157	9	A1897395	A1897395	EST26638
786	15	9.3	157	14	R36155	R36155	YH2N01.s1
789	15	9.3	160	9	AA585483	AA585483	JTH124 HT
790	15	9.3	160	28	CC101623	CC101623	CSU-K34.1
791	15	9.3	162	9	AL697631	AL697631	DFE2P686L
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Job time : 820.155 sec

OM nucleic - nucleic search, using sw model

Run on: October 14, 2004, 09:12:14 ; Search time 831.586 Seconds
(without alignments) 8443.595 Million cell updates/sec

Title: US-09-407-804A-7

Perfect score: 162

Sequence: 1 atgagacacacattatataaag.....aatgcttttcaagaataaa 162

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	144.4	89.1	43594	6	BD245634	BD245634 Developme
5	142.8	88.1	1408	6	AR354422	AR354422 Sequence
6	142.8	88.1	43604	7	AF424781	AF424781 Staphyloc
7	141.4	87.3	159	6	AK618544	AK618544 Sequence
8	141.2	87.2	291150	1	AP003135	AP003135 Staphyloc
9	138.2	85.3	159	6	AK583668	AK583668 Sequence
10	138	85.2	42722	7	AF424783	AF424783 Staphyloc
11	138	85.2	272850	1	AP004828	AP004828 Developme
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41 33.2 20.5 156181 2 AC101833
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ALIGNMENTS

RESULT 1
BD245278 162 bp DNA linear PAT 17-JUL-2003
LOCUS BD245278
DEFINITION Development of novel antibiotics based on bacteriophage genomics.
ACCESSION BD245278.1 GI:33055048
VERSION JP 2002531107-A/13.
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 162)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Development of novel antibiotics based on bacteriophage genomics
JOURNAL Patent: JP 2002531107-A 13 24-SEP-2002;
PUBTECH INC
COMMENT OS Staphylococcus aureus bacteriophage 77
PN JP 2002531107-A/13
PD 24-SEP-2002
PF 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR
01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454252 PT JERRY
PELLETIER,PHILIPPE GROS,MICHAEL DUBOW
PC C12N15/09,A01N63/00,A61K45/00,A61P31/04,C07K14/005,
PC C12N15/00,
PC C12N1/21,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/566, PC
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PC A61K37/02
CC Coding Sequence
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FT aureus bacteriophage 77,
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DB 121 GCAACATTCATGTAACACAAAGATGCTTTTCAAGATTA 162

RESULT 2
BD245281 41708 bp DNA linear PAT 17-JUL-2003
LOCUS BD245281
DEFINITION Development of novel antibiotics based on bacteriophage genomics.
ACCESSION BD245281
VERSION JP 2002531107-A/16.
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 41708)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Development of novel antibiotics based on bacteriophage genomics
JOURNAL Patent: JP 2002531107-A 16 24-SEP-2002;
PUBTECH INC
COMMENT OS Staphylococcus aureus bacteriophage 77
PN JP 2002531107-A/16
PD 24-SEP-2002
PF 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR
01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454252 PT JERRY
PELLETIER,PHILIPPE GROS,MICHAEL DUBOW
PC C12N15/09,A01N63/00,A61K45/00,A61P31/04,C07K14/005,
PC C12N1/21,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/566, PC
C12N15/00,
PC A61K37/02
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FT source 1..41708
FT aureus bacteriophage 77,
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 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 29171 GCAACATTCATGTACTACAAAGATGCTTTTCAAGATTA 29212

RESULT 3
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 LOCUS AR368770 41708 bp DNA linear PAT 12-SEP-2003
 DEFINITION Sequence 3 from patent US 637652.
 ACCESSION AR368770
 VERSION AR368770.1 GI:34603077
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 41708)
 AUTHORS Palletier,J., Gros,P. and Dubow,M.
 TITLE Compositions and methods involving an essential *Staphylococcus aureus* gene and its encoded protein
 JOURNAL Patent: US 637652-A 3 23-APR-2002;
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ORIGIN

Query Match 100.0%; Score 162; DB 6; Length 41708;
 Best Local Similarity 100.0%; Pred. No. 2.8e-36;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 29171 GCAACATTCATGTACTACAAAGATGCTTTTCAAGATTA 29212

RESULT 4

BD245634 43594 bp DNA linear PAT 17-JUL-2003
 LOCUS BD245634
 DEFINITION Development of novel antibiotics based on bacteriophage genomics.
 ACCESSION BD245634
 VERSION BD245634.1 GI:33055404
 KEYWORDS JP 2002531107-A/369.
 SOURCE JP 2002531107-A/369.
 ORGANISM unidentified
 SOURCE unidentified
 ORGANISM unidentified

REFERENCE 1 (bases 1 to 43594)
 AUTHORS Palletier,J., Gros,P. and Dubow,M.
 TITLE Development of novel antibiotics based on bacteriophage genomics
 JOURNAL Patent: JP 2002531107-A 369 24-SEP-2002;
 COMMENT PHAGEGEN INC
 OS *Staphylococcus aureus* bacteriophage 96
 PN JP 2002531107-A/369

PD 24-SEP-2002
 PF 03-DEC-1999 JP 2000585456
 PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR
 28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR
 01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454252 PI JERRY
 PELLETIER, PHILIPPE GROS, MICHAEL DUBOW
 PC C12N1/00, A01N63/00, A61K38/00, A61K45/00, A61P31/04, C07K14/005,
 PC C12N1/21, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/566, PC
 C12N15/00,
 PC A61K37/02
 CC Genome Sequence
 CC Key Location/Qualifiers
 FT source 1..43594
 FT aureus bacteriophage /organism="Staphylococcus aureus bacteriophage 96".
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 /db_xref="taxon:32644"

ORIGIN

Query Match 89.1%; Score 144.4; DB 6; Length 43594;
 Best Local Similarity 93.2%; Pred. No. 3.2e-31;
 Matches 151; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ATAGCAACATTATATAAGCTAGTACAGATATTGCTTCAAGCTCTAGCGATT 60
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 DB 4456 ATAGCAACATTATATAAGCTAGTACAGATATTGCTTCAAGCTCTAGCGATT 4515
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 QY 61 GTACTATGCGGTTTCTATCTCACTACAGATGTCATTCGCGGATTGCGAAGTATC 120
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 DB 4516 GTACTATGCGGTTTCTATCTCACTACAGATGTCATTCGCGGATTGCGAAGTATC 4575
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 QY 121 GCAACATTCATGTACTACAAAGATGCTTTTCAAGATTA 162
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 DB 4576 GCAACATTCATGTACTACAAAGATGCTTTTCAAGATTA 4617

RESULT 5
AR354422/c 1408 bp DNA linear PAT 17-AUG-2003
LOCUS AR354422
DEFINITION Sequence 540 from patent US 6593114.
ACCESSION AR354422
VERSION AR354422.1 GI:33760306
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1408)
AUTHORS Kunach,C.A., Choi,G.H., Barash,S., Dillon,P.J., Fannon,M.R. and Rosen,C.A.
TITLE Staphylococcus aureus polynucleotides and sequences
JOURNAL Patent: US 6593114-A 540 15-JUL-2003;
FEATURES
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ORIGIN
Query Match 88.1%; Score 142.8; DB 6; Length 1408;
Best Local Similarity 92.6%; Pred. No. 1.4e-30;
Matches 150; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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DB 339 ATGACGACATTATATAAGCTAGTACGATATTGCTTACAGCTCTTACGATT 280
61 GTACTTATGCGCTTTCTATCTACTACGATGATGATGCGGATTCGCAAGTAC 120
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DB 279 GTACTTATGCGCTTTCTATCTACTACGATGATGATGCGGATTCGCAAGTAC 220
QY 121 GCGACATTCGCTACTACGAAGATGCTTTTCAAGATTA 162
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DB 219 GCGACATTCGCTACTACGAAGATGCTTTTCAAGATTA 178
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RESULT 6
AF424781 43604 bp DNA linear PHG 10-JUN-2002
LOCUS AF424781
DEFINITION Staphylococcus aureus phage phi 11, complete genome.
ACCESSION AF424781
VERSION AF424781.1 GI:18920487
KEYWORDS
SOURCE Staphylococcus aureus phage phi 11
ORGANISM Staphylococcus aureus phage phi 11
REFERENCE 1 (bases 1 to 43604)
AUTHORS Vltusovs,dadna viruses, no RNA stages; Caudovirales; Siphoviridae.
Iandolo,J.J., Worrell,V., Grocher,K.H., Qian,Y., Tian,R.,
Kenton,S., Dorman,A., Ji,H., Lin,S., Lon,P., Qi,S., Zhu,H. and
Roo,B.A.
TITLE Comparative analysis of the genomes of the temperate bacteriophages
JOURNAL ph11, ph12 and ph13 of Staphylococcus aureus 8325
Gene 289 (1-2), 109-118 (2002)
MEDLINE 22032962
PUBMED 12036589
REFERENCE 2 (bases 1 to 43604)
AUTHORS Iandolo,J.J., Worrell,V., Roe,B., Qian,Y., Dorman,A., Tian,R.,
Lin,S. and Jia,H.
TITLE Direct Submission
JOURNAL Submitted (26-SEP-2001) Microbiology and Immunology, Univ. of
Oklahoma Health Sciences Center, 940 S.E. Young Blvd, Oklahoma City,
OK 73190, USA
FEATURES
source location/Qualifiers
1..43604
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KINSNRKEINLKRESKGIIPENLRKLNINNESSRKIPDNYFIKGGEL
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NANDLPASLRKTOLETVNDQFEYHIVAVDCNSERKILATSLILGRALEIMCRLI
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complement(2901..3620)

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 6696..7016
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 MSQSNPFWNANGPIEINDDLF"
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 GENNGRSIVDKT"
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SMGPTAVSEVTEQIARVIFILGVLVAVFDGSLILANGALFPAANGAIGIFPLM
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GALSIVGIPSQLQDIFENLANSNKIVMIPYSISAGAVSLIPYITRTAEGRLEEM
HHQIRTSIGVLEITVPASIGMALAQPLETFVGYDPIYLGHDNDGSRLLFYAP
VALIISLSTVASMLOGIDROKLTVYVILASVIRKLANPLIMLFTFPALISTIA
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VITSLQNNNGFASNTDFFYKQLEGEVYVNSLTADPPSSNSGVMDNFVYTD
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INQONTDOVDTTNOAVNAIDVEAEVYIRKALADIEKAVKQOQIDSLDSTON
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LDEANOLISDTLKQAOEINTNDQADATVDRQOTKAEQIKRKRARRRAALDSIE
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NIAIAQVEKELIKAQOIASAVTNADVAILHDEKREIEIEEPYINRKASAREDTLL
FNDKQAEIANIOATVEERSIILAQONIVYTAIGQIDODRSNNOVDRKASAREDTLL
DLDVHPIKRPDAKTIINDLARTALNONVYKRNKSNRNKALKATITALQOMDELEKT
ARTNADVAVLKRNVALSIDVATTEKENSILARTINQQTAKRKALATBEOLAKV
KYLIDQVADGNRTDEDAIDNDIKQHTQVLDVILAILKPAEXTVSPKEIQAPARY
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Query Match 87.2%; Score 141.2; DB 1; Length 291150;
Best Local Similarity 92.0%; Pred. No. 2,1e-30;
Matches 149; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 ATGAGCAACATTATATAAGCTAGTAGCAAGTATTGCTTCAAGCTTAGCAATT 60
Db 240786 ATGAGTAAACCTATATAAGCTAGTAGCAAGTATTGCTTCAAGCTTAGCAATT 60
240727
QY 61 GTACTTATGCCGTTTCTATACTCTACACAGCATGTCGAATGCGGAGATTGCGCAATATC 120
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Db 240726 GTACTTATGCCGTTTCTATACTCTACACAGCATGTCGAATGCGGAGATTGCGCAATATC 240667
QY 121 GCAACATTCATGACTACAAAGATGCTTTTCAAGAATTA 162
Db 240666 GCAACATTCATGACTACAAAGATGCTTTTCAAGAATTA 240625
RESULT 9
LOCUS AX583668 159 bp DNA linear PAT 10-JAN-2003
DEFINITION Sequence 45 from Patent WO20059148.
ACCESSION AX583668
VERSION AX583668.1 GI:27655478
KEYWORDS
SOURCE
Staphylococcus aureus
Staphylococcus aureus
ORGANISM
Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE
1 Meinke, A., Nagy, E., von Absen, U., Klade, C., Henics, T., Zauner, W.,
Mlinh, D. B., Vytvytska, O., Etz, H., Dryla, A., Welchhart, T., Hefner, M.,
Tempelmeier, B., Fraser, C. M. and Gill, S.
A method for identification, isolation and production of antigens
to a specific pathogen
Patent: WO 02059148-A 45 01-AUG-2002;
Cistern Biotechnologies GmbH (AT)
FEATURES
source
1..159
/organism="Staphylococcus aureus"
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Query Match 85.3%; Score 138.2; DB 6; Length 159;
Best Local Similarity 91.8%; Pred. No. 3.8e-29;
Matches 146; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 1 ATGAGCAACATTATATAAGCTAGTAGCAAGTATTGCTTCAAGCTTAGCAATT 60
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QY 61 GTACTTATGCCGTTTCTATACTCTACACAGCATGTCGAATGCGGAGATTGCGCAATATC 120
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QY 121 GCAACATTCATGACTACAAAGATGCTTTTCAAGAATTA 159
Db 121 GCAACATTCATGACTACAAAGATGCTTTTCAAGAATTA 159
RESULT 10
AF424783 42722 bp DNA linear FIG 10-JUN-2002
LOCUS AF424783
DEFINITION Staphylococcus aureus phase phi 13, complete genome.
ACCESSION AF424783
VERSION AF424783.1 GI:18920591
KEYWORDS

ORGANISM	Staphylococcus aureus phage phi 13
SOURCE	Staphylococcus aureus phage phi 13
REFERENCE AUTHORS	Virtunen, dudu virtunen, no RNA stage; Caudovirales; Siphoviridae. 1 (bases 1 to 42722) Iandolo,J.J., Worrell,V., Groicher,K.H., Qian,Y., Tian,R., Kanton,S., Dorman,A., Ji,H., Lin,S., Loh,P., Qi,S., Zhu,H. and Roe,B.A.
TITLE	Comparative analysis of the genomes of the temperate bacteriophages phi11, phi12 and phi13 of Staphylococcus aureus 8325
JOURNAL MEDLINE	Gene 269 (1-2), 109-116 (2002)
PUBLISHED	22032962
REFERENCE AUTHORS	2 (bases 1 to 42722) Iandolo,J.J., Worrell,V., Roe,B., Qian,Y., Dorman,A., Tian,R., Lin,S. and Jia,H.
TITLE	Direct Submision
JOURNAL	Submitted (26-SEP-2001) Microbiology and Immunology, Univ. of Oklahoma Health Sciences Center, 940 S.L. Young Blvd, Oklahoma City, OK 73190, USA
FEATURES	Location/Qualifiers 1..42722 /organism="Staphylococcus aureus phage phi 13" /proviral /mol_type="genomic DNA" /specific_host="Staphylococcus aureus strain 8325" /db_xref=taxon:186153" complement(59..10956) /codon_start=1 /transl_table=1 /product="integrase" /protein_id="AAL82331.1" /db_xref=Gt:18920592" /translation="MKTRCYDGRKMYEFKEGKRVRKRGFRTRKANSAGLDKINELRSQINDVITLAEYENMIKTYKOPVKENTYRHYRNALOHOKHIGQELESKIRNGVOAKINDYSKEHAKETIKRTNKAIRSDALDLGIKNPDKAVNNYKAGKPRTSEDEKFTSYTEYLIDKHVRKRRRSSIALPLMICGCCGSGANIKIEHINOVNIPTIDEKTIQTSRYSTAKSKDKHMVDISTPAISYDGYFPGASITINDOAINNALMSACRVNNIPTTSHALNRTHCSILANGVSIRITHRLGHNAIIATITSVSHLEEKNEEDKMTKITELSW" 1204..1818 /note="OfcC" /codon_start=1 /transl_table=1 /product="unknown" /protein_id="AAL82332.1" /db_xref=Gt:18920593" /translation="MTOFGALLLTGLGVIPYKTLTMIGLVSEKKRIINTPVLLIFSIECTLIWFYTEFIENNVDLRNLSSLLQLTGKANIFLLIFVLVYFNPLVAFKIWIHLNHTKRFNPLDCISILDNRDLGNNGNKRPVIYKGFENRIIEEGELTKTVNSASDSFDLLEVRODFKVSDDLSENDELIVGHTLVLDLKQIKMLDLYLMNEY"
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Query Match 85.2%; Score 138; DB 7; Length 42722;
Best Local Similarity 90.7%; Pred. No. 2.2e-29;
Matches 147; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 ATAGCAACATTATTAAGCTACCTAGTACGAGATTTATGCTTACAGCTTAGCATT 60
DB 6585 ATAGCAACATTATTAAGCTACCTAGTACGAGCTGCTTACAGCTTAGCATT 6644
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DB 6645 GTACTTATGCCGTTCTATATCTCACTACAGCATGTCATTGCCGATTCGCAAGTATC 6704
QY 121 GCAACATTCATGTACTACAAAGAAATGCTTTTCAAGATTA 162
DB 6705 GCAACATTCATGTACTACAAAGAAATGCTTTTCAAGATTA 6746
RESULT 11
AP004828/c 272850 bp DNA linear BCT 20-DEC-2002
LOCUS
DEFINITION
Staphylococcus aureus subsp. aureus MW2 DNA, complete genome,
strain:MW2, section 7/10.
ACCESSION
AP004828 BA000033
VERSION
AP004828.1 GI:21204850
KEYWORDS
Staphylococcus aureus subsp. aureus MW2
SOURCE
Staphylococcus aureus subsp. aureus MW2
ORGANISM
Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE
1 Baba,T., Takeuchi,F., Kuroda,M., Yuzawa,H., Aoki,K., Oguchi,A.,
Nagai,Y., Iwama,N., Asano,K., Naimi,T., Kuroda,H., Cui,L.,
Yamamoto,K. and Hiramatsu,K.

TITLE	Genome and virulence determinants of high virulence community-acquired MRSA	CDS	complement(2472. .3785)
JOURNAL	Lancet 359 (9320), 1819-1827 (2002)		/gene="murC"
PUBLISHED	22040717		/note="ORFID:MM1683"
REFERENCE	12044378		/codon_start=1
AUTHORS	2 (bases 1 to 272850) Director-General, Biotechnology Center, Aoki,K., Oguchi,A., Nagai,Y., Asano,K., Iwama,N., Baba,T., Kuroda,M., Hiratsatsu,K. and Kikuchi,H.		/transl_table=1
TITLE	Direct Submission	gene	/product="UDP-N-Acercylmuramate-aldolase ligase"
JOURNAL	Submitted (06-MAR-2002) Director-General, Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center/ 2chome 49-10 Nishihara, Shibuya-Ku, Tokyo 151-0066, Japan (E-mail:biomite-go-jp, URL:http://www.bio.nite.go.jp/, Tel:81-3-3481-1933, Fax:81-3-3481-8424)		/db_xref="GI:21204853"
FEATURES	Location/Qualifiers		/translacion="MTHFVGIKSGWSSIAQIMHDIQHEVGSID ENYVEFEVALR NKGI KILFEDANNIKEDMVAIOGNASSHEELVRAHQLOKIDVVSVIDEQIIDPOYTS SVAYGAGHGTSTTGGLSHWNGDKTSFLLGDGTQAGTSDVEFAEACEYRRHFLS KYRDAIIMTNIIDPDPYFOINDIVDFDAFOAMANKKIKIAMDDEHILRKIEDADVI LYXGKGSDDIYKONIOITDKGAFAPVVDPEEFVDSPOGHVUVALAKVIAISVY LEDLVNVIKEALEFEGGVRNRENETANOVYDDYVAHREHRSATITRARKKYPHK EYVAVFOHFTSRTOAFINERFASLSKADRVFICEFGSIEKNGALITQDILIDETIG ASLINESIVLVEQDUNAVLFWGAGDIQKIDNAYIDIKGKNAF"
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Query Match 85.2%; Score 138; DB 1; Length 272850;
Best Local Similarity 90.7%; Pred. No. 1.8e-29;
Matches 147; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
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DB 257045 ATGACGACATTATTAAGTACCTAGTACGAGATATGCTTACAGCTTACGATT 60
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DB 256985 GTACTTATGCCGTTTCTATACCTACACGAGATGTCATTGCCGAGTTCGAGATATC 120
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DB 256925 GCAACATTCATGACTACAAAGATGCTTTTCAAGATTA 162
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BD245282
LOCUS BD245282 43095 bp DNA linear PAT 17-JUL-2003
DEFINITION Development of novel antibiotics based on bacteriophage genomes.
ACCESSION BD245282
VERSION BD245282.1 GI:33055052
KEYWORDS JP 2002531107-A/17.
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 43095)
AUTHORS Polletier,J., Gros,P. and Dubou,M.
TITLE Development of novel antibiotics based on bacteriophage genomes
JOURNAL Patent: JP 2002531107-A 17 24-SEP-2002;
PHARTECH INC
OS Stephylococcus aureus bacteriophage 3A
PN JP 2002531107-A/17
PD 24-SEP-2002
PF 03-DEC-1999 JP 2000585456
PR 03-DEC-1999 US 60/110992,03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR

01-DEC-1999 US 60/168777.02-DEC-1999 US 09/454252 P1 JERRY
PELLETIER, PHILLIPPE GNOS, MICHAEL DUBOW
PC C12N15/00, A01N63/00, A61K38/00, A61K45/00, A61P31/04, C07K14/005,
PC C12M1/00,
PC C12N1/21, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/566, PC
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ORIGIN
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Best Local Similarity 89.5%; Pred. No. 1.9e-28;
Matches 145; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
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DB 29502 GTACTATGCGCTTTCTATATCTTACATACGATGTCATTCGCGGATTCGCAATTC 29561
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LOCUS AB009866
DEFINITION Bacteriophage phi PVL proviral DNA, complete sequence.
ACCESSION AB009866
VERSION AB009866.2 GI:8051688
KEYWORDS dUTPase; ssDNA binding protein; anti repressor; repressor;
integrase; LukE-PV; LukS-PV; holin; amidase (peptidoglycan
hydrolase); capsid protein; portal protein.
SOURCE
ORGANISM Staphylococcus aureus bacteriophage PVL
Staphylococcus aureus bacteriophage PVL
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
REFERENCE
1 (et al.)
AUTHORS Kaneko, J., Kimura, T., Naito, S., Tomita, T. and Kamio, Y.
TITLE Pantom-valentine leukocidin genes in a phage-like particle isolated
from mitomycin C-treated Staphylococcus aureus V8 (ATCC 49775)
JOURNAL Bioest. Biotechnol. Blochem. 61 (11), 1960-1962 (1997)
MEDLINE 98067870
PUBMED 9404084
REFERENCE 2 (et al.)
AUTHORS Kaneko, J., Kimura, T., Naito, S., Tomita, T. and Kamio, Y.
TITLE Complete nucleotide sequence and molecular characterization of the
temperate staphylococcal bacteriophage phiPVL carrying
Panton-Valentine leukocidin genes
JOURNAL Gene 215 (1), 57-67 (1998)
MEDLINE 9832719
PUBMED 966077
REFERENCE 3 (bases 1 to 41401)
AUTHORS Kaneko, J., Kimura, T., Naito, S., Tomita, T. and Kamio, Y.
TITLE Direct Submission
JOURNAL Submitted (17-DEC-1997) Jun Kaneko, Tohoku University, Dept. Appl.
Biol. Chem., Faculty of Agriculture, 1-1 Tsutsumi-dori
Aramiyamachi, Aoba-ku, Sendai, Miyagi 981, Japan
(E-mail: jkaneko@biochem.tohoku.ac.jp, Tel: 81-22-717-8781,
Fax: 81-22-717-8780)
COMMENT On May 24, 2000 this sequence version replaced gi:3341907.
Sequence updated (06-Feb-1998)
Sequence updated (22-May-2000).
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gene
CDS

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VERSION AP003360.2 GI:14246398
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1 Bacteriol. Firmicutes; Bacillales; Staphylococcus.
AUTHORS
Kuroda, M., Ohta, T., Uchiyama, I., Baba, T., Yuzawa, H., Kobayashi, I.,
Cui, L., Oguchi, A., Aoki, K., Nagai, Y., Imai, J., Ito, T., Kanamori, M.,
Matsunari, H., Maruyama, A., Murakami, H., Hosoyama, A.,
Mizutani-U, Y., Takahashi, N. K., Sawano, T., Inoue, R., Kaito, C.,
Sekimizu, K., Hiraoka, H., Kuhara, S., Goto, S., Yabuuchi, J.,
Kanoh, M., Yamashita, A., Oshima, K., Furuya, K., Yoshino, C.,
Shiba, T., Hattori, M., Ogasawara, N., Hayashi, H. and Hirumatsu, K.
Whole genome sequencing of methicillin-resistant Staphylococcus
aureus
JOURNAL Lancet 357 (9264), 1225-1240 (2001)
MEDLINE 21311952
PUBMED 11418146
REFERENCE 2 (bases 1 to 348527)
AUTHORS Ohta, T.
JOURNAL Submitted (28-FEB-2001) Toshiko Ohta, University of Tsukuba College
of Medical Technology and Nursing, Department of Medical
Technology 1-1-1 Ten-nodai, Tsukuba, Ibaraki 305-8577, Japan
(E-mail:tohta@tsukuba.ac.jp, Tel:81-298-53-3454,
Fax:81-298-53-3454)
COMMENT On May 29, 2001 this sequence version replaced gi:13874937.
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6: geneseqn2001bs:*
7: geneseqn2002s:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2004s:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	162	100.0	162	3	AA666231	Bacteriophage
2	162	100.0	41708	4	AA666247	Bacteriophage
3	162	100.0	41708	4	AA666106	Bacteriophage
4	144.4	89.1	43576	3	AA666609	Complete
5	142.8	88.1	1408	2	AAV74651	Bacteriophage
6	141.4	87.3	159	7	ACF73074	Staphylococcus
7	136.2	85.3	159	7	ABU14900	Staphylococcus

XX	Staphylococcus aureus; bacteriophage 77.
OS	
XX	
XX	WO200032825-A2.
XX	
XX	
PD	08-JUN-2000.
XX	
XX	
PE	03-DEC-1999; 99MO-IB002040.
PR	
PR	03-DEC-1999; 98US-0110992P.
PR	03-JUN-1999; 99US-00326144.
PR	28-SEP-1999; 99US-00407604.
PR	30-SEP-1999; 99US-0157218P.
PR	01-DEC-1999; 99US-0168771P.
PR	02-DEC-1999; 99US-00454252.
XX	
PA	(PHAG-) PHAGETECH INC.
XX	
PI	Pelletier J, Gros P, Dubow M;
DR	
DR	WPI: 2000-412361/35.
DR	P-PSDB: AAB16526.
XX	
PT	Identifying a bacteriophage coding region for treating bacterial
PT	infections comprises identifying a nucleic acid encoding a product that
XX	inhibits bacteria when a bacteriophage infects a bacterium.
XX	
PS	Disclosure; Page 159; 456pp; English.
XX	
CC	The present invention describes a method for identifying a bacteriophage
CC	coding region encoding a product active on an essential bacterial target.
CC	The method comprises identifying a nucleic acid sequence encoding a gene
CC	product that provides a bacteria-inhibiting function when an
CC	uncharacterised bacteriophage infects a pathogenic bacterium. The
CC	compound active on a target of a bacteriophage inhibitor protein in a
CC	bacteria is used to treat or prevent a bacterial infection in an animal.
CC	AA686243 to AA689442 and AAB16523 to AAB16934 represent bacteriophage
CC	nucleotide and protein sequences which are used in the exemplification of
CC	

XX

Query Match	100.0%	Score 162	DB 3	Length 162
Best Local Similarity	100.0%	Pred. No. 8.9e-42		
Matches 162	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	ATGACCAACATTATATAAAGCTACTAGTAGCAGATTATGCTTACAGCTTACGATT	60	
DB	1	ATGACCAACATTATATAAAGCTACTAGTAGCAGATTATGCTTACAGCTTACGATT	60	
QY	61	GCACATTAGCCCTTCTCATCTTACACAGATGTCATTGCGGGATTCGCAAGATTC	120	
DB	61	GTACTTATGCCGTTTCTCATCTTACACAGATGTCATTGCGGGATTCGCAAGATTC	120	
QY	121	GCACATTATGCTTACCAAGATGCTTTTCAAAGATTA	162	

DB 121 GCACATTCATCTACTACAAAGATGCTTTCCAAAGATTA 162

RESULT 2

AAA68247

ID AAA68247 standard; DNA; 41708 BP.

XX

AC AAA68247;

XX

DT 15-SEP-2003 (revised)

DT 06-AUG-2003 (revised)

DT 27-OCT-2000 (first entry)

XX

DE Bacteriophage 77 complete genome sequence.

XX

KW Bacteriophage; antimicrobial; genome; identification; antibacterial;

KW bacterial growth inhibition; bacterial infection; de.

XX

OS Staphylococcus aureus; bacteriophage 77.

XX

PN WO200032825-A2.

XX

PD 08-JUN-2000.

XX

PF 03-DEC-1999; 99WO-1B002040.

XX

PR 03-DEC-1998; 98US-0110992P.

PR 03-JUN-1999; 99US-00326144.

PR 28-SEP-1999; 99US-00407804.

PR 30-SEP-1999; 99US-0157218P.

PR 01-DEC-1999; 99US-0168777P.

PR 02-DEC-1999; 99US-00454252.

XX

PA (PHAG-) PHAGETECH INC.

XX

PI Pelletier J, Gros P, Dubow M;

XX

DR WPI; 2000-412361/35.

XX

PT Identifying a bacteriophage coding region for treating bacterial

PT infections comprises identifying a nucleic acid encoding a product that

PT inhibits bacteria when a bacteriophage infects a bacterium.

XX

PS Example 3; Page 141-151; 456pp; English.

XX

CC The present invention describes a method for identifying a bacteriophage

CC coding region encoding a product active on an essential bacterial target.

CC The method comprises identifying a nucleic acid sequence encoding a gene

CC product that provides a bacteria-inhibiting function when an

CC uncharacterised bacteriophage infects a pathogenic bacterium. The

CC compound active on a target of a bacteriophage inhibitor protein in a

CC bacterium is used to treat or prevent a bacterial infection in an animal.

CC AAA68243 to AAA69442 and AAB16523 to AAB16954 represent bacteriophage

CC nucleotide and protein sequences which are used in the exemplification of

CC the present invention. (Updated on 06-AUG-2003 to correct OS field.)

CC (Updated on 15-SEP-2003 to standardise OS field)

XX

SQ Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 U; 0 Other;

Query Match 100.0%; Score 162; DB 3; Length 41708;

Best Local Similarity 100.0%; Pred. No. 4e-41;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGAGCACATTATATAAGCTACCTAGTAGCAGATATTATGCTTCAACAGTCTTAGCATT 60

DB 29051 ATGAGCACATTATATAAGCTACCTAGTAGCAGATATTATGCTTCAACAGTCTTAGCATT 29110

OY 61 GTACTTAGCGGTTCTATCTATCTACACAGCATGTCATTGCGGATTCGCAAGTATC 120

DB 29111 GTACTTAGCGGTTCTATCTATCTACACAGCATGTCATTGCGGATTCGCAAGTATC 29170

OY 121 GCACATTCATCTACTACAAAGATGCTTTCCAAAGATTA 162

DB 29171 GCACATTCATCTACTACAAAGATGCTTTCCAAAGATTA 29212

RESULT 3

AAC86106

ID AAC86106 standard; cDNA; 41708 BP.

XX

AC AAC86106;

XX

DT 06-AUG-2003 (revised)

DT 29-AUG-2001 (first entry)

XX

DE Complete genome of bacteriophage 77.

XX

KW Dnal1; S. aureus; inhibitor; bacteriophage 77; ORF 104; phage 77ORF104;

KW screening assay; ss.

XX

OS Bacteriophage.

XX

PN WO200146383-A2.

XX

PD 28-JUN-2001.

XX

PF 21-DEC-2000; 2000WO-US035180.

XX

PR 22-DEC-1999; 99US-00470512.

PR 12-OCT-2000; 2000US-00689952.

XX

PA (PHAG-) PHAGETECH INC.

PA (WILLIAMS K M.

XX

PI Pelletier J, Gros P, Dubow M;

XX

DR WPI; 2001-418052/44.

XX

PT Novel Dnal polypeptides useful for treating and diagnosing microbial,

PT preferably bacterial, diseases such as those caused by Staphylococcus

PT aureus.

XX

PS Disclosure; Fig 2; 107pp; English.

XX

KW skin infection; surgical wound infection; scalded skin syndrome;
 KW toxic shock syndrome; ds.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1081..1140
 FT /tag= a
 FT /note= "these bases represent a line of missing text in
 FT the sequence listing in the specification. They are
 FT included to maintain the nucleotide numbering given in
 FT the specification for this DNA sequence"
 XX
 PN EP786519-A2.
 XX
 PD 30-JUL-1997.
 XX
 PF 07-JAN-1997; 97EP-00100117.
 XX
 PR 05-JAN-1996; 96US-0009861P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Kunesch CA, Choi GH, Barash SC, Dillon PJ, Fannon KR, Rosen CA;
 XX WPI; 1997-374922/35.
 DR
 XX
 PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -
 PT stored on computer readable medium and used in the production of anti-
 PT S. aureus vaccines.
 XX
 PS Claim 1; Page 1475-1476; 3271pp; English.
 CC
 CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences
 CC of the invention. The DNA sequences are recorded on a computer readable
 CC medium, preferably selected from a floppy or hard disk, random access
 CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
 CC the S. aureus DNA sequences allows putative functions to be assigned so
 CC that protein-encoding or regulatory regions of commercial, therapeutic or
 CC industrial importance can be obtained. Specifically, sequences which are
 CC likely to encode antigens have been identified and these polypeptides can
 CC be used in a vaccine composition against S. aureus infection. The
 CC polypeptides can also be used in a kit for the immunodetection of
 CC S. aureus in a sample. S. aureus is implicated in numerous human diseases,
 CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
 CC skin and surgical wound infections, scalded skin syndrome, toxic shock
 CC syndrome, etc. Organisms transformed with the DNA sequences can be used
 CC for recombinant production of the polypeptides. The new DNA sequences
 CC (and their fragments) are useful as primers or probes for isolating
 CC homologues of any of the S. aureus DNA sequences contained on the computer
 CC readable medium
 XX
 SQ Sequence 1408 BP; 332 A; 250 C; 218 G; 543 T; 0 U; 65 Other;
 XX
 Query Match 88.1%; Score 142.8; DB 2; Length 1408;
 Best Local Similarity 92.6%; Prod. No. 2.1e-35;
 Matches 150; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ATGAGCAACATTATTAAGGCTACCTAGTACAGTATTGCTTCACAGTCTTACGCATT 60
 DB 339 ATGATTAACATTATTAAGGCTACCTAGTACAGTATTGCTTCACAGTCTTACGCATT 280
 QY 61 GTACTTATGCCGTTTCTATCTTACATCAACAGATGTCGAGATTGCGAGATTC 120
 DB 279 GTACTTATGCCGTTTCTATCTTACATCAACAGATGTCGAGATTGCGAGATTC 220
 QY 121 GCAACATTCATGACTACAAAGATGCTTTCAAGATTA 162
 DB 219 GCAACATTCATTCATTAAGGAATCTTTATGAAGATGA 178
 RESULT 6
 ACF73074
 ID ACF73074 standard; DNA; 159 BP.
 XX
 AC ACF73074;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Staphylococcus aureus DNA #754.
 XX
 KW Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
 KW enzymatic assay; antibiotic target; gene; ds.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO200294868-A2.
 PD 28-NOV-2002.
 XX
 PF 27-MAR-2002; 2002WO-1B002637.
 XX
 PR 27-MAR-2001; 2001GB-00007661.
 XX
 PA (CHIR-) CHIRON SPA.
 XX
 PI Maignani V, More M, Scarselli M;
 XX WPI; 2003-120786/11.
 DR P-PSDB; ABMT1514.
 DR
 XX
 PT New Staphylococcus aureus protein, useful as a vaccine for treating or
 PT preventing Staphylococcal infection, specifically an infection caused by
 PT S. aureus, e.g. sepsis.
 XX
 PS Claim 6; SEQ ID NO 1507; 49pp; English.
 XX
 CC The invention relates to novel genes and encoded proteins from
 CC Staphylococcus aureus. A composition comprising the S. aureus protein, a
 CC nucleic acid encoding the protein, or an antibody to the protein, is
 CC useful as a pharmaceutical, particularly as a vaccine for treating or
 CC preventing infection due to Staphylococcus bacteria, specifically an
 CC infection caused by S. aureus. The composition is particularly useful for
 CC treating or preventing sepsis in a patient. The composition can also be

CC used for diagnostics. The protein is also used in an assay for enzymatic
 CC studies and as a target for antibiotics. This sequence represents one of
 CC the novel *S. aureus* genes of the invention
 XX
 XX
 SQ Sequence 159 BP; 51 A; 30 C; 26 G; 52 T; 0 U; 0 Other;

Query Match 87.3%; Score 141.4; DB 7; Length 159;
 Best Local Similarity 93.1%; Pred. No. 3.2e-35;
 Matches 148; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ATGAGCAACATTATTAAGCTACCTAGTAGCAGATATTGCTTCACAGTCTTAGCGATT 60
 DB 1 ATGAGTAGACATTATTAAGCTACCTAGTAGCAGATATTGCTTCACAGTCTTAGCGATT 60
 QY 61 GTACTTATGCCGTTTCTATTACTTCACTACAGCATGGTCATTGGCGGATTGCCAAGTATC 120
 DB 61 GTACTTATGCCGTTTCTATTACTTCACTACAGCATGGTCATTGGCGGATTGCCAAGTATC 120
 QY 121 GCAACATTCATGTACTACAAAGATGCTTTTCAAGAA 159
 DB 121 GCAACATTCATGTACTATTAAGAAATCTTTATGAAGA 159

RESULT 7
 ABT14900
 ID ABT14900 standard; DNA; 159 BP.
 XX
 AC ABT14900;
 XX
 DT 06-MAR-2003 (first entry)
 XX
 DE Pathogen specific antigen related staphylococcal DNA SEQ ID No 45.
 XX
 KW Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
 KW hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
 KW auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
 KW auto-immune diseases; HIV; hepatitis; gene; ds.
 XX
 OS Staphylococcus sp.
 XX
 PN W0200259148-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 21-JAN-2002; 2002WD-EP000546.
 XX
 PR 26-JAN-2001; 2001AT-00000130.
 XX
 PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
 XX
 PI Melinke A, Nagy E, Von Ahnson U, Klade C, Herlitz T, Zauner W;
 PI Mlinh DB, Vytvyvka O, Eitz H, Dryla A, Weichhart T, Hafner M;
 PI Tempelmeier B;
 XX
 XX WPI; 2003-075410/07.
 DR
 XX
 PT Identifying, isolating and producing hyperimmune serum-reactive antigens

PT from a pathogen, for preparing vaccine or medicament for treating or
 PT preventing e.g. staphylococcal infections, comprises providing antibody
 PT preparation.
 XX
 XX
 PS Example 7; Page 152; 252pp; English.

CC The invention relates to a novel method for identifying, isolating and
 CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
 CC allergen, a tissue or host prone to auto-immunity, where the antigens are
 CC used in a vaccine, comprises providing antibody preparation from a plasma
 CC pool of a type of animal, or individual sera with antibodies against the
 CC specific pathogen, tumour, allergen, tissue or host prone to auto-
 CC immunity. The hyperimmune serum-reactive antigens comprising any of the
 CC 62 sequences of 53-2261 amino acids fully defined in the specification,
 CC or their hyperimmune fragments are useful for the manufacture of a
 CC pharmaceutical preparation, particularly a vaccine against staphylococcal
 CC infections or colonisation against *S. aureus* or *S. epidermidis*. The
 CC preparation of antibodies is useful for the manufacture of a medicament
 CC for treating or preventing staphylococcal infections or colonisation
 CC against *S. aureus* or *S. epidermidis*. The antibody preparations may also
 CC be used for diagnostic and imaging purposes. Other conditions that can be
 CC treated include cancer, autoimmune diseases or infections caused by viral
 CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
 CC polynucleotide sequence represents staphylococcal DNA relating to the
 CC method for identifying and producing pathogen specific antigens of the
 CC invention
 XX
 XX

Sequence 159 BP; 52 A; 31 C; 26 G; 50 T; 0 U; 0 Other;

Query Match 85.3%; Score 138.2; DB 7; Length 159;
 Best Local Similarity 91.8%; Pred. No. 3.4e-34;
 Matches 146; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 ATGAGCAACATTATTAAGCTACCTAGTAGCAGATATTGCTTCACAGTCTTAGCGATT 60
 DB 1 ATGAGTAGACATTATTAAGCTACCTAGTAGCAGATATTGCTTCACAGTCTTAGCGATT 60
 QY 61 GTACTTATGCCGTTTCTATTACTTCACTACAGCATGGTCATTGGCGGATTGCCAAGTATC 120
 DB 61 GTACTTATGCCGTTTCTATTACTTCACTACAGCATGGTCATTGGCGGATTGCCAAGTATC 120
 QY 121 GCAACATTCATGTACTACAAAGATGCTTTTCAAGAA 159
 DB 121 GCAACATTCATGTACTATTAAGAAATCTTTATGAAGA 159

Search completed: October 14, 2004, 12:48:17
 Job time : 111 secs

OM nucleole - nucleole search, using sw model

Run on: October 14, 2004, 12:03:47 ; Search time 736.65 Seconds

(without alignments)
6393.544 Million cell updates/sec

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

28: gb_gss1:.*
29: gb_gss2:.*

US-09-407-804A-7
Perfect score: 162
Sequence: 1 atgagacacattcacaanaag.....aatgcctttccaaagaataaa 162
Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0
Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 08
Maximum Match 100%
Listing first 45 summaries

Database :
EST:.*
1: em_ests:.*
2: em_esth:.*
3: em_estl:.*
4: em_estm:.*
5: em_estov:.*
6: em_estpl:.*
7: em_estro:.*
8: em_hic:.*
9: gb_est1:.*
10: gb_est2:.*
11: gb_hic:.*
12: gb_est3:.*
13: gb_est4:.*
14: gb_est5:.*
15: em_estfun:.*
16: em_estom:.*
17: em_gss_hum:.*
18: em_gss_inv:.*
19: em_gss_pln:.*
20: em_gss_vit:.*
21: em_gss_fun:.*
22: em_gss_man:.*
23: em_gss_mus:.*
24: em_gss_pro:.*
25: em_gss_rnd:.*
26: em_gss_phg:.*
27: em_gss_vit:.*

Result No.	Score	Query Match	Length	DB ID	Description
1	37.8	23.3	592	29	CC962715
2	37.8	23.3	622	29	CC962715
3	37.8	23.3	746	29	CC965697
4	36.2	22.3	598	28	BH733956
5	36.2	22.3	637	29	CC951970
6	36.2	22.3	685	28	BH432658
7	36.2	22.3	821	28	BH496295
8	34.6	21.4	694	28	B2043339
9	34.6	21.4	694	28	B2043339
10	34.6	21.4	828	29	CC942125
11	34	21.0	899	29	CC9825379
12	33.8	20.9	332	28	A2017923
13	33.6	20.7	636	28	B2138306
14	33.2	20.5	441	12	BM933696
15	33.2	20.5	441	12	BM933696
16	33.2	20.5	448	10	BE993185
17	33.2	20.5	654	10	BB475101
18	33.2	20.5	807	12	BJ403671
19	33	20.4	521	12	BJ577935
20	33	20.4	643	13	BX507709
21	32.8	20.2	502	13	BX558882
22	32.6	20.1	347	29	CG765378
23	32.6	20.1	585	28	CC113035
24	32.6	20.1	694	28	B2389867
25	32.4	20.0	661	12	BJ574708
26	32.4	20.0	724	28	BH567725
27	32.2	19.9	675	28	B2015314
28	32	19.8	723	28	A2656529
29	32	19.8	723	28	A2656529
30	32	19.8	1518	28	CC185828
31	31.8	19.6	461	28	AQ587116
32	31.8	19.6	526	13	BY708493
33	31.8	19.6	645	29	CC955595
34	31.8	19.6	834	28	BH687466
35	31.8	19.6	2525	11	BC036519
36	31.6	19.5	1201	29	CNS0150V
37	31.4	19.4	386	28	AQ133541
38	31.4	19.4	488	9	A1240366
39	31.4	19.4	681	12	BJ570871
40	31.4	19.4	741	28	BH460398
41	31.4	19.4	777	28	BH725123
42	31.4	19.4	806	14	CD826219
43	31.4	19.4	811	12	BM007305
44	31.4	19.4	1201	13	BX379698
45	31.2	19.3	360	13	BX550058

Search completed: October 14, 2004, 18:55:16
Job time : 760.63 secs

OM nucleic - nucleic search, using aw model

Run on: October 14, 2004, 19:00:14 ; Search time 816.257 Seconds
(without alignments)
8442.862 Million cell updates/sec

Title: US-09-407-804A-8

Perfect score: 159
Sequence: 1 atgttaaccacagaattttt.....ccgctacgtcgaaatttaa 159

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 2167151695 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : GenEmbl: +
1: gb_ba: +
2: gb_hg: +
3: gb_in: +
4: gb_cm: +
5: gb_ov: +
6: gb_pat: +
7: gb_ph: +
8: gb_pl: +
9: gb_pr: +
10: gb_ro: +
11: gb_sta: +
12: gb_sy: +
13: gb_un: +
14: gb_vl: +
15: em_da: +
16: em_fun: +
17: em_hum: +
18: em_in: +
19: em_mu: +
20: em_om: +
21: em_or: +
22: em_ov: +
23: em_pat: +
24: em_ph: +
25: em_pl: +
26: em_ro: +
27: em_sta: +

28: em_un: +
29: em_vl: +
30: em_hg_hum: +
31: em_hg_inv: +
32: em_hg_other: +
33: em_hg_mus: +
34: em_hg_pin: +
35: em_hg_rnd: +
36: em_hg_mam: +
37: em_hg_vrt: +
38: em_sy: +
39: em_higo_hum: +
40: em_higo_mus: +
41: em_higo_other: +

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	159	100.0	159	6	BD245279
2	159	100.0	159	6	AR368771
3	159	100.0	41708	6	BD245281
4	159	100.0	41708	6	AR368770
5	62	39.0	348527	1	AP003360
6	60	37.7	42942	7	AB045978
7	42	26.4	42722	7	AF424783
8	25	15.7	232473	2	AC14212
9	23	14.5	178469	2	BX248504
10	22	13.8	188989	2	AC125363
11	22	13.8	224661	2	AC098164
12	21	13.2	757	1	MC210
13	21	13.2	141704	9	AC007993
14	21	13.2	142163	9	AC061975
15	21	13.2	196421	2	AC078837
16	21	13.2	215705	9	AL589931
17	21	13.2	246441	2	AC098542
18	20	12.6	45636	7	AB044554
19	20	12.6	77028	9	AC093716
20	20	12.6	86829	9	AC093716
21	20	12.6	109710	9	AC011382
22	20	12.6	138376	8	AP003578
23	20	12.6	145491	8	AP002883
24	20	12.6	148202	10	AC125108
25	20	12.6	148326	10	AL732503
26	20	12.6	155415	2	AC108886
27	20	12.6	166712	2	AC118065
28	20	12.6	188932	2	AC011150
29	20	12.6	192499	2	AC133913
30	20	12.6	193514	2	AC121674
31	20	12.6	200769	2	AC137118
32	20	12.6	204632	2	AC097583
33	20	12.6	216490	10	AC100953

c 34	20	12.6	224659	10	AL806518	AC106675	9	AC106675	AC106675 Homo sapi
c 35	20	12.6	232001	2	AC121540	AL596025	10	AL596025	AL596025 Mouse DNA
c 36	20	12.6	234728	2	AC126570	AC074304	9	AC074304	AC074304 Mus muscu
c 37	20	12.6	234804	2	AC133409	AC013464	9	AC013464	AC013464 Homo sapi
c 38	20	12.6	235079	2	AC124475	AC140240	9	AC140240	AC140240 Mus muscu
c 39	20	12.6	237263	2	AC097686	AC084378	9	AC084378	AC084378 Homo sapi
c 40	20	12.6	253127	2	AC094585	AC114007	10	AC114007	AC114007 Homo sapi
c 41	20	12.6	255861	2	AC106603	AC073734	9	AC073734	AC073734 Mus muscu
c 42	20	12.6	268850	2	AC110949	AC016734	9	AC016734	AC016734 Homo sapi
c 43	20	12.6	274799	2	AC109721	AL731732	10	AL731732	AL731732 Mouse DNA
c 44	19	11.9	504	6	AR394629	AC099428	9	AC099428	AC099428 Rattus no
c 45	19	11.9	673	6	BD194110	AC10102	9	AC10102	AC10102 Rattus no
c 46	19	11.9	10476	1	AE014951	AC079994	9	AC079994	AC079994 Homo sapi
c 47	19	11.9	15671	1	AF343914	AC094823	9	AC094823	AC094823 Rattus no
c 48	19	11.9	32129	3	CET23F11	AC095450	9	AC095450	AC095450 Rattus no
c 49	19	11.9	43487	3	AF016420	AC133279	9	AC133279	AC133279 Rattus no
c 50	19	11.9	48993	9	AC133605	AC107412	9	AC107412	AC107412 Rattus no
c 51	19	11.9	51952	6	AR110591	AC122854	9	AC122854	AC122854 Mus muscu
c 52	19	11.9	51953	8	LEU81378	AL596167	9	AL596167	AL596167 Listeria
c 53	19	11.9	54149	10	AL833772	AC133732	9	AC133732	AC133732 Rattus no
c 54	19	11.9	72054	5	AC140935	AC125947	9	AC125947	AC125947 Rattus no
c 55	19	11.9	79923	9	AL596178	AC117040	9	AC117040	AC117040 Sequence
c 56	19	11.9	93177	9	AC098678	AC11829	9	AC11829	AC11829 Rattus no
c 57	19	11.9	104948	9	AC015751	AC098041	9	AC098041	AC098041 Rattus no
c 58	19	11.9	110000	2	AC096086	AC094212	9	AC094212	AC094212 Rattus no
c 59	19	11.9	112732	2	AC092367	AC091428	9	AC091428	AC091428 Mus muscu
c 60	19	11.9	113060	2	AC121133	AE016955	9	AE016955	AE016955 Enterococ
c 61	19	11.9	122613	9	AL596422	AK417043	9	AK417043	AK417043 Sequence
c 62	19	11.9	131056	2	AC137985	AY461844	9	AY461844	AY461844 Bartonell
c 63	19	11.9	135964	9	AC005914	AF006409	9	AF006409	AF006409 Lynx cana
c 64	19	11.9	139773	2	AC067806	AF314054	9	AF314054	AF314054 Rhizobium
c 65	19	11.9	145242	9	AC013457	AX789619	9	AX789619	AX789619 Sequence
c 66	19	11.9	145353	2	AC034177	G88718	9	G88718	G88718 S208P643RA
c 67	19	11.9	149224	2	AC022753	BD092877	9	BD092877	BD092877 Identifit
c 68	19	11.9	150312	9	CNS01R1J	AX794162	9	AX794162	AX794162 Sequence
c 69	19	11.9	150350	9	CNS01DMV	AF117382	9	AF117382	AF117382 Mus muscu
c 70	19	11.9	151171	2	AC020775	AK069473	9	AK069473	AK069473 Oryza sat
c 71	19	11.9	151673	10	AC087102	AK103512	9	AK103512	AK103512 Oryza sat
c 72	19	11.9	152186	2	AC084284	AK129266	9	AK129266	AK129266 Mus muscu
c 73	19	11.9	154396	2	AC068930	AE001180	9	AE001180	AE001180 Borrelia
c 74	19	11.9	159981	9	AC016817	AE000559	9	AE000559	AE000559 Helicobac
c 75	19	11.9	160521	2	AC127728	AE014229	9	AE014229	AE014229 Streptococ
c 76	19	11.9	160810	9	AC009953	AC014089	9	AC014089	AC014089 Drosophil
c 77	19	11.9	162721	10	AC079638	AX602188	9	AX602188	AX602188 Sequence
c 78	19	11.9	166014	9	AC022538	Z82090	9	Z82090	Z82090 Caenorhabd1
c 79	19	11.9	168065	9	CNS05TC6	U64848	9	U64848	U64848 Caenorhabd1
c 80	19	11.9	169266	2	AC102458	AL365449	9	AL365449	AL365449 Human DNA
c 81	19	11.9	169314	2	AC102458	Z11115	9	Z11115	Z11115 Caenorhabd1
c 82	19	11.9	170511	2	AC116263	AC004076	9	AC004076	AC004076 Homo sapi
c 83	19	11.9	171051	2	AC023528	AC101358	9	AC101358	AC101358 Mus muscu
c 84	19	11.9	173728	9	AL365496	AP003838	9	AP003838	AP003838 Oryza sat
c 85	19	11.9	174537	9	AC027233	AL512592	9	AL512592	AL512592 Human DNA
c 86	19	11.9	183773	9	AC119299	AC101023	9	AC101023	AC101023 Mus muscu
c 87	19	11.9	185156	9	HSB8212L9	AC100364	9	AC100364	AC100364 Mus muscu
c 88	19	11.9	185636	2	AC027109	AC087493	9	AC087493	AC087493 Homo sapi
c 89	19	11.9	186479	2	AC118083				
c 90	19	11.9	188826	9	AL359380				

148	18	11.3	73390	9	AC012938	AC012938 Homo sapi	205	18	11.3	135569	2	AC073997	AC073997 Homo sapi
149	18	11.3	73484	2	AC133530	AC133530 Homo sapi	206	18	11.3	135934	2	AC018925	AC018925 Homo sapi
150	18	11.3	77910	2	AP000452	AP000452 Homo sapi	207	18	11.3	139266	2	AC068747	AC068747 Homo sapi
151	18	11.3	78331	9	AC098692	AC098692 Homo sapi	208	18	11.3	139357	9	AC010907	AC010907 Homo sapi
152	18	11.3	80485	9	AB026899	AB026899 Homo sapi	209	18	11.3	140935	9	AC025173	AC025173 Homo sapi
153	18	11.3	83547	2	AC022890	AC022890 Homo sapi	210	18	11.3	141771	2	AC16512	AC16512 Homo sapi
154	18	11.3	84731	2	AC068885	AC068885 Homo sapi	211	18	11.3	141997	10	AL844482	AL844482 Homo sapi
155	18	11.3	90136	9	HS330012	AL031731 Human DNA	212	18	11.3	143861	10	AL391994	AL391994 Mouse DNA
156	18	11.3	90864	8	AP004949	AP004949 Letus cor	213	18	11.3	144449	2	AC067926	AC067926 Mus muscu
157	18	11.3	91587	1	AE016970	AE016970 Mycoplasma	214	18	11.3	145795	2	AC025548	AC025548 Homo sapi
158	18	11.3	93521	2	AC135555	AC135555 Gallus ga	215	18	11.3	145866	9	AC104771	AC104771 Homo sapi
159	18	11.3	96312	2	AP005554	AP005554 Oryza sat	216	18	11.3	146960	2	AC101960	AC101960 Mus muscu
160	18	11.3	97234	9	AL137859	AL137859 Human DNA	217	18	11.3	147418	10	AC140210	AC140210 Mus muscu
161	18	11.3	99479	9	AL136089	AL136089 Human DNA	218	18	11.3	148179	9	AC093677	AC093677 Homo sapi
162	18	11.3	100090	10	AL1772162	AL1772162 Mouse DNA	219	18	11.3	148567	9	AL451054	AL451054 Homo sapi
163	18	11.3	100170	9	AL161743	AL161743 Human DNA	220	18	11.3	149214	2	AC024535	AC024535 Homo sapi
164	18	11.3	104762	2	AC108086	AC108086 Homo sapi	221	18	11.3	150792	5	EX004972	EX004972 Zebrafish
165	18	11.3	107909	9	AL359847	AL359847 Human DNA	222	18	11.3	150891	2	EX640520	EX640520 Danio rer
166	18	11.3	108785	9	AL354682	AL354682 Human DNA	223	18	11.3	151340	2	AC121621	AC121621 Rattus no
167	18	11.3	110000	2	AC091229_09	Continuation (10 o	224	18	11.3	152548	2	AC100741	AC100741 Mus muscu
168	18	11.3	110000	2	AC091360_3	Continuation (4 of	225	18	11.3	152586	9	AC016968	AC016968 Homo sapi
169	18	11.3	110000	2	AC092921_3	Continuation (4 of	226	18	11.3	152632	2	AC145246	AC145246 Homo sapi
170	18	11.3	110000	2	AC095121_1	Continuation (4 of	227	18	11.3	152861	9	AC104779	AC104779 Homo sapi
171	18	11.3	110000	2	AC095121_2	Continuation (3 of	228	18	11.3	153803	2	AC055722	AC055722 Homo sapi
172	18	11.3	110000	2	AC095531_1	Continuation (4 of	229	18	11.3	153929	2	AC011883	AC011883 Homo sapi
173	18	11.3	110000	2	AC106241_3	Continuation (5 of	230	18	11.3	154889	2	AL351842	AL351842 Homo sapi
174	18	11.3	110000	2	AC106241_4	Continuation (2 of	231	18	11.3	154931	2	AL356781	AL356781 Homo sapi
175	18	11.3	110000	2	AC106552_0	Continuation (2 of	232	18	11.3	155491	9	AC068339	AC068339 Homo sapi
176	18	11.3	110000	2	AC106552_1	Continuation (2 of	233	18	11.3	155666	9	AC068696	AC068696 Homo sapi
177	18	11.3	110000	2	AC114698_0	Continuation (2 of	234	18	11.3	156170	5	EX005472	EX005472 Zebrafish
178	18	11.3	110000	2	AC115185_0	Continuation (2 of	235	18	11.3	156497	2	AL353192	AL353192 Rattus no
179	18	11.3	110000	2	AC126728_1	Continuation (2 of	236	18	11.3	156780	9	AP003034	AP003034 Homo sapi
180	18	11.3	110000	2	AC126728_1	Continuation (3 of	237	18	11.3	156989	10	AC124387	AC124387 Homo sapi
181	18	11.3	110000	2	AL360016_2	Continuation (3 of	238	18	11.3	157533	9	AL354709	AL354709 Human DNA
182	18	11.3	110000	2	AL713858_2	Continuation (3 of	239	18	11.3	158121	2	AC026594	AC026594 Homo sapi
183	18	11.3	110000	6	AR409405_0	BD061520 Genome DN	240	18	11.3	158170	5	EX005472	EX005472 Zebrafish
184	18	11.3	110000	6	BD061520_0	AC097470 Homo sapi	241	18	11.3	158497	2	AL353192	AL353192 Rattus no
185	18	11.3	110702	9	AC097470	AC097470 Homo sapi	242	18	11.3	158596	2	AL353192	AL353192 Rattus no
186	18	11.3	112398	9	AP003179	AP003179 Homo sapi	243	18	11.3	158780	9	AP003034	AP003034 Homo sapi
187	18	11.3	113387	9	AL390702	AL390702 Human DNA	244	18	11.3	159689	10	AC124387	AC124387 Homo sapi
188	18	11.3	113797	9	AL390628	AL390628 Human DNA	245	18	11.3	160035	2	EX465852	EX465852 Danio rer
189	18	11.3	115932	9	HS1107	AL031589 Human DNA	246	18	11.3	160901	9	CNS01DMW	AL137228 Human chr
190	18	11.3	118425	2	AC146562	AC146562 Medicago	247	18	11.3	160920	2	AC027087	AC027087 Homo sapi
191	18	11.3	119393	9	AC003658	AC003658 Homo sapi	248	18	11.3	161602	9	AC022634	AC022634 Homo sapi
192	18	11.3	119453	9	AC004006	AC004006 Homo sapi	249	18	11.3	162043	2	AC018803	AC018803 Homo sapi
193	18	11.3	121245	9	AC034240	AC034240 Homo sapi	250	18	11.3	162322	2	AC093027	AC093027 Homo sapi
194	18	11.3	122042	9	AC008924	AC008924 Homo sapi	251	18	11.3	162387	2	AC021213	AC021213 Homo sapi
195	18	11.3	122168	9	AC127383	AC127383 Homo sapi	252	18	11.3	162450	6	AR211792	AR211792 Sequence
196	18	11.3	123205	10	AL293155	AL293155 Mouse DNA	253	18	11.3	162641	2	AC143910	AC143910 Mus muscu
197	18	11.3	124446	9	AL512484	AL512484 Human DNA	254	18	11.3	162930	2	AC147593	AC147593 Canis fam
198	18	11.3	125765	2	AC141355	AC141355 Tetradon	255	18	11.3	163249	10	AC113559	AC113559 Mus muscu
199	18	11.3	129705	2	AC133358	AC133358 Rattus no	256	18	11.3	163348	10	AC119236	AC119236 Mus muscu
200	18	11.3	130040	8	AC135415	AC135415 Medicago	257	18	11.3	163520	9	AL391239	AL391239 Human DNA
201	18	11.3	130177	9	HSB27987	AL078644 Human DNA	258	18	11.3	163531	2	AC102289	AC102289 Mus muscu
202	18	11.3	130932	9	AC092658	AC092658 Homo sapi	259	18	11.3				
203	18	11.3	132444	9	AC019226	AC019226 Homo sapi	260	18	11.3				
204	18	11.3	133468	2	AC129971	AC129971 Felle cat	261	18	11.3				

c 262	18	11.3	16373	9	AL359854	Human DNA	c 319	18	11.3	180778	9	AL355596	AL355596 Human DNA
c 263	18	11.3	163623	9	AP005203	Homo sapi	320	18	11.3	181016	2	AC073129	AC073129 Homo sapi
c 264	18	11.3	163731	9	AC008949	Homo sapi	321	18	11.3	181467	10	AL844586	AL844586 Mouse DNA
c 265	18	11.3	164310	2	AC016156	Homo sapi	c 322	18	11.3	182184	2	AC022891	AC022891 Homo sapi
c 266	18	11.3	165147	2	AC021342	Homo sapi	323	18	11.3	182440	1	AP000994	AP000994 Homo sapi
c 267	18	11.3	165459	9	AC090587	Homo sapi	324	18	11.3	182481	1	AC007056	AC007056 Homo sapi
c 268	18	11.3	165789	2	AL591029	Homo sapi	325	18	11.3	182608	2	BX530059	BX530059 Homo sapi
c 269	18	11.3	165957	9	AC113558	Homo sapi	c 326	18	11.3	182618	9	AC095349	AC095349 Homo sapi
c 270	18	11.3	166192	9	AC096737	Homo sapi	c 327	18	11.3	183391	2	AC147319	AC147319 Pan trogl
c 271	18	11.3	166588	2	AC021870	Homo sapi	328	18	11.3	183461	9	AC006121	AC006121 Homo sapi
c 272	18	11.3	166876	2	AL356864	Homo sapi	c 329	18	11.3	183976	9	AC100821	AC100821 Homo sapi
c 273	18	11.3	166913	2	AC013708	Homo sapi	c 330	18	11.3	184106	9	AC060812	AC060812 Homo sapi
c 274	18	11.3	167050	1	SAG766847	Streptococ	331	18	11.3	184111	9	AC006821	AC006821 Homo sapi
c 275	18	11.3	167263	9	AC092417	Homo sapi	332	18	11.3	184119	2	AC133424	AC133424 Homo sapi
c 276	18	11.3	167778	2	AC132618	Mus muscu	c 333	18	11.3	184555	9	AC025427	AC025427 Homo sapi
c 277	18	11.3	168026	9	AL445670	Human DNA	c 334	18	11.3	184557	10	AC116657	AC116657 Homo sapi
c 278	18	11.3	168205	2	AC058819	Homo sapi	c 335	18	11.3	184560	2	AC021124	AC021124 Homo sapi
c 279	18	11.3	168741	2	AC013573	Homo sapi	c 336	18	11.3	185229	9	AL157762	AL157762 Homo sapi
c 280	18	11.3	168947	9	AC009453	Homo sapi	337	18	11.3	185598	2	AC132909	AC132909 Homo sapi
c 281	18	11.3	169371	2	AC125014	Mus muscu	338	18	11.3	186360	9	AC007982	AC007982 Homo sapi
c 282	18	11.3	169457	2	AC009216	Drosophil	339	18	11.3	186748	3	AC012163	AC012163 Homo sapi
c 283	18	11.3	169771	9	AC079163	Homo sapi	340	18	11.3	187914	9	AC104126	AC104126 Homo sapi
c 284	18	11.3	169775	9	AL139120	Human DNA	341	18	11.3	187993	2	AC139292	AC139292 Homo sapi
c 285	18	11.3	170026	2	AC016421	Homo sapi	342	18	11.3	188303	2	AC115256	AC115256 Homo sapi
c 286	18	11.3	170070	2	BX548039	Homo sapi	c 343	18	11.3	188303	2	AC115256	AC115256 Homo sapi
c 287	18	11.3	170163	2	AC064844	Homo sapi	344	18	11.3	188373	9	AC145920	AC145920 Homo sapi
c 288	18	11.3	170233	2	AC147091	Pan trogl	c 345	18	11.3	189196	10	AL603804	AL603804 Mouse DNA
c 289	18	11.3	171073	9	AC074254	Homo sapi	c 346	18	11.3	189217	10	AC122858	AC122858 Homo sapi
c 290	18	11.3	171515	9	AC068389	Homo sapi	347	18	11.3	190173	10	AC110573	AC110573 Homo sapi
c 291	18	11.3	171619	9	AC008082	Homo sapi	348	18	11.3	190690	9	HSX324122	HSX324122 Homo sapi
c 292	18	11.3	171726	2	AC136269	Rattus no	349	18	11.3	190802	10	AC124424	AC124424 Homo sapi
c 293	18	11.3	172022	2	AC145440	Bos tauru	c 350	18	11.3	191122	2	AL359769	AL359769 Homo sapi
c 294	18	11.3	172144	4	AC092497	Sus scrofa	351	18	11.3	191452	2	AC118966	AC118966 Homo sapi
c 295	18	11.3	172157	2	BX571698	Danio rer	352	18	11.3	191841	2	AC112827	AC112827 Homo sapi
c 296	18	11.3	173012	2	AC013728	Homo sapi	353	18	11.3	192670	9	AC008592	AC008592 Homo sapi
c 297	18	11.3	174040	2	AC073950	Homo sapi	354	18	11.3	192712	2	BX537285	BX537285 Homo sapi
c 298	18	11.3	174640	2	AC024479	Homo sapi	c 355	18	11.3	193625	2	AP001194	AP001194 Homo sapi
c 299	18	11.3	174712	4	AC091624	Canis fam	356	18	11.3	193867	2	AC105512	AC105512 Homo sapi
c 300	18	11.3	174790	2	AC134864	Canis fam	357	18	11.3	194247	2	AC128060	AC128060 Homo sapi
c 301	18	11.3	175263	9	AC023102	Homo sapi	358	18	11.3	194250	2	AC140094	AC140094 Bos tauru
c 302	18	11.3	175354	9	AP003503	Homo sapi	c 359	18	11.3	194541	2	AC011119	AC011119 Homo sapi
c 303	18	11.3	175946	9	AP002088	Homo sapi	360	18	11.3	194663	2	BX890578	BX890578 Homo sapi
c 304	18	11.3	176468	2	AC102928	Homo sapi	c 361	18	11.3	195066	10	AC122215	AC122215 Homo sapi
c 305	18	11.3	177056	2	AC132579	Mus muscu	c 362	18	11.3	195665	2	BX322638	BX322638 Homo sapi
c 306	18	11.3	177136	2	AC103584	Bos tauru	c 363	18	11.3	196492	3	AC139725	AC139725 Homo sapi
c 307	18	11.3	177268	2	AC145286	Homo sapi	c 364	18	11.3	196877	9	AC063947	AC063947 Homo sapi
c 308	18	11.3	177417	2	AC133160	Mus muscu	365	18	11.3	197013	2	AC079552	AC079552 Homo sapi
c 309	18	11.3	177470	9	AL357140	Human DNA	366	18	11.3	197437	2	AF303736	AF303736 Homo sapi
c 310	18	11.3	177552	2	BX510351	Danio rer	367	18	11.3	198647	2	AC023056	AC023056 Homo sapi
c 311	18	11.3	178210	2	AC023884	Homo sapi	368	18	11.3	198656	2	AC108431	AC108431 Homo sapi
c 312	18	11.3	178254	2	AC125160	Mus muscu	369	18	11.3	198693	2	AC115912	AC115912 Homo sapi
c 313	18	11.3	178679	2	AC113946	Mus muscu	370	18	11.3	199016	9	HS48612	HS48612 Homo sapi
c 314	18	11.3	178914	9	AL590807	Human DNA	c 371	18	11.3	199315	2	AC087801	AC087801 Homo sapi
c 315	18	11.3	179605	9	AC008507	Homo sapi	c 372	18	11.3	200306	2	AC128157	AC128157 Homo sapi
c 316	18	11.3	179262	2	AC079507	Mus muscu	373	18	11.3	201673	2	AC099747	AC099747 Homo sapi
c 317	18	11.3	179442	2	AP003051	Homo sapi	c 374	18	11.3	202370	2	AC102899	AC102899 Homo sapi
c 318	18	11.3	180137	2	AC023081	Homo sapi	c 375	18	11.3	202726	5	AL773593	AL773593 Zebrafish

376	18	11.3	203279	9	AL354826	AL354826 Human DNA	c 433	18	11.3	259599	2	AC123087	AC123087 Rattus no
377	18	11.3	203924	2	AC012159	AC012159 Drosophila	c 434	18	11.3	264412	2	AC128074	AC128074 Rattus no
378	18	11.3	205834	5	AP006193	AP006193 Homo sapi	435	18	11.3	266461	2	AC120718	AC120718 Rattus no
379	18	11.3	205870	5	BX088695	BX088695 Zebrafish	436	18	11.3	266583	2	AC111344	AC111344 Rattus no
380	18	11.3	206436	2	AC112605	AC112605 Rattus no	437	18	11.3	274480	2	AC115513	AC115513 Rattus no
c 381	18	11.3	209326	2	AC106407	AC106407 Rattus no	438	18	11.3	276049	2	AC128259	AC128259 Rattus no
382	18	11.3	209643	10	AC080018	AC080018 Mus muscu	c 439	18	11.3	285256	2	AC118492	AC118492 Rattus no
c 383	18	11.3	209901	2	AC102707	AC102707 Mus muscu	c 440	18	11.3	286008	2	AC134828	AC134828 Mus muscu
c 384	18	11.3	210740	2	AC120321	AC120321 Rattus no	441	18	11.3	286395	2	AC125732	AC125732 Rattus no
c 385	18	11.3	216571	9	AC009961	AC009961 Homo sapi	c 442	18	11.3	290633	2	AC099180	AC099180 Rattus no
c 386	18	11.3	217916	2	AC099190	AC099190 Rattus no	443	18	11.3	292171	2	AC091244	AC091244 Rattus no
c 387	18	11.3	219488	2	AC095440	AC095440 Rattus no	444	18	11.3	298532	2	AC129468	AC129468 Rattus no
c 388	18	11.3	220084	2	AL445521	AL445521 Homo sapi	445	18	11.3	299804	2	AE003507	AE003507 Rattus no
c 389	18	11.3	220216	9	AC021019	AC021019 Homo sapi	446	18	11.3	300355	1	AE017162	AE017162 Picrochloro
c 390	18	11.3	220231	2	AC125358	AC125358 Rattus no	447	18	11.3	301697	2	AC136490	AC136490 Rattus no
391	18	11.3	220248	10	AL772385	AL772385 Mouse DNA	448	18	11.3	302960	1	AE016935	AE016935 Bacteroid
392	18	11.3	220320	2	AC132527	AC132527 Mus muscu	c 449	18	11.3	304642	2	AC123398	AC123398 Rattus no
393	18	11.3	221787	2	AC073690	AC073690 Mus muscu	c 450	18	11.3	322781	2	AC103396	AC103396 Rattus no
394	18	11.3	221969	2	AC139955	AC139955 Rattus no	451	18	11.3	324462	2	AC137263	AC137263 Rattus no
395	18	11.3	221974	2	AC099118	AC099118 Rattus no	c 452	18	11.3	326700	2	AC134362	AC134362 Rattus no
396	18	11.3	222570	2	AC103995	AC103995 Rattus no	c 453	18	11.3	327812	2	AC115555	AC115555 Rattus no
397	18	11.3	222975	2	AC130905	AC130905 Rattus no	454	18	11.3	331314	2	AC125550	AC125550 Rattus no
c 398	18	11.3	223366	2	AC091366	AC091366 Rattus no	455	18	11.3	333622	2	AC111475	AC111475 Rattus no
c 399	18	11.3	225118	2	AC117168	AC117168 Rattus no	c 456	18	11.3	340899	2	AC095219	AC095219 Rattus no
400	18	11.3	225216	10	AL844888	AL844888 Mouse DNA	c 457	18	11.3	341944	2	AC079158	AC079158 Homo sapi
401	18	11.3	225651	2	AC106065	AC106065 Rattus no	c 458	18	11.3	345434	2	AC098412	AC098412 Rattus no
402	18	11.3	226450	2	BX088714	BX088714 Danto fer	459	18	11.3	345992	2	AC107197	AC107197 Rattus no
403	18	11.3	226872	2	AC108645	AC108645 Rattus no	460	18	11.3	346354	2	AC095850	AC095850 Rattus no
c 404	18	11.3	227457	2	AC129997	AC129997 Rattus no	461	18	11.3	346865	2	AC097921	AC097921 Rattus no
c 405	18	11.3	227876	2	AC097192	AC097192 Rattus no	c 462	18	11.3	346865	2	AC097921	AC097921 Rattus no
c 406	18	11.3	228353	2	AL445583	AL445583 Homo sapi	463	18	11.3	347550	1	AB001118	AB001118 Buchnera
407	18	11.3	228655	2	AC096829	AC096829 Rattus no	c 464	18	11.3	348650	1	AB003364	AB003364 Staphyloc
408	18	11.3	230378	2	AC102893	AC102893 Mus muscu	465	17	10.7	179	9	HS69D11F	HS69D11F
409	18	11.3	230575	2	AC128992	AC128992 Rattus no	c 466	17	10.7	303	11	BV048861	BV048861 S212P6034
410	18	11.3	231529	2	AC125102	AC125102 Mus muscu	c 467	17	10.7	358	3	EZAS06154	EZAS06154 Euscorpili
411	18	11.3	232552	2	AC103111	AC103111 Rattus no	c 468	17	10.7	375	8	ATHS23814	ATHS23814 Arabidops
412	18	11.3	233645	2	AC130670	AC130670 Mus muscu	c 469	17	10.7	375	8	ATHS23827	ATHS23827 Arabidops
413	18	11.3	233645	2	AC097282	AC097282 Rattus no	c 470	17	10.7	375	8	ATHS23827	ATHS23827 Arabidops
c 414	18	11.3	234072	2	AC099135	AC099135 Rattus no	c 471	17	10.7	425	6	AX431960	AX431960 Sequence
c 415	18	11.3	236629	2	AC120586	AC120586 Rattus no	472	17	10.7	445	8	AJ592834	AJ592834 Arabidops
c 416	18	11.3	236766	2	AC115491	AC115491 Rattus no	473	17	10.7	486	6	AX311732	AX311732 Sequence
c 417	18	11.3	238009	2	AC103650	AC103650 Mus muscu	474	17	10.7	534	11	BV029827	BV029827 S212P6020
418	18	11.3	239113	2	AC094034	AC094034 Rattus no	475	17	10.7	594	9	HSN324265	HSN324265 Homo sapi
c 419	18	11.3	240830	2	AC095615	AC095615 Rattus no	c 476	17	10.7	629	6	AX371038	AX371038 Sequence
c 420	18	11.3	241407	2	AC130827	AC130827 Mus muscu	c 477	17	10.7	641	11	BV001915	BV001915 S208P6122
c 421	18	11.3	242269	2	AC133719	AC133719 Rattus no	478	17	10.7	759	6	AR348254	AR348254 Sequence
422	18	11.3	247402	10	AC125187	AC125187 Mus muscu	479	17	10.7	760	4	AY285283	AY285283 Sus scrofa
423	18	11.3	249987	2	AC098279	AC098279 Rattus no	c 480	17	10.7	811	6	AX136583	AX136583 Sequence
424	18	11.3	251645	2	AC105549	AC105549 Rattus no	c 481	17	10.7	811	6	BD123823	BD123823 Secretory
425	18	11.3	251766	2	AC106117	AC106117 Rattus no	c 482	17	10.7	848	8	AT022	AT022 Arabidops
426	18	11.3	252402	2	BX005425	BX005425 Danto fer	483	17	10.7	868	11	BV056539	BV056539 S212P6790
427	18	11.3	252632	2	AC123197	AC123197 Rattus no	484	17	10.7	906	8	AF362487	AF362487 Arabidops
c 428	18	11.3	253589	2	AC113741	AC113741 Rattus no	c 485	17	10.7	972	8	AF207978	AF207978 Ipomopsis
c 429	18	11.3	253638	2	AC102537	AC102537 Mus muscu	486	17	10.7	1014	8	AF362486	AF362486 Arabidops
c 430	18	11.3	254114	2	AC129431	AC129431 Rattus no	487	17	10.7	1050	3	AF438021	AF438021 Apocynaceae
c 431	18	11.3	254437	9	AP000500	AP000500 Homo sapi	488	17	10.7	1147	5	LD1300147	LD1300147 Lopnur d
c 432	18	11.3	258789	2	AC113921	AC113921 Rattus no	489	17	10.7	1232	3	DNMC70F	DNMC70F D.melanogaster

c 490	17	10.7	1438	6	AX154644	Sequence	c 547	17	10.7	5683	6	AX825986	AX825986	Sequence
c 491	17	10.7	1463	6	AX136329	Sequence	c 548	17	10.7	5683	6	AX826114	AX826114	Sequence
c 492	17	10.7	1463	6	BD123617	Secretary	c 549	17	10.7	5880	6	AX251085	AX251085	Sequence
c 493	17	10.7	1463	9	AK075525	Homo sapi	c 550	17	10.7	5880	6	AX323563	AX323563	Sequence
c 494	17	10.7	1565	3	AK113875	AK113875	c 551	17	10.7	6076	6	AX251418	AX251418	Sequence
c 495	17	10.7	1799	10	AY082332	AY082332	c 552	17	10.7	6301	6	AX344955	AX344955	Sequence
c 496	17	10.7	1827	10	BC050206	BC050206	c 553	17	10.7	6316	6	AX251105	AX251105	Sequence
c 497	17	10.7	1831	3	DROGACATRA	L22205	c 554	17	10.7	6316	6	AX251866	AX251866	Sequence
c 498	17	10.7	1905	1	AF056335	Bacillus	c 555	17	10.7	6316	6	AX251866	AX251866	Sequence
c 499	17	10.7	1968	1	AY128680	AY128680	c 556	17	10.7	6321	6	AX348647	AX348647	Sequence
c 500	17	10.7	1969	7	BADLGDH	M62697	c 557	17	10.7	6321	6	AX458547	AX458547	Sequence
c 501	17	10.7	1992	6	BC040866	BC040866	c 558	17	10.7	6475	6	AX347150	AX347150	Sequence
c 502	17	10.7	2000	6	AKS09766	AKS09766	c 559	17	10.7	6534	6	AX277948	AX277948	Sequence
c 503	17	10.7	2087	9	AK093752	AK093752	c 560	17	10.7	6534	6	AX323637	AX323637	Sequence
c 504	17	10.7	2153	3	AY069651	AY069651	c 561	17	10.7	6534	6	AX344776	AX344776	Sequence
c 505	17	10.7	2246	6	AR395926	AR395926	c 562	17	10.7	6534	6	AX346328	AX346328	Sequence
c 506	17	10.7	2261	6	AX544449	AX544449	c 563	17	10.7	6950	2	AC014419	AC014419	Sequence
c 507	17	10.7	2400	1	AF092086	AF092086	c 564	17	10.7	7262	9	HSW806281	HSW806281	Sequence
c 508	17	10.7	2447	8	AY114653	AY114653	c 565	17	10.7	8588	6	AX278015	AX278015	Sequence
c 509	17	10.7	2398	8	AY227363S2	AY264885	c 566	17	10.7	8588	6	AX323712	AX323712	Sequence
c 510	17	10.7	2612	8	AY062594	AY062594	c 567	17	10.7	9265	6	AX339183	AX339183	Sequence
c 511	17	10.7	2682	9	CAU64206	U64206	c 568	17	10.7	9265	6	AX347055	AX347055	Sequence
c 512	17	10.7	2814	10	BC023094	BC023094	c 569	17	10.7	10279	6	AX279995	AX279995	Sequence
c 513	17	10.7	2882	6	AX747740	AX747740	c 570	17	10.7	10279	6	AX346492	AX346492	Sequence
c 514	17	10.7	2882	9	AK092806	AK092806	c 571	17	10.7	10279	6	AX356451	AX356451	Sequence
c 515	17	10.7	3360	1	STXSAU3A1M	M32470	c 572	17	10.7	10401	9	HSX297551	HSX297551	Sequence
c 516	17	10.7	3360	6	AT7958	AT7958	c 573	17	10.7	10988	1	AE007626	AE007626	Sequence
c 517	17	10.7	3478	8	SCOR273C	SCOR273C	c 574	17	10.7	11147	6	AX598807	AX598807	Sequence
c 518	17	10.7	3759	3	DMJ18386	DMJ18386	c 575	17	10.7	11147	6	AX598853	AX598853	Sequence
c 519	17	10.7	3776	1	LAJ10153	LAJ10153	c 576	17	10.7	11196	1	AE006318	AE006318	Sequence
c 520	17	10.7	4043	9	HSW806088	HSW806088	c 577	17	10.7	11279	1	AE009840	AE009840	Sequence
c 521	17	10.7	4300	8	AF279129	AF279129	c 578	17	10.7	11502	9	AC138607	AC138607	Sequence
c 522	17	10.7	4313	3	DMW68563	DMW68563	c 579	17	10.7	11964	6	AX458509	AX458509	Sequence
c 523	17	10.7	4353	6	AX252138	AX252138	c 580	17	10.7	12203	3	AF016653	AF016653	Sequence
c 524	17	10.7	4353	6	AX344498	AX344498	c 581	17	10.7	12221	1	AE015001	AE015001	Sequence
c 525	17	10.7	4353	6	AX348905	AX348905	c 582	17	10.7	12523	1	AE010575	AE010575	Sequence
c 526	17	10.7	4915	9	HSW807057	HSW807057	c 583	17	10.7	13377	8	AF341860511	AF341860511	Sequence
c 527	17	10.7	5031	6	AX085162	AX085162	c 584	17	10.7	13779	3	DMX35042	DMX35042	Sequence
c 528	17	10.7	5031	6	AX085359	AX085359	c 585	17	10.7	14147	6	AX251501	AX251501	Sequence
c 529	17	10.7	5142	6	AX367152	AX367152	c 586	17	10.7	14147	6	AX347392	AX347392	Sequence
c 530	17	10.7	5218	9	HSW806829	HSW806829	c 587	17	10.7	14147	6	AX349113	AX349113	Sequence
c 531	17	10.7	5236	6	AX345252	AX345252	c 588	17	10.7	14147	6	AX657806	AX657806	Sequence
c 532	17	10.7	5278	6	AX251130	AX251130	c 589	17	10.7	14147	6	AX659080	AX659080	Sequence
c 533	17	10.7	5278	6	AX345725	AX345725	c 590	17	10.7	14147	6	AX767435	AX767435	Sequence
c 534	17	10.7	5360	6	AX281201	AX281201	c 591	17	10.7	14147	6	AX795753	AX795753	Sequence
c 535	17	10.7	5360	6	AX346839	AX346839	c 592	17	10.7	14147	6	AX795869	AX795869	Sequence
c 536	17	10.7	5360	6	AX356472	AX356472	c 593	17	10.7	14147	6	AX822261	AX822261	Sequence
c 537	17	10.7	5683	6	AX281480	AX281480	c 594	17	10.7	14147	6	AX822385	AX822385	Sequence
c 538	17	10.7	5683	6	AX346709	AX346709	c 595	17	10.7	14147	6	AX8225901	AX8225901	Sequence
c 539	17	10.7	5683	6	AX348832	AX348832	c 596	17	10.7	14147	6	AX826029	AX826029	Sequence
c 540	17	10.7	5683	6	AX795708	AX795708	c 597	17	10.7	14287	6	AX344624	AX344624	Sequence
c 541	17	10.7	5683	6	AX795834	AX795834	c 598	17	10.7	14946	8	AF362474	AF362474	Sequence
c 542	17	10.7	5683	6	AX795950	AX795950	c 599	17	10.7	15479	6	AX348350	AX348350	Sequence
c 543	17	10.7	5683	6	AX822161	AX822161	c 600	17	10.7	15479	6	AX347057	AX347057	Sequence
c 544	17	10.7	5683	6	AX822346	AX822346	c 601	17	10.7	15498	8	AF362475	AF362475	Sequence
c 545	17	10.7	5683	6	AX822474	AX822474	c 602	17	10.7	15498	8	AF362475	AF362475	Sequence
c 546	17	10.7	5683	6	AX825801	AX825801	c 603	17	10.7	18611	10	AF330048	AF330048	Sequence

604	17	10.7	19000	3	CER05D4	292804 Caenorhabdi	c 661	17	10.7	61469	2	AC107910	AC107910 Homo sapi
605	17	10.7	19605	9	AC103746	AC103746 Homo sapi	c 662	17	10.7	61818	2	AC106008	AC106008 Homo sapi
606	17	10.7	20720	3	CERC0762	Z3840 Caenorhabdi	c 663	17	10.7	61824	2	AC101450	AC101450 Mus muscu
607	17	10.7	20723	3	AC024839	AC024839 Caenorhab	c 664	17	10.7	62880	2	AC026926	AC026926 Homo sapi
608	17	10.7	20723	3	AC024839	AC024839 Caenorhab	c 665	17	10.7	63142	9	AP0000279	AP0000279 Homo sapi
609	17	10.7	20941	1	AEO00976	AEO00976 Archaeogl	c 666	17	10.7	63266	9	AL607038	AL607038 Homo sapi
610	17	10.7	23652	8	T15D22	AC012189 Arabidops	c 667	17	10.7	63918	9	AL672104	AL672104 Homo sapi
611	17	10.7	23992	9	AC110298	AC110298 Homo sapi	c 668	17	10.7	64524	2	AC087195	AC087195 Homo sapi
612	17	10.7	26726	9	AY194117	AY194117 Homo sapi	c 669	17	10.7	64550	2	AC125427	AC125427 Homo sapi
613	17	10.7	30051	9	AL732446	AL732446 Human DNA	c 670	17	10.7	65361	2	AC091863	AC091863 Homo sapi
614	17	10.7	30060	2	AC017401	AC017401 Drosophill	c 671	17	10.7	65752	2	AC018627	AC018627 Homo sapi
615	17	10.7	31226	3	U39998	U39998 Caenorhabdi	c 672	17	10.7	65838	2	AC115758	AC115758 Mus muscu
616	17	10.7	32819	2	CER37L19	Z92838 Caenorhabdi	c 673	17	10.7	66009	2	AC101250	AC101250 Mus muscu
617	17	10.7	33399	3	CERC09H6	Z81466 Caenorhabdi	c 674	17	10.7	66152	2	AC137709	AC137709 Homo sapi
618	17	10.7	34101	3	U64837	U64837 Caenorhabdi	c 675	17	10.7	66686	2	AC087669	AC087669 Homo sapi
619	17	10.7	35503	3	CER09D6	Z82078 Caenorhabdi	c 676	17	10.7	66833	2	AC101655	AC101655 Mus muscu
620	17	10.7	36242	9	AL360228	AL360228 Human DNA	c 677	17	10.7	66874	9	AC069310	AC069310 Homo sapi
621	17	10.7	37467	3	DMC14E2	Z98254 Drosophilla	c 678	17	10.7	66959	9	AL591214	AL591214 Homo sapi
622	17	10.7	37672	8	SCV050M6N	X89633 S. cerevisia	c 679	17	10.7	67179	2	AC084787	AC084787 Homo sapi
623	17	10.7	38020	9	AC122131	AC122131 Homo sapi	c 680	17	10.7	67340	2	AC113954	AC113954 Mus muscu
624	17	10.7	38225	3	CER13611	Z83317 Caenorhabdi	c 681	17	10.7	67575	9	HSBR211L9	HSBR211L9 Homo sapi
625	17	10.7	39057	3	AF078788	AF078788 Caenorhab	c 682	17	10.7	67680	9	AC026426	AC026426 Homo sapi
626	17	10.7	39550	9	HSU85B5	Z69724 Human DNA	c 683	17	10.7	66648	9	HS635G19	HS635G19 Homo sapi
627	17	10.7	39982	6	AR308846	AR308846 Sequence	c 684	17	10.7	68986	2	AC020283	AC020283 Homo sapi
628	17	10.7	40198	9	HS1261H12	Z54072 Human DNA	c 685	17	10.7	70687	8	AP006376	AP006376 Homo sapi
629	17	10.7	40873	2	CER04109	Z92846 Caenorhabdi	c 686	17	10.7	71118	9	AL390375	AL390375 Homo sapi
630	17	10.7	41509	2	AC140536	AC140536 Homo sapi	c 687	17	10.7	71327	8	AP001300	AP001300 Homo sapi
631	17	10.7	41735	9	AC134050	AC134050 Homo sapi	c 688	17	10.7	74515	9	AL355482	AL355482 Homo sapi
632	17	10.7	42042	3	CERC34B4	Z78059 Caenorhabdi	c 689	17	10.7	74546	9	BX296564	BX296564 Homo sapi
633	17	10.7	42065	3	CER02E15	AC084480 Caenorhab	c 690	17	10.7	75551	3	AC005111	AC005111 Homo sapi
634	17	10.7	42141	3	CER5469A	AL032648 Caenorhab	c 691	17	10.7	78241	9	AL358392	AL358392 Homo sapi
635	17	10.7	42612	2	AC091325	AC091325 Mus muscu	c 692	17	10.7	78689	9	AC108668	AC108668 Homo sapi
636	17	10.7	43585	3	U97593	U97593 Caenorhabdi	c 693	17	10.7	81278	9	AC091062	AC091062 Homo sapi
637	17	10.7	43785	7	LBA131519	AJ131519 Lactobaci	c 694	17	10.7	82168	9	AC092769	AC092769 Homo sapi
638	17	10.7	43955	2	AC100238	AC100238 Mus muscu	c 695	17	10.7	82415	8	AB005244	AB005244 Homo sapi
639	17	10.7	44443	9	HSU72E5	Z68328 Human DNA	c 696	17	10.7	82452	9	AL138763	AL138763 Homo sapi
640	17	10.7	44722	9	AC107396	AC107396 Homo sapi	c 697	17	10.7	82453	9	AC004558	AC004558 Homo sapi
641	17	10.7	45983	9	BX004861	BX004861 Human DNA	c 698	17	10.7	82646	10	AL928620	AL928620 Homo sapi
642	17	10.7	49137	2	AC106018	AC106018 Homo sapi	c 699	17	10.7	83391	6	AX458577	AX458577 Sequence
643	17	10.7	49137	2	AC106018	AC106018 Homo sapi	c 700	17	10.7	85836	2	AC108384	AC108384 Pan trogl
644	17	10.7	49349	9	AL451134	AL451134 Human DNA	c 701	17	10.7	86203	9	AC017116	AC017116 Homo sapi
645	17	10.7	49499	9	AF184110	AF184110 Homo sapi	c 702	17	10.7	87243	9	AC117497	AC117497 Homo sapi
646	17	10.7	49743	2	AC017211	AC017211 Drosophill	c 703	17	10.7	87347	9	AC133530	AC133530 Homo sapi
647	17	10.7	50572	2	AC023899	AC023899 Mus muscu	c 704	17	10.7	88783	9	AC026398	AC026398 Homo sapi
648	17	10.7	51070	9	AC116303	AC116303 Homo sapi	c 705	17	10.7	88900	2	AC020204	AC020204 Homo sapi
649	17	10.7	51921	9	AC016145	AC016145 Homo sapi	c 706	17	10.7	89089	9	HS260B21	HS260B21 Homo sapi
650	17	10.7	54161	9	BX276189	BX276189 Human DNA	c 707	17	10.7	89354	9	AC008957	AC008957 Homo sapi
651	17	10.7	54626	2	AC103762	AC103762 Homo sapi	c 708	17	10.7	89690	8	AC079374	AC079374 Homo sapi
652	17	10.7	55335	9	AL592227	AL592227 Human DNA	c 709	17	10.7	90599	8	AC130275	AC130275 Homo sapi
653	17	10.7	56287	8	AP002060	AP002060 Arabidops	c 710	17	10.7	90940	9	AC104052	AC104052 Homo sapi
654	17	10.7	57493	9	AC004505	AC004505 Homo sapi	c 711	17	10.7	91516	9	AL731577	AL731577 Homo sapi
655	17	10.7	58484	9	AL337160	AL337160 Human DNA	c 712	17	10.7	91722	8	AP004976	AP004976 Lotus cor
656	17	10.7	58749	2	AC139006	AC139006 Homo sapi	c 713	17	10.7	92250	9	AC026693	AC026693 Homo sapi
657	17	10.7	59266	2	AC131282	AC131282 Homo sapi	c 714	17	10.7	93214	2	AC013107	AC013107 Homo sapi
658	17	10.7	60036	2	AC009610	AC009610 Homo sapi	c 715	17	10.7	93974	9	AC084421	AC084421 Homo sapi
659	17	10.7	60565	2	AC023852	AC023852 Homo sapi	c 716	17	10.7	94038	8	AC004401	AC004401 Arabidops
660	17	10.7	61404	9	AL513546	AL513546 Human DNA	c 717	17	10.7	95214	8	AC006526	AC006526 Arabidops

c 718	17	10.7	95337	2	AC138691	AC138691 Homo sapi
c 719	17	10.7	95302	9	AC010380	AC010380 Homo sapi
c 720	17	10.7	96726	2	HS1178F13	AL118500 Homo sapi
c 721	17	10.7	97101	2	AL450308	AL450308 Homo sapi
c 722	17	10.7	97434	9	AC087882	AC087882 Homo sapi
c 723	17	10.7	99332	9	HSJ298J18	AL096764 Homo sapi
c 724	17	10.7	100000	9	AP000038	AP000038 Homo sapi
c 725	17	10.7	100000	9	AP000106	AP000106 Homo sapi
c 726	17	10.7	100000	9	AP000182	AP000182 Homo sapi
c 727	17	10.7	100028	8	ATF3C22	AL353912 Arabidops
c 728	17	10.7	100057	10	AL929178	AL929178 Mouse DNA
c 729	17	10.7	101324	9	AC010386	AC010386 Homo sapi
c 730	17	10.7	101640	3	AC024810	AC024810 Caenorhab
c 731	17	10.7	101640	3	AC024810	AC024810 Caenorhab
c 732	17	10.7	102507	9	HSJ328N14	AL109938 Homo sapi
c 733	17	10.7	103187	9	AC093659	AC093659 Homo sapi
c 734	17	10.7	103820	5	AL929560	AL929560 Zebrafish
c 735	17	10.7	103822	9	AL353639	AL353639 Human DNA
c 736	17	10.7	103952	9	AC008852	AC008852 Homo sapi
c 737	17	10.7	104246	2	AC084785	AC084785 Arabidops
c 738	17	10.7	104972	2	AC025176	AC025176 Homo sapi
c 739	17	10.7	105391	2	AC144728	AC144728 Medicago
c 740	17	10.7	105643	9	AC005629	AC005629 Homo sapi
c 741	17	10.7	105960	9	HS209A6	AL035401 Human DNA
c 742	17	10.7	106710	9	HSB711C4	AL590012 Homo sapi
c 743	17	10.7	106773	9	AL590012	AL590012 Human DNA
c 744	17	10.7	107100	2	AC117377	AC117377 Homo sapi
c 745	17	10.7	107341	2	AC136973	AC136973 Medicago
c 746	17	10.7	107895	9	AC078929	AC078929 Homo sapi
c 747	17	10.7	108881	8	AC002391	AC002391 Arabidops
c 748	17	10.7	108933	2	AC146692	AC146692 Medicago
c 749	17	10.7	109450	2	AC019498	AC019498 Drosophila
c 750	17	10.7	109586	9	AC093059	AC093059 Homo sapi
c 751	17	10.7	109588	9	AC010461	AC010461 Homo sapi
c 752	17	10.7	110000	2	AC095363	AC095363 Rattus no
c 753	17	10.7	110000	2	AC095857	AC095857 Rattus no
c 754	17	10.7	110000	2	AC099211	AC099211 Rattus no
c 755	17	10.7	110000	2	AC110868	AC110868 Rattus no
c 756	17	10.7	110000	2	AC111335	AC111335 Rattus no
c 757	17	10.7	110000	2	AC111335	AC111335 Rattus no
c 758	17	10.7	110000	2	AC114471	AC114471 Rattus no
c 759	17	10.7	110000	2	AC117022	AC117022 Rattus no
c 760	17	10.7	110000	2	AC118422	AC118422 Rattus no
c 761	17	10.7	110000	2	AC120234	AC120234 Rattus no
c 762	17	10.7	110000	2	AC125151	AC125151 Rattus no
c 763	17	10.7	110000	2	AC125156	AC125156 Rattus no
c 764	17	10.7	110000	2	AC125156	AC125156 Rattus no
c 765	17	10.7	110000	2	AC130479	AC130479 Rattus no
c 766	17	10.7	110000	2	AC132284	AC132284 Rattus no
c 767	17	10.7	110000	2	AL390202	AL390202 Rattus no
c 768	17	10.7	110000	2	BX253515	BX253515 Drosophila
c 769	17	10.7	110000	2	PFMAL13_21	PFMAL13_21 Homo sapi
c 770	17	10.7	110000	2	PFMAL13P2_0	PFMAL13P2_0 Homo sapi
c 771	17	10.7	110000	2	PFMAL13P1_01	PFMAL13P1_01 Homo sapi
c 772	17	10.7	110312	10	AF131866	AF131866 Mus muscu
c 773	17	10.7	110520	9	AL603757	AL603757 Human DNA
c 774	17	10.7	110626	9	AC005541	AC005541 Homo sapi
c 775	17	10.7	110811	8	AP004520	AP004520 Lotus cor
c 776	17	10.7	110907	14	AY229987	AY229987 Cryptoph
c 777	17	10.7	111104	9	AC117389	AC117389 Homo sapi
c 778	17	10.7	111255	8	AC125478	AC125478 Medicago
c 779	17	10.7	112088	9	AC005216	AC005216 Homo sapi
c 780	17	10.7	112656	9	AC112253	AC112253 Homo sapi
c 781	17	10.7	114688	9	AC125437	AC125437 Homo sapi
c 782	17	10.7	115038	10	AL929270	AL929270 Mouse DNA
c 783	17	10.7	115279	9	AC112506	AC112506 Homo sapi
c 784	17	10.7	115512	9	AC114744	AC114744 Homo sapi
c 785	17	10.7	115568	9	AC092120	AC092120 Homo sapi
c 786	17	10.7	115626	9	AC010631	AC010631 Homo sapi
c 787	17	10.7	116763	8	ATF211	AL773543 Arabidops
c 788	17	10.7	117303	9	AC010792	AC010792 Homo sapi
c 789	17	10.7	117406	10	AL844550	AL844550 Mouse DNA
c 790	17	10.7	118080	10	HSN75335	HSN75335 Human DNA
c 791	17	10.7	118280	2	AC108843	AC108843 Mus muscu
c 792	17	10.7	118696	2	AC136141	AC136141 Medicago
c 793	17	10.7	119065	2	AC139336	AC139336 Human DNA
c 794	17	10.7	119077	9	AL354982	AL354982 Human DNA
c 795	17	10.7	119753	8	AC006248	AC006248 Arabidops
c 796	17	10.7	120316	2	AC025984	AC025984 Homo sapi
c 797	17	10.7	120461	2	AC131654	AC131654 Mus muscu
c 798	17	10.7	120586	8	AL590322	AL590322 Human DNA
c 799	17	10.7	120921	8	AC139336	AC139336 Medicago
c 800	17	10.7	121151	9	HS705D16	AL034428 Human DNA
c 801	17	10.7	121289	2	CNS05TD8	AL356018 Human chr
c 802	17	10.7	121372	2	AC145851	AC145851 Drosophila
c 803	17	10.7	121524	8	AF041468	AF041468 Gallardi
c 804	17	10.7	122042	8	AC008924	AC008924 Homo sapi
c 805	17	10.7	122371	2	BX253508	BX253508 Drosophila
c 806	17	10.7	123209	8	ATF4F15	AL045711 Arabidops
c 807	17	10.7	123291	9	AC104070	AC104070 Homo sapi
c 808	17	10.7	124211	8	AC126787	AC126787 Medicago
c 809	17	10.7	126154	10	AL935159	AL935159 Mouse DNA
c 810	17	10.7	126231	9	AC004139	AC004139 Homo sapi
c 811	17	10.7	126270	9	AC005283	AC005283 Homo sapi
c 812	17	10.7	126414	9	AC108084	AC108084 Homo sapi
c 813	17	10.7	126761	2	AC084129	AC084129 Homo sapi
c 814	17	10.7	126803	9	AC007032	AC007032 Homo sapi
c 815	17	10.7	127703	9	AL357034	AL357034 Human DNA
c 816	17	10.7	128428	2	AC144889	AC144889 Bos tauru
c 817	17	10.7	128554	9	AL162500	AL162500 Human DNA
c 818	17	10.7	128856	2	AC126779	AC126779 Medicago
c 819	17	10.7	129196	10	BX005080	BX005080 Macropus
c 820	17	10.7	129708	4	AC145407	AC145407 Homo sapi
c 821	17	10.7	129802	2	AC136701	AC136701 Homo sapi
c 822	17	10.7	129819	9	AC104049	AC104049 Homo sapi
c 823	17	10.7	129858	10	AL772272	AL772272 Mouse DNA
c 824	17	10.7	129989	9	AC005681	AC005681 Homo sapi
c 825	17	10.7	129996	2	AC133462	AC133462 Mus muscu
c 826	17	10.7	130878	9	AL450063	AL450063 Mouse DNA
c 827	17	10.7	131355	2	AC139655	AC139655 Rattus no
c 828	17	10.7	131402	10	AL773583	AL773583 Mouse DNA
c 829	17	10.7	131743	8	AC004561	AC004561 Arabidops
c 830	17	10.7	131743	8	AC004561	AC004561 Arabidops
c 831	17	10.7	131944	9	AC097659	AC097659 Homo sapi

c 832	17	10.7	132473	8	AC136451	AC136451 Medicago	c 889	17	10.7	146742	2	AC016275	AC016275 Homo sapi
833	17	10.7	132501	9	AC107613	AC107613 Homo sapi	890	17	10.7	146921	9	AC007992	AC007992 Homo sapi
834	17	10.7	132641	9	AP00679-	AP00679 Homo sapi	891	17	10.7	147002	2	AC126914	AC126914 Rattus no
c 835	17	10.7	134043	2	AC146717	AC146717 Rattus no	892	17	10.7	147047	9	AL353778	AL353778 Human DNA
c 836	17	10.7	134457	9	AC001231	AC001231 Homo sapi	893	17	10.7	147179	2	AC117937	AC117937 Canis fam
837	17	10.7	134825	10	AC108420	AC108420 Mus muscu	894	17	10.7	147250	2	AC011778	AC011778 Homo sapi
838	17	10.7	134878	9	AC140847	AC140847 Homo sapi	895	17	10.7	147260	2	AC016340	AC016340 Homo sapi
c 839	17	10.7	135240	9	AL136362	AL136362 Human DNA	896	17	10.7	147595	2	AC136834	AC136834 Rattus no
c 840	17	10.7	135280	5	BX296520	BX296520 Zebrafish	c 898	17	10.7	147810	9	AL353730	AL353730 Human DNA
c 841	17	10.7	135638	1	SYCSLNG	D64005 Synchocyst	c 899	17	10.7	148293	9	AC087730	AC087730 Pan trogl
c 842	17	10.7	135862	10	AC132576	AC132576 Mus muscu	c 900	17	10.7	148317	5	BX649477	BX649477 Zebrafish
c 843	17	10.7	135966	2	AL356007	AL356007 Homo sapi	c 901	17	10.7	148328	10	AL808120	AL808120 Mouse DNA
c 844	17	10.7	136311	2	AC146972	AC146972 Medicago	c 902	17	10.7	148338	2	AC022831	AC022831 Homo sapi
c 845	17	10.7	136372	9	AC103828	AC103828 Homo sapi	c 903	17	10.7	148380	2	AL139325	AL139325 Homo sapi
c 846	17	10.7	136485	10	BX294008	BX294008 Mouse DNA	c 904	17	10.7	148438	9	AC019072	AC019072 Homo sapi
c 847	17	10.7	136723	9	AC074000	AC074000 Homo sapi	c 905	17	10.7	148498	2	AC034225	AC034225 Homo sapi
c 848	17	10.7	136943	9	AL359842	AL359842 Human DNA	c 906	17	10.7	148504	2	AC138732	AC138732 Pongo pyg
849	17	10.7	137343	9	AP000946	AP000946 Homo sapi	c 907	17	10.7	148573	2	AC066693	AC066693 Homo sapi
c 850	17	10.7	137484	10	AC126021	AC126021 Mus muscu	c 908	17	10.7	148641	9	HS111909	HS111909 Homo sapi
851	17	10.7	137580	2	AC146553	AC146553 Medicago	c 909	17	10.7	148751	2	AC144694	AC144694 Sus scrof
852	17	10.7	137890	9	AB045364	AB045364 Homo sapi	c 910	17	10.7	148915	9	AC005030	AC005030 Homo sapi
853	17	10.7	137897	9	AL161913	AL161913 Human DNA	c 911	17	10.7	149050	9	AC024697	AC024697 Homo sapi
854	17	10.7	138007	2	AC141282	AC141282 Homo sapi	c 912	17	10.7	149059	9	AC027779	AC027779 Homo sapi
c 855	17	10.7	138209	9	HS044211	AL078597 Human DNA	c 913	17	10.7	149114	9	AP001172	AP001172 Homo sapi
c 856	17	10.7	138215	2	AC023523	AC023523 Homo sapi	814	17	10.7	149114	9	AP001172	AP001172 Homo sapi
c 857	17	10.7	138573	9	AL354211	AL354211 Pan trogl	915	17	10.7	149169	9	HS3323A24	HS3323A24 Homo sapi
c 858	17	10.7	139056	2	AC141691	AC141691 Apis mell	916	17	10.7	149981	2	AC011929	AC011929 Homo sapi
859	17	10.7	139189	10	AL935138	AL935138 Mouse DNA	917	17	10.7	150001	9	AC006063	AC006063 Homo sapi
c 860	17	10.7	139881	9	AL160254	AL160254 Human DNA	918	17	10.7	150136	9	BS000056	BS000056 Pan trogl
c 861	17	10.7	140806	2	AC137198	AC137198 Rattus no	919	17	10.7	150375	10	AC124404	AC124404 Mus muscu
862	17	10.7	140869	2	AC116515	AC116515 Mus muscu	920	17	10.7	150375	10	AC124404	AC124404 Mus muscu
c 863	17	10.7	141000	9	AC121756	AC121756 Homo sapi	921	17	10.7	150489	2	AC069491	AC069491 Homo sapi
c 864	17	10.7	141882	2	AC138465	AC138465 Medicago	922	17	10.7	150951	10	RN52A6	AC146246 Pan trogl
c 865	17	10.7	141920	2	AC068008	AC068008 Homo sapi	923	17	10.7	150954	9	AC146246	AC146246 Pan trogl
c 866	17	10.7	141913	9	AL512452	BS000037 Pan trogl	924	17	10.7	151494	2	AL339886	AL339886 Rattus no
c 867	17	10.7	142800	9	BS000037	BS000037 Pan trogl	925	17	10.7	151578	9	AL589986	AL589986 Homo sapi
868	17	10.7	142829	2	AC145415	AC145415 Felle cat	926	17	10.7	151588	2	AC105370	AC105370 Sus scrof
869	17	10.7	142908	2	AL513172	AL513172 Homo sapi	927	17	10.7	151603	9	AL157361	AL157361 Homo sapi
c 870	17	10.7	143324	9	AL137881	AL137881 Human DNA	928	17	10.7	151923	10	AL845499	AL845499 Mouse DNA
c 871	17	10.7	143527	9	AC011353	AC011353 Homo sapi	929	17	10.7	152190	2	AC113048	AC113048 Mus muscu
c 872	17	10.7	143577	9	AC013828	AC013828 Homo sapi	930	17	10.7	152205	2	AC041037	AC041037 Homo sapi
873	17	10.7	144290	9	AC098866	AC098866 Homo sapi	931	17	10.7	152248	2	AC027522	AC027522 Homo sapi
c 874	17	10.7	144301	9	AC010467	AC010467 Homo sapi	932	17	10.7	152344	9	CNS05TE3	CNS05TE3 Homo sapi
875	17	10.7	144311	2	AC133934	AC133934 Mus muscu	933	17	10.7	152558	2	AC013487	AC013487 Homo sapi
c 876	17	10.7	144566	9	BS000025	BS000025 Pan trogl	934	17	10.7	152580	2	AC107694	AC107694 Mus muscu
877	17	10.7	144749	2	AC025912	AC025912 Mus muscu	935	17	10.7	153022	2	AC137708	AC137708 Homo sapi
c 878	17	10.7	144768	9	AC010273	AC010273 Homo sapi	936	17	10.7	153176	2	AC132666	AC132666 Rattus no
c 879	17	10.7	144781	9	HS585114	AL121782 Human DNA	c 937	17	10.7	153203	2	AL359812	AL359812 Homo sapi
c 880	17	10.7	145256	9	AL360182	AL360182 Human DNA	c 938	17	10.7	153688	9	AC073225	AC073225 Homo sapi
c 881	17	10.7	145307	2	AP004745	AP004745 Oryza sat	c 939	17	10.7	153926	9	AL1671885	AL1671885 Homo sapi
c 882	17	10.7	145578	10	AC126548	AC126548 Mus muscu	940	17	10.7	154019	10	AL671885	AL671885 Homo sapi
883	17	10.7	145726	2	AC021807	AC021807 Homo sapi	941	17	10.7	154071	9	AL354794	AL354794 Homo sapi
884	17	10.7	145789	9	AC122694	AC122694 Homo sapi	942	17	10.7	154353	9	AC027820	AC027820 Homo sapi
885	17	10.7	146158	9	AL136136	AL136136 Human DNA	943	17	10.7	154612	9	AL365504	AL365504 Human DNA
c 886	17	10.7	146170	2	AC079224	AC079224 Homo sapi	944	17	10.7	154618	2	AC094013	AC094013 Papio anu
887	17	10.7	146267	2	AC008815	AC008815 Homo sapi	c 945	17	10.7	154640	9	AC096659	AC096659 Homo sapi
888	17	10.7	146610	9	AC006575	AC006575 Homo sapi							

c 946	17	10.7	154803	9	AC119713	AC119713 Homo sapi
c 947	17	10.7	154856	2	AC119792	AC119792 Rattus no
c 948	17	10.7	154957	2	AC080126	AC080126 Homo sapi
c 949	17	10.7	155064	9	CNS01DUP	AL133312 Human chr
c 950	17	10.7	155172	2	AC021110	AC021110 Homo sapi
c 951	17	10.7	155185	2	AC074374	AC074374 Homo sapi
c 952	17	10.7	155214	10	AL627406	AL627406 Mouse DNA
c 953	17	10.7	155375	2	AC098854	AC098854 Homo sapi
c 954	17	10.7	155377	2	AC103599	AC103599 Mus muscu
c 955	17	10.7	155331	2	AL1592213	AL1592213 Homo sapi
c 956	17	10.7	155367	9	HS1125A11	AL034549 Human DNA
c 957	17	10.7	155587	10	AC131768	AC131768 Mus muscu
c 958	17	10.7	155798	2	AC144919	AC144919 Mus muscu
c 959	17	10.7	155874	2	BX004782	BX004782 Homo sapi
c 960	17	10.7	155881	9	AC002465	AC002465 Human BAC
c 961	17	10.7	156080	9	AC146010	AC146010 Pan trogl
c 962	17	10.7	156248	9	AC027322	AC027322 Homo sapi
c 963	17	10.7	156563	2	BX511161	BX511161 Dantio rer
c 964	17	10.7	156705	10	AL929037	AL929037 Mouse DNA
c 965	17	10.7	156873	9	AC015598	AC015598 Homo sapi
c 966	17	10.7	156881	5	BX088345	BX088345 Zebrafish
c 967	17	10.7	156933	2	AC147274	AC147274 Pan trogl
c 968	17	10.7	157138	2	AC145505	AC145505 Fells cat
c 969	17	10.7	157212	2	AC102481	AC102481 Mus muscu
c 970	17	10.7	157250	2	AC087305	AC087305 Homo sapi
c 971	17	10.7	157398	9	BX005266	BX005266 Human DNA
c 972	17	10.7	157392	2	AC129984	AC129984 Homo sapi
c 973	17	10.7	157493	2	AC027068	AC027068 Homo sapi
c 974	17	10.7	157564	8	AP001389	AP001389 Oryza sat
c 975	17	10.7	157574	2	AC025996	AC025996 Homo sapi
c 976	17	10.7	157573	9	AL1592293	AL1592293 Human DNA
c 977	17	10.7	157573	9	AC087555	AC087555 Papio anu
c 978	17	10.7	157725	2	AC026240	AC026240 Homo sapi
c 979	17	10.7	157999	2	AC117088	AC117088 Rattus no
c 980	17	10.7	158052	9	AC027612	AC027612 Homo sapi
c 981	17	10.7	158089	9	AL1592492	AL1592492 Human DNA
c 982	17	10.7	158387	2	AC095020	AC095020 Bos tauri
c 983	17	10.7	158698	2	AC018625	AC018625 Homo sapi
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c 992	17	10.7	159322	9	AC096631	AC096631 Homo sapi
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c 994	17	10.7	159512	9	AC133552	AC133552 Homo sapi
c 995	17	10.7	159539	9	AL1512625	AL1512625 Human DNA
c 996	17	10.7	159560	2	AC022955	AC022955 Homo sapi
c 997	17	10.7	159575	2	AC141407	AC141407 Homo sapi
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ALIGNMENTS

RESULT 1					159 bp	DNA	linear	PAR 17-JUL-2003
BD245279								
LOCUS					BD245279			
DEFINITION					Development of novel antibiotics based on bacteriophage genomics.			
ACCESSION					BD245279.1	GI:33055049		
VERSION					JP 2002531107-A/14.			
KEYWORDS					unidentified			
SOURCE					unclassified			
ORGANISM					unclassified			
REFERENCE					1 (bases 1 to 159)			
AUTHORS					Pelleiter,J., Gros,P. and Dubow,M.			
TITLE					Development of novel antibiotics based on bacteriophage genomics			
JOURNAL					Patent: JP 2002531107-A 14 24-SEP-2002;			
COMMENT					PHARTECH INC			
OS					Staphylococcus aureus bacteriophage 77			
PN					JP 2002531107-A/14			
PD					24-SEP-2002			
PF					03-DEC-1999 JP 2000585456			
PR					03-DEC-1998 US 60/110992, 03-JUN-1999 US 09/326144 PR			
28-SEP-1999 US					09/407804, 30-SEP-1999 US 60/157218 PR			
01-DEC-1999 US					60/168777, 02-DEC-1999 US 09/454252 PT JERRY			
PC					PELLETER,PHILIPPE GROS,MICHAEL DUBOW			
PC					C12M15/09,A01N63/00,A61K38/00,A61K45/00,A61P31/04,C07K14/005,			
PC					C12M1/00,			
PC					C12M1/21,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/566, PC			
PC					C12M15/00,			
PC					A61K37/02			
CC					Coding Sequence			
FH					Key			
FT					source			
FT					source			
FT					aureus bacteriophage 77'.			
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Query Match					100.0%; Score 159; DB 6; Length 159;			
Best local Similarity					100.0%; Pred. No. 6; le-79;			
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
QY					1 ATGGTACCAAGATTTTAAAACTGATGTTCAATATGTAAGCTCAAAA 60			
Db					1 ATGGTACCAAGATTTTAAAACTGATGTTCAATATGTAAGCTCAAAA 60			
QY					61 CTGATGATGAGGACAGGGCGAATAGGTTAGAGACTTATTCAAAACTT 120			
Db					61 CTGATGATGAGGACAGGGCGAATAGGTTAGAGACTTATTCAAAACTT 120			
QY					121 GCAAGCGTCAATACAGCCCGCTATGTCGATATTAA 159			

Db 121 GCAGAACGTCAACACCCCGCTATGTCGAATATTAA 159

RESULT 2
LOCUS AR368771 159 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 4 from patent US 6376652.
ACCESSION AR368771
VERSION AR368771.1 GI:34603078
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 159)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Compositions and methods involving an essential Staphylococcus aureus gene and its encoded protein
JOURNAL Patent: US 6376652-A 4 23-Apr-2002;
FEATURES
source Location/Qualifiers
1..159
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/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 159; DB 6; Length 159;
Best Local Similarity 100.0%; Pred. No. 6.1e-79;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTAACCAAGAAATTTTAAACCTGAAGTTCAGATATGACGCTCAAAA 60
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QY 61 CTCATAGATGAGGACAGGCGCATGAATAAGTTGTACAGACCTATTATCAAAA 120
DB 61 CTCATAGATGAGGACAGGCGCATGAATAAGTTGTACAGACCTATTATCAAAA 120
QY 121 GCAGAACGTCAACACCCCGCTATGTCGAATATTAA 159
DB 121 GCAGAACGTCAACACCCCGCTATGTCGAATATTAA 159

RESULT 3
LOCUS BD245281 41708 bp DNA linear PAT 17-JUL-2003
DEFINITION Development of novel antibiotics based on bacteriophage genomics.
ACCESSION BD245281
VERSION BD245281.1 GI:33055051
KEYWORDS JP 2002531107-A/16.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 41708)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Development of novel antibiotics based on bacteriophage genomics
JOURNAL Patent: JP 2002531107-A 16 24-Sep-2002;
PHARTECH INC

COMMENT OS Staphylococcus aureus bacteriophage 77
PN JP 2002531107-A/16

PD 24-SEP-2002
PF 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992, 03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804, 30-SEP-1999 US 60/157218 PR
01-DEC-1999 US 60/168777, 02-DEC-1999 US 09/454252 PI JERRY
PC PELLETIER, PHILIPPE GROS, MICHAEL DUBOW
PC C12N15/09, A01N63/00, A61K45/00, A61P31/04, C07K14/009,
PC C12M1/00,
PC C12N1/21, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/566, PC
C12N15/00,
PC A61K37/02
CC Genome Sequence
FH Key Location/Qualifiers
FT source 1..41708
FT /organism="Staphylococcus
aureus bacteriophage 77".

FEATURES

source Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 159; DB 6; Length 41708;
Best Local Similarity 100.0%; Pred. No. 7.6e-79;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTAACCAAGAAATTTTAAACCTGAAGTTCAGATATGACGCTCAAAA 60
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QY 61 CTCATAGATGAGGACAGGCGCATGAATAAGTTGTACAGACCTATTATCAAAA 120
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QY 121 GCAGAACGTCAACACCCCGCTATGTCGAATATTAA 159
DB 34513 GCAGAACGTCAACACCCCGCTATGTCGAATATTAA 34551

RESULT 4
LOCUS AR368770 41708 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 3 from patent US 6376652.
ACCESSION AR368770
VERSION AR368770.1 GI:34603077
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 41708)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Compositions and methods involving an essential Staphylococcus aureus gene and its encoded protein

JOURNAL Patent: US 6376652-A 3 23-APR-2002;
FEATURES Location/Qualifiers
source 1..41708
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FEATURES
source

Location/Qualifiers

ORIGIN

Query Match 100.0%; Score 159; DB 6; Length 41708;
Best Local Similarity 100.0%; Pred. No. 7,66-79;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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CDS

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QY 61 CTCATGATGAGGCAAGGCGCATGAAATAGGTGTACACCTATTATTCAAAACTT 120
DB 34453 CTCATGATGAGGCAAGGCGCATGAAATAGGTGTACACCTATTATTCAAAACTT 34512

QY 121 GCAGAGCTCATACAGCCCGCTATGCTGCAATTAA 159
DB 34513 GCAGAGCTCATACAGCCCGCTATGCTGCAATTAA 34551

gene
CDS

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/db_xref="GI:14246390"

RESULT 5
LOCUS AP003360 348527 bp DNA linear BCT 07-FEB-2002
DEFINITION Staphylococcus aureus subsp. aureus Mu50 genomic DNA, complete
ACCESSION AP003360 BA000017
VERSION AP003360.2 GI:14246388
KEYWORDS

SOURCE
ORGANISM
REFERENCE
AUTHORS

Staphylococcus aureus subsp. aureus Mu50
Staphylococcus aureus subsp. aureus Mu50
Bacteria; Firmicutes; Bacillales; Staphylococcus.

TITLE
AUTHORS
Cui,L., Oguchi,A., Aoki,K., Nagai,Y., Iian,J., Ito,T., Kanamori,M.,
Matsumaru,H., Maruyama,A., Murakami,H., Hosoyama,A.,
Mitsunaka,U.I., Takahashi,N.K., Sawano,T., Inoue,R., Kato,C.,
Sekiizu,K., Hirakawa,H., Kunita,S., Goto,S., Yabuzaki,J.,
Koshida,M., Yamashita,A., Oshima,K., Furuya,K., Yoshino,C.,
Shiba,T., Hattori,M., Ogasawara,N., Hayashi,H. and Hiramatsu,K.
Whole genome sequencing of methicillin-resistant Staphylococcus
aureus

gene
CDS

2807..3139
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/db_xref="GI:14246391"

REFERENCE
AUTHORS
TITLE

JOURNAL Lancet 357 (9264), 1225-1240 (2001)
MEDLINE 2131952
PUBMED 11418146
2 (bases 1 to 348527)
Ohta,T.
Direct Submission
Submitted (28-FEB-2001) Toshiko Ohta, University of Tsukuba College
of Medical Technology and Nursing, Department of Medical
Technology/1-1-1 Ten-no-odai, Tsukuba, Ibaraki 305-8577, Japan
(E-mail:tohts@tsukuba.ac.jp, Tel:81-298-53-3454,
Fax:81-298-53-3454)
On May 29, 2001 this sequence version replaced gi:13674937.

COMMENT

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LOCUS	AB045978	42942 bp	DNA	linear
DEFINITION	Staphylococcus aureus temperate phage phiSLT genomic DNA, complete sequence.			
ACCESSION	AB045978			
VERSION	AB045978.1	GI:12697822		
KEYWORDS				
SOURCE	Staphylococcus aureus temperate phage phiSLT			
ORGANISM	Staphylococcus aureus temperate phage phiSLT			
REFERENCE	Viruses; dsDNA viruses, not RNA stage; Caudovirales; Siphoviridae. 1 (altos)			
AUTHORS	Narita,S., Kaneko,J., Chiba,J., Pilemont,Y., Jarraud,S., Etienne,J. and Kamio,Y.			
TITLE	Phage conversion of Panton-Valentine leukocidin in Staphylococcus aureus: molecular analysis of a PVL-converting phage, phiSLT			
JOURNAL	Gene 268 (1-2), 195-206 (2001)			
MEDLINE	21261956			
PUBMED	11368915			
REFERENCE	2 (bases 1 to 42942)			
AUTHORS	Kaneko,J., Narita,S. and Kamio,Y.			
TITLE	Direct Submision			
JOURNAL	Submitted (12-JUL-2000) Jun Kaneko, Tohoku University, Graduate School of Agricultural Science, 1-1 Tsutsuimidori Amemiyamachi, Sendai, Miyagi 981-8535, Japan (E-mail:j.kaneko@biochem.tohoku.ac.jp, Tel:81-22-717-8781, Fax:81-22-747-8780)			
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VERSION	AF424783.1	GI:18920591						
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ORGANISM	Staphylococcus aureus phage phi 13							
SOURCE	Viruses; DNA viruses, no RNA stage; Caudovirales; Siphoviridae.							
REFERENCE	1 (bases 1 to 42722)							
AUTHORS	Iandolo,J.J., Worrell,V., Grodcher,K.H., Qian,Y., Tian,R., Kenton,S., Dorman,A., Ji,H., Lin,S., Loh,P., Qi,S., Zhu,H. and Roe,B.A.							
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JOURNAL	Gene 289 (1-2), 109-116 (2002)							
MEDLINE	22032862							
PUBMED	12035589							
REFERENCE	2 (bases 1 to 42722)							
AUTHORS	Iandolo,J.J., Worrell,V., Roe,B., Qian,Y., Dorman,A., Tian,R., Lin,S. and Jia,H.							
TITLE	Direct Submission							
JOURNAL	Submitted (26-SEP-2001) Microbiology and Immunology, Univ. of Oklahoma Health Sciences Center, 940 S.L. Young Bvd, Oklahoma City, OK 73190, USA							
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DB 129782 TTTTAAACTAACTGAGTGT 129758

Search completed: October 15, 2004, 03:32:43
Job time : 879.423 secs

GenCore version 5.1.6
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OW nucleic - nucleic search, using sw model

Run on: October 14, 2004, 18:55:29 ; Search time 106.071 Seconds
(without alignments)

6368.040 Million cell updates/sec

Title: US-09-407-804A-8

Perfect score: 159

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Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
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Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	12	18	11.3	405	8	ACH18258	Human adu	c	69	17	10.7	5683	6	AB133807	AB133807 Human imm
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c 142	16	10.1	422	9	ADD33185	Adi33185 Human mlt	c 199	16	10.1	1083	7	ACA30327	Aca30327 Prokaryot
c 143	16	10.1	428	7	ABV35997	Abv35997 Bovine ES	c 200	16	10.1	1086	7	ABZ81912	Abz81912 Tobacco D
c 144	16	10.1	431	5	ABV17652	Abv17652 Human pro	c 201	16	10.1	1104	2	AAV75129	Aav75129 Stephyloc
c 145	16	10.1	437	7	ABK50178	Abk50178 Bovine ES	c 202	16	10.1	1111	3	AAA09306	Aaa09306 Human alp
c 146	16	10.1	442	6	ABJ78441	Abj78441 Human ova	c 203	16	10.1	1111	5	AAH76472	Aah76472 CDNA cor
c 147	16	10.1	452	8	ABV19176	Abv19176 Human pro	c 204	16	10.1	1111	6	ABJ61814	Abj61814 Colon ade
c 148	16	10.1	465	8	ACH24294	Ach24294 Human adu	c 205	16	10.1	1111	6	ABJ92125	Abj92125 Human tum
c 149	16	10.1	475	6	ABJ37743	Abj37743 Human col	c 206	16	10.1	1111	7	ACD19378	Acd19378 CDNA enco
c 150	16	10.1	479	5	AAH81583	Aah81583 Human dlf	c 207	16	10.1	1111	7	ABX72050	Abx72050 DNA enco
c 151	16	10.1	482	5	ABV48952	Abv48952 Human pro	c 208	16	10.1	1111	7	ACE12940	Ace12940 Human cor
c 152	16	10.1	499	5	ABV47446	Abv47446 Human pro	c 209	16	10.1	1193	3	AAK59711	Aak59711 Human sec
c 153	16	10.1	515	9	ADD59601	Adi59601 Human pdc	c 210	16	10.1	1198	4	AAH31383	Aah31383 Human sec
c 154	16	10.1	522	9	ADB37434	Adi37434 Human can	c 211	16	10.1	1354	2	AAT87431	Aat87431 Clone H17
c 155	16	10.1	528	2	AAV84661	Aav84661 EST clone	c 212	16	10.1	1354	3	AAA30224	Aaa30224 Human non
c 156	16	10.1	532	4	AAH92665	Aah92665 Human inf	c 213	16	10.1	1354	9	ADC38647	Adc38647 Human cDN
c 157	16	10.1	544	5	ABV55726	Abv55726 Human pro	c 214	16	10.1	1371	2	AAK33332	Aak33332 Human CXC
c 158	16	10.1	546	4	AAK78241	Aak78241 Human tum	c 215	16	10.1	1445	2	AAH74176	Aah74176 Human che
c 159	16	10.1	576	2	AAT68039	Aat68039 H. pylori	c 216	16	10.1	1481	9	ADZ25640	Adz25640 Human cDN
c 160	16	10.1	600	5	ABV53353	Abv53353 Human pro	c 217	16	10.1	1493	6	ABT07758	Abt07758 Breast ca
c 161	16	10.1	600	5	ABV50792	Abv50792 Human pro	c 218	16	10.1	1493	7	ACC72819	Aac72819 Human can
c 162	16	10.1	602	5	ABV58326	Abv58326 Human pro	c 219	16	10.1	1493	7	ACC51010	Aac51010 Human bla
c 163	16	10.1	620	2	AAZ24594	Aaz24594 Human lun	c 220	16	10.1	1493	7	ABX76375	Abx76375 Lung can
c 164	16	10.1	620	2	AAZ24594	Aaz24594 Human lun	c 221	16	10.1	1493	9	ADC78926	Adc78926 Human PRO
c 165	16	10.1	620	3	AAZ24594	Aaz24594 Human lun	c 222	16	10.1	1518	4	AAH16511	Aah16511 Human cDN
c 166	16	10.1	620	3	AAZ24594	Aaz24594 Human lun	c 223	16	10.1	1539	2	AAT75304	Aat75304 Nucleotid
c 167	16	10.1	620	3	AAZ24594	Aaz24594 Human lun	c 224	16	10.1	1556	3	AAZ24594	Aaz24594 Human sec
c 168	16	10.1	620	6	ABJ49104	Abj49104 Human lun	c 225	16	10.1	1641	3	AAZ24594	Aaz24594 Human sec
c 169	16	10.1	620	6	ABJ49104	Abj49104 Human lun	c 226	16	10.1	1725	8	ADZ25640	Adz25640 Human HSP
c 170	16	10.1	620	6	ABJ49104	Abj49104 Human lun	c 227	16	10.1	1741	3	AAZ25640	Aaz25640 Human ORF
c 171	16	10.1	620	8	ADA28653	Ada28653 Human lun	c 228	16	10.1	1747	5	AAH64872	Aah64872 Human sec
c 172	16	10.1	620	8	ADA28653	Ada28653 Human lun	c 229	16	10.1	1757	4	AAH78964	Aah78964 Human D-H
c 173	16	10.1	620	9	ADZ28239	Adz28239 Human lun	c 230	16	10.1	1849	4	AAI59812	Aai59812 Human pol
c 174	16	10.1	620	9	ADZ28239	Adz28239 Human lun	c 231	16	10.1	1881	4	AAI58026	Aai58026 Human pol
c 175	16	10.1	645	6	ABQ57035	Abq57035 Human col	c 232	16	10.1	1896	7	ACA43105	Aca43105 Prokaryot
c 176	16	10.1	646	6	ABX66909	Abx66909 Helicobac	c 233	16	10.1	2036	4	ABJ11823	Abj11823 Drosophila
c 177	16	10.1	664	6	ABX66909	Abx66909 Helicobac	c 234	16	10.1	2115	4	AAH13699	Aah13699 Human cDN
c 178	16	10.1	684	3	AACT9836	Aact9836 Human sec	c 235	16	10.1	2196	6	ABJ99480	Abj99480 Mouse 1sc

236	16	10.1	2226	3	AACT7975	AACT7975 Human can
237	16	10.1	2248	6	AAAG2481	AAAG2481 cDNA sequ
238	16	10.1	2254	5	AAAG4401	AAAG4401 Human DNA
239	16	10.1	2263	9	AADE2974	AADE2974 Human end
240	16	10.1	2289	4	AAAS3785	AAAS3785 Helicobac
241	16	10.1	2289	7	AAAC34700	AAAC34700 Prokaryot
242	16	10.1	2395	4	AAAT8432	AAAT8432 Nucleotid
243	16	10.1	2396	3	AAAG6334	AAAG6334 Human cel
244	16	10.1	2492	4	AAEL2854	AAEL2854 Drosophi1
245	16	10.1	2532	4	AAEL2826	AAEL2826 Drosophi1
246	16	10.1	2656	5	AAAG67350	AAAG67350 DNA encod
247	16	10.1	2678	7	AACT5521	AACT5521 Clostridi
248	16	10.1	2811	7	AAAG34595	AAAG34595 Human med
249	16	10.1	2859	7	AAAG62811	AAAG62811 Human act
250	16	10.1	2875	3	AAAG6857	AAAG6857 Essential
251	16	10.1	2875	4	AAAG1539	AAAG1539 Stephyloc
252	16	10.1	2875	4	AAAG08008	AAAG08008 Stephyloc
253	16	10.1	2875	9	AAAD67386	AAAD67386 Antibacte
254	16	10.1	2875	9	AADE73610	AADE73610 Mutant ba
255	16	10.1	3154	4	AAEL18228	AAEL18228 Drosophi1
256	16	10.1	3202	4	AAAG4410	AAAG4410 S. epider
257	16	10.1	3288	7	AACT2030	AACT2030 BCU0571 g
258	16	10.1	3636	8	AAAG32554	AAAG32554 DNA encod
259	16	10.1	3652	4	AAH16223	AAH16223 Human cDN
260	16	10.1	3660	2	AAV74483	AAV74483 Stephyloc
261	16	10.1	3706	3	AAAG3312	AAAG3312 Sequence
262	16	10.1	3736	6	AAAG35771	AAAG35771 Human gen
263	16	10.1	3764	4	AAEL23312	AAEL23312 Drosophi1
264	16	10.1	3785	6	AAAG8640	AAAG8640 Wheat car
265	16	10.1	3814	10	AADE77089	AADE77089 Human cDN
266	16	10.1	4050	9	AAAG53325	AAAG53325 Primary r
267	16	10.1	4055	7	AAAG69144	AAAG69144 M. gentia
268	16	10.1	4169	3	AAAG09331	AAAG09331 Human can
269	16	10.1	4169	9	AAAG35131	AAAG35131 Human bre
270	16	10.1	4344	6	AAAG95256	AAAG95256 Gene #175
271	16	10.1	4388	2	AAAT75302	AAAT75302 Nucleotid
272	16	10.1	4544	5	AAAL15386	AAAL15386 Human ner
273	16	10.1	4563	7	AAAG62910	AAAG62910 Human act
274	16	10.1	4870	4	AAAG57564	AAAG57564 Human bra
275	16	10.1	4870	7	AAAG63121	AAAG63121 Human cDN
276	16	10.1	5265	6	AAAG28419	AAAG28419 DNA trans
277	16	10.1	5267	6	AAAG67043	AAAG67043 Human ang
278	16	10.1	5282	6	AAAG1407	AAAG1407 Human gen
279	16	10.1	5581	4	AAAG80802	AAAG80802 Human imm
280	16	10.1	5581	4	AAAG80803	AAAG80803 Human imm
281	16	10.1	5602	4	AAAG80801	AAAG80801 Human imm
282	16	10.1	5717	9	AAAD14637	AAAD14637 Human src
283	16	10.1	5718	5	AAAG64495	AAAG64495 DNA encod
284	16	10.1	5728	6	AAAL32100	AAAL32100 Human imm
285	16	10.1	5788	6	AAAG39442	AAAG39442 Human che
286	16	10.1	5864	6	AAAL33440	AAAL33440 Human imm
287	16	10.1	5864	6	AAAL34361	AAAL34361 Chemtcell
288	16	10.1	5883	6	AAAL37333	AAAL37333 Human imm
289	16	10.1	5931	4	AAAG46702	AAAG46702 Tumour su
290	16	10.1	6015	4	AAAG46684	AAAG46684 Tumour su
291	16	10.1	6203	4	AAAG45475	AAAG45475 Chemtcell
292	16	10.1	6203	6	AAAG28399	AAAG28399 DNA trans
293	16	10.1	6306	6	AAAL49350	AAAL49350 Human pol
294	16	10.1	6385	4	AAAG45353	AAAG45353 Chemtcell
295	16	10.1	6385	6	AAAG28186	AAAG28186 DNA trans
296	16	10.1	6418	6	AAAL32322	AAAL32322 Human imm
297	16	10.1	6418	6	AAAG61073	AAAG61073 Human gen
298	16	10.1	6636	6	AAAG80022	AAAG80022 Human che
299	16	10.1	6664	6	AAAG61368	AAAG61368 Human gen
300	16	10.1	6664	9	AAAG54321	AAAG54321 Pretreaste
301	16	10.1	6664	9	AAAG54193	AAAG54193 Pretreaste
302	16	10.1	6736	2	AAAG68473	AAAG68473 A. pleuro
303	16	10.1	6736	2	AAAG68471	AAAG68471 A. pleuro
304	16	10.1	6863	4	AAAG64618	AAAG64618 Tumour su
305	16	10.1	7297	4	AAAG89535	AAAG89535 Human dig
306	16	10.1	7547	4	AAAG45301	AAAG45301 Chemtcell
307	16	10.1	7544	6	AAAG28140	AAAG28140 DNA trans
308	16	10.1	8323	6	AAAL2059	AAAL2059 Human imm
309	16	10.1	8420	4	AAAG89536	AAAG89536 Human dig
310	16	10.1	10417	4	AAAG81192	AAAG81192 Human imm
311	16	10.1	10417	7	AAAG57772	AAAG57772 BAC fragm
312	16	10.1	10417	7	AAAG41640	AAAG41640 Human sec
313	16	10.1	10717	6	AAAL33695	AAAL33695 Human imm
314	16	10.1	10717	6	AAAG80211	AAAG80211 Human che
315	16	10.1	10754	2	AAAG28236	AAAG28236 Human ade
316	16	10.1	10754	2	AAAG61442	AAAG61442 Partial s
317	16	10.1	10754	5	AAAG90294	AAAG90294 Nucleotid
318	16	10.1	11327	4	AAAG46432	AAAG46432 Tumour su
319	16	10.1	11899	7	AAAG69142	AAAG69142 M. gentia
320	16	10.1	12889	4	AAAG07412	AAAG07412 Human pan
321	16	10.1	12889	4	AAAG91143	AAAG91144 Human dig
322	16	10.1	13024	4	AAAL04739	AAAL04739 Human rep
323	16	10.1	13024	4	AAEL97644	AAEL97644 Human tes
324	16	10.1	13919	6	AAAG29304	AAAG29304 Chemtcell
325	16	10.1	14143	4	AAAG07413	AAAG07413 Human pan
326	16	10.1	14143	4	AAAG91144	AAAG91144 Human dig
327	16	10.1	15016	2	AAAG95560	AAAG95560 Nucleic a
328	16	10.1	15018	7	AAAG52817	AAAG52817 Prokaryot
329	16	10.1	15069	4	AAAL05378	AAAL05378 Drosophi1
330	16	10.1	15282	6	AAAG70190	AAAG70190 Human gen
331	16	10.1	15282	6	AAAG61140	AAAG61140 Human gen
332	16	10.1	15649	4	AAAG45397	AAAG45397 Chemtcell
333	16	10.1	15649	6	AAAG28242	AAAG28242 DNA trans
334	16	10.1	15866	4	AAAG90892	AAAG90892 Human dig
335	16	10.1	17249	4	AAAG71137	AAAG71137 Human imm
336	16	10.1	17848	4	AAAG45323	AAAG45323 Chemtcell
337	16	10.1	17848	6	AAAG3976	AAAG3976 Human che
338	16	10.1	17848	6	AAAG28164	AAAG28164 DNA trans
339	16	10.1	17959	6	AAAL32575	AAAL32575 Human imm
340	16	10.1	17959	6	AAAL54342	AAAL54342 Chemtcell
341	16	10.1	17970	4	AAAG80740	AAAG80740 Human imm
342	16	10.1	19653	6	AAAL33335	AAAL33335 Human imm
343	16	10.1	19802	4	AAAG90894	AAAG90894 Human dig
344	16	10.1	19802	4	AAAL04554	AAAL04554 Human rep
345	16	10.1	19802	4	AAAL97477	AAAL97477 Human tes
346	16	10.1	19966	3	AAAG23035	AAAG23035 Nucleotid
347	16	10.1	19966	3	AAAG42528	AAAG42528 DNA encod
348	16	10.1	21358	4	AAAG90363	AAAG90363 Human dig
349	16	10.1	21358	4	AAAG73090	AAAG73090 Human imm

350	16	10.1	21358	4	AAK87446	AbK87446 Human imm	407	16	10.1	143068	6	AB1168124	Ab1168124 Ovary can	
c 351	16	10.1	21358	4	AAK87558	AAK87558 Human imm	408	16	10.1	143068	6	AB111034	Ab111034 Human bre	
352	16	10.1	21358	4	AA106419	AA106419 Human rep	409	16	10.1	143068	7	AB296966	Ab296966 Human nuc	
353	16	10.1	21358	5	AA39919	AA39919 Genomic s	410	16	10.1	143068	7	AB296799	Ab296799 Human nuc	
354	16	10.1	21358	8	ADB32879	ADB32879 Human nov	c 411	16	10.1	144460	3	AA293815	AA293815 Olfactory	
c 355	16	10.1	21403	4	AAK90893	AAK90893 Human rep	412	16	10.1	149412	3	AA335151	AA335151 Human ade	
c 356	16	10.1	21403	4	AA104555	AA104555 Human dig	413	16	10.1	152740	3	AA21273	AA21273 Human low	
c 357	16	10.1	21403	4	AB197478	AB197478 Human tes	414	16	10.1	152740	7	AA296967	AA296967 Human nuc	
358	16	10.1	21676	4	AAK90362	AAK90362 Human dig	415	16	10.1	154465	6	AA28763	AA28763 Human nuc	
c 359	16	10.1	21676	4	AAK87549	AAK87549 Human imm	416	16	10.1	158245	6	AA28762	AA28762 Human nuc	
c 360	16	10.1	21676	4	AAK73081	AAK73081 Human imm	417	16	10.1	161425	4	AAH02340	AAH02340 Human AKA	
361	16	10.1	21676	4	AAK87445	AAK87445 Human imm	418	16	10.1	162025	4	AAH02339	AAH02339 Human AKA	
362	16	10.1	21676	4	AA106418	AA106418 Human rep	419	16	10.1	162025	6	AA287738	AA287738 Human AKA	
363	16	10.1	21676	5	AA39918	AA39918 Genomic s	c 420	16	10.1	162025	6	AA287739	AA287739 Human AKA	
364	16	10.1	22676	8	ADB32878	ADB32878 Human nov	c 421	16	10.1	169998	6	AA287739	AA287739 Human AKA	
365	16	10.1	23241	4	AAK87225	AAK87225 Human imm	422	16	10.1	183337	7	ABQ77402	ABQ77402 Human EDN	
366	16	10.1	23241	4	AAK84291	AAK84291 Human imm	423	16	10.1	183337	7	ABQ77402	ABQ77402 Human EDN	
c 367	16	10.1	23763	4	AAK90895	AAK90895 Human dig	424	16	10.1	188888	6	ABQ77562	ABQ77562 Human EGF	
c 368	16	10.1	23763	4	AA104558	AA104558 Human rep	c 424	16	10.1	197496	6	ABN85584	ABN85584 Human EGF	
c 369	16	10.1	23763	4	AB197481	AB197481 Human tes	425	16	10.1	198161	6	ABN85584	ABN85584 Human EGF	
370	16	10.1	25392	4	AAK82159	AAK82159 Human imm	426	16	10.1	302250	6	AB167703	AB167703 Oesophagu	
371	16	10.1	32185	4	AA136606	AA136606 Human mus	c 427	16	10.1	322101	9	AA258431	AA258431 Human PAO	
372	16	10.1	32185	7	ABK59794	ABK59794 cDNA enco	c 428	16	10.1	334462	9	ADC24763	ADC24763 Human w11	
c 373	16	10.1	32885	4	AB119560	AB119560 Drosophila	c 429	16	10.1	335913	5	AA161371	AA161371 Soybean 2	
c 374	16	10.1	33053	6	ABQ67006	ABQ67006 Human ang	c 430	16	10.1	335913	5	AA161372	AA161372 Soybean 2	
375	16	10.1	50000	3	AA644140	AA644140 Nucleotid	c 431	16	10.1	349901	9	ADC86940	ADC86940 Human GPC	
c 376	16	10.1	56423	9	ADC85728	ADC85728 Human GPC	c 432	16	10.1	349980	6	ABQ81848	ABQ81848 Bifidobac	
377	16	10.1	57248	6	ABR83563	ABR83563 Human cDN	c 433	15	9.4	116	41	6	ABR86236	ABR86236 Arginyl t
378	16	10.1	65787	8	ADA02603	ADA02603 Mouse 112	c 434	15	9.4	116	41	6	ABR86236	ABR86236 Arginyl t
379	16	10.1	65787	9	ADA72341	ADA72341 Mouse 112	c 435	15	9.4	173	3	AA029217	AA029217 Human sec	
380	16	10.1	84539	6	AB164158	AB164158 Stomach c	c 436	15	9.4	187	6	AB178987	AB178987 Human ova	
c 381	16	10.1	96595	8	ADN03068	ADN03068 Human PEP	c 437	15	9.4	216	6	AB178987	AB178987 Human ova	
c 382	16	10.1	96595	9	AD872806	AD872806 Human PEP	c 438	15	9.4	240	2	AA169363	AA169363 Murine me	
c 383	16	10.1	96596	8	ADA66352	ADA66352 Human PEP	c 439	15	9.4	240	2	AA169363	AA169363 Murine me	
384	16	10.1	96599	9	ADC85298	ADC85298 Human Egr	c 440	15	9.4	252	6	ABN66415	ABN66415 Streptococ	
385	16	10.1	96600	8	ADA02819	ADA02819 Mouse Sos	c 441	15	9.4	270	4	AAK61270	AAK61270 Human imm	
386	16	10.1	96600	9	ADB72557	ADB72557 Mouse Sos	442	15	9.4	276	6	ABT03058	ABT03058 Human bre	
c 387	16	10.1	97662	4	AA893908	AA893908 Genomic s	443	15	9.4	279	7	ABT2531	ABT2531 Breast ca	
c 388	16	10.1	100543	6	AB552816	AB552816 Genomic D	444	15	9.4	299	3	AA025407	AA025407 Human sec	
389	16	10.1	106746	3	AA110225	AA110225 Human PCT	c 445	15	9.4	312	3	AA025407	AA025407 Human sec	
c 390	16	10.1	110000	2	AA758840_0	AA758840 Mycoplasma	446	15	9.4	317	7	ABX55277	ABX55277 Bovine ES	
391	16	10.1	110000	2	AA758840_4	AA758840 Mycoplasma	c 447	15	9.4	317	9	ADC75289	ADC75289 T harzian	
c 392	16	10.1	110000	2	AA758840_4	AA758840 Mycoplasma	448	15	9.4	321	7	ACA38992	ACA38992 Prokaryot	
c 393	16	10.1	110000	2	AA758840_4	AA758840 Mycoplasma	c 449	15	9.4	325	3	AA025228	AA025228 Human sec	
c 394	16	10.1	110000	6	ABA92787_5	ABA92787_5 of	c 450	15	9.4	335	3	AA444083	AA444083 Human sec	
395	16	10.1	110000	6	ABQ67196_4	ABQ67196_4 of	451	15	9.4	341	4	AAK59210	AAK59210 Human imm	
c 396	16	10.1	110000	6	ABQ69245_28	ABQ69245_28 of	c 452	15	9.4	341	8	ACG31558	ACG31558 Human bon	
c 397	16	10.1	110000	7	ACF42745_0	ACF42745_0 of	c 453	15	9.4	344	3	AA055076	AA055076 Arabidops	
c 398	16	10.1	110000	7	ABQ83210_1	ABQ83210_1 of	c 454	15	9.4	350	5	ABV30283	ABV30283 Human pro	
399	16	10.1	110000	7	AA053223_2	AA053223_2 of	c 455	15	9.4	351	5	ABV33666	ABV33666 Human pro	
c 400	16	10.1	113306	9	ADC86534	ADC86534 Human GPC	c 456	15	9.4	353	4	AAH93826	AAH93826 Human pro	
c 401	16	10.1	113315	6	AB134175	AB134175 Human imm	457	15	9.4	355	5	AAH94334	AAH94334 Human imm	
402	16	10.1	116624	2	AAV52850	AAV52850 Human eye	c 458	15	9.4	356	7	ABT41722	ABT41722 Toxicity	
403	16	10.1	143068	3	AAA34983	AAA34983 Human ade	c 459	15	9.4	356	8	ADB52368	ADB52368 Primary r	
404	16	10.1	143068	3	AAA35150	AAA35150 Human ade	460	15	9.4	357	8	ADB52368	ADB52368 Primary r	
405	16	10.1	143068	3	AA212172	AA212172 Human low	461	15	9.4	360	5	ABH15418	ABH15418 Human nec	
406	16	10.1	143068	3	AA212172	AA212172 Human low	c 462	15	9.4	363	3	AA019690	AA019690 Human sec	
							c 463	15	9.4	364	4	AA185003	AA185003 Human pol	

464	15	9.4	366	7	ACA282929	AcA282929	Prokaryot
c 465	15	9.4	370	8	ACH31547	Act31547	Human bon
466	15	9.4	372	4	AAK74731	AAK74731	Human imm
467	15	9.4	372	4	ABK55205	AbK55205	Bovine ES
468	15	9.4	376	7	ABK54968	AbK54968	Bovine ES
469	15	9.4	377	4	AA189286	AA189286	Human pol
470	15	9.4	381	7	ABK39567	AbK39567	Bovine ES
471	15	9.4	388	4	AA185553	AA185553	Human pol
472	15	9.4	394	5	ABV17897	AbV17897	Human pro
473	15	9.4	398	4	AA187937	AA187937	Human pol
c 474	15	9.4	398	8	ACH31014	Act31014	Human bon
475	15	9.4	399	6	ABN16543	AbN16543	Human ORF
476	15	9.4	399	7	ABK40689	AbK40689	Bovine ES
c 477	15	9.4	401	4	AAK95891	AAK95891	Human ES
478	15	9.4	401	4	AAK93866	AAK93866	Human neu
c 479	15	9.4	401	4	AAK97359	AAK97359	Human neu
c 480	15	9.4	401	4	AAK97384	AAK97384	Human neu
c 481	15	9.4	401	6	ABT00661	AbT00661	Human neu
482	15	9.4	401	6	ABT00636	AbT00636	Human neu
c 483	15	9.4	401	6	ABT02154	AbT02154	Human neu
484	15	9.4	401	6	ABT02129	AbT02129	Human neu
c 485	15	9.4	401	7	ABK55085	AbK55085	Bovine ES
c 486	15	9.4	403	4	AA190677	AA190677	Human pol
c 487	15	9.4	403	7	ABK37575	AbK37575	Bovine ES
c 488	15	9.4	406	5	ABV51599	AbV51599	Human pro
c 489	15	9.4	408	4	AB115789	Ab115789	Drosophila
c 490	15	9.4	409	4	AA111114	AA111114	Probe #10
c 491	15	9.4	409	4	ABK52773	AbK52773	Human foe
c 492	15	9.4	409	4	AA132379	AA132379	Probe #10
c 493	15	9.4	409	4	ABK42347	AbK42347	Human bre
c 494	15	9.4	409	4	ABK22558	AbK22558	Probe #10
c 495	15	9.4	409	4	AAK26484	AAK26484	Human bon
c 496	15	9.4	409	4	AAK01026	AAK01026	Human bra
c 497	15	9.4	409	4	ABK26076	AbK26076	Human liv
c 498	15	9.4	409	5	AA101032	AA101032	Probe #10
c 499	15	9.4	409	5	ABK01074	AbK01074	Human gen
500	15	9.4	414	5	ABV47687	AbV47687	Human pro
c 501	15	9.4	416	5	ABV17926	AbV17926	Human pro
c 502	15	9.4	417	4	AAK72248	AAK72248	Human imm
c 503	15	9.4	417	5	ABV45814	AbV45814	Human pro
c 504	15	9.4	418	4	AAK79731	AAK79731	Human imm
c 505	15	9.4	419	6	ABQ98581	AbQ98581	Human ORF
c 506	15	9.4	420	8	ACH18985	Act18985	Human adu
c 507	15	9.4	421	3	AAK32214	AAK32214	Human sec
508	15	9.4	421	7	ABK43038	AbK43038	Bovine ES
509	15	9.4	428	7	ABK35359	AbK35359	Bovine ES
510	15	9.4	429	7	ABK42396	AbK42396	Bovine ES
c 511	15	9.4	432	4	AA183048	AA183048	Human pol
c 512	15	9.4	438	5	ABV58602	AbV58602	Human pro
513	15	9.4	438	6	ABQ96389	AbQ96389	Tumour su
514	15	9.4	440	8	ACH49504	Act49504	Human leu
c 515	15	9.4	444	6	ABK12607	AbK12607	Arabidops
c 516	15	9.4	446	5	AAK57185	AAK57185	DNA encod
517	15	9.4	451	8	ACH17490	Act17490	Human adu
518	15	9.4	453	4	AA186781	AA186781	Human pol
519	15	9.4	456	6	ABQ96388	AbQ96388	Tumour su
520	15	9.4	457	9	ADK84923	ADK84923	Ferney51
521	15	9.4	459	4	AAK67407	AAK67407	Human imm
522	15	9.4	463	4	AAK87996	AAK87996	Human dig
523	15	9.4	464	4	AAK56123	AAK56123	Human imm
c 524	15	9.4	464	8	ACH45481	Act45481	Human foe
525	15	9.4	467	2	AAK83836	AAK83836	DNA encod
526	15	9.4	467	4	AAK35283	AAK35283	Human car
527	15	9.4	467	9	ABK45362	AbK45362	Human car
528	15	9.4	468	6	AB191329	Ab191329	Human exc
529	15	9.4	469	4	AA198762	AA198762	Human kid
530	15	9.4	470	5	ABQ96387	AbQ96387	Tumour su
531	15	9.4	470	8	ACH50808	Act50808	Human mam
532	15	9.4	471	8	ACH37766	Act37766	Human end
533	15	9.4	474	4	AA139334	AA139334	Probe #80
c 534	15	9.4	474	6	ABQ90253	AbQ90253	M. capsul
c 535	15	9.4	475	8	ACH48413	Act48413	Human leu
c 536	15	9.4	480	6	ABQ96391	AbQ96391	Tumour su
537	15	9.4	493	4	AA161679	AA161679	Human bre
c 538	15	9.4	493	6	ABQ96390	AbQ96390	Tumour su
539	15	9.4	494	4	AAK57130	AAK57130	Human imm
c 540	15	9.4	500	3	AAK95176	AAK95176	Cat flea
c 541	15	9.4	502	6	ABK39323	AbK39323	DNA encod
c 542	15	9.4	502	7	ACH11652	Act11652	Human lun
c 543	15	9.4	502	7	ACH02838	Act02838	Lung canc
c 544	15	9.4	502	5	ABK20924	AbK20924	Human ner
c 545	15	9.4	512	5	ABK20925	AbK20925	Human ner
c 546	15	9.4	512	5	ABK20927	AbK20927	Human ner
c 547	15	9.4	512	5	ABK20928	AbK20928	Human ner
c 548	15	9.4	512	7	ABK25894	AbK25894	Aspergill
549	15	9.4	512	9	ADK30463	ADK30463	Human nov
550	15	9.4	513	3	AAK45955	AAK45955	Human met
c 551	15	9.4	517	3	ABV47716	AbV47716	Human pro
552	15	9.4	521	9	ADK81244	ADK81244	Arabidops
553	15	9.4	530	5	ABV07485	AbV07485	Human pro
554	15	9.4	532	2	AAQ24835	AAQ24835	Peroxidase
555	15	9.4	533	3	AAZ98840	AAZ98840	Horrearedi
c 556	15	9.4	534	5	ABV12105	AbV12105	Human pro
c 557	15	9.4	535	6	ABK60606	AbK60606	Human can
558	15	9.4	546	6	ABK87699	AbK87699	Human pro
559	15	9.4	550	9	ADD19049	ADD19049	Human dis
560	15	9.4	555	6	ABQ50104	AbQ50104	Oligonuc
561	15	9.4	555	8	ABQ50105	AbQ50105	Oligonuc
c 562	15	9.4	555	8	ACH41943	Act41943	Human foe
563	15	9.4	563	5	ABK57035	AbK57035	Human pro
c 564	15	9.4	583	4	AAH12711	AAH12711	Human cin
565	15	9.4	590	4	AAH13368	AAH13368	Human cin
566	15	9.4	597	6	ABQ24336	AbQ24336	Oligonuc
567	15	9.4	597	6	ABQ24337	AbQ24337	Oligonuc
c 568	15	9.4	603	5	ABV19942	AbV19942	Human pro
c 569	15	9.4	612	6	ABK64177	AbK64177	Human can
c 570	15	9.4	616	5	ABK55734	AbK55734	Human pro
c 571	15	9.4	621	5	ABV49703	AbV49703	Human pro
c 572	15	9.4	633	7	ACH37372	Act37372	Prokaryot
573	15	9.4	633	7	AA124154	AA124154	Human bre
574	15	9.4	638	4	ABK92382	AbK92382	Stephyloc
575	15	9.4	648	6	ABK65878	AbK65878	Human can
c 576	15	9.4	656	6	ABK65878	AbK65878	Human can
c 577	15	9.4	656	6	ABK65878	AbK65878	Human can

c 578	15	9.4	659	6	AB065847	Ab065847 Arabidops	635	15	9.4	942	6	AB065793	Ab065793 Listeria
c 579	15	9.4	674	7	ACF63950	AcF63950 Phototrab	636	15	9.4	942	7	ACF63697	Ac636897 Prokaryot
c 580	15	9.4	676	7	ACF63954	AcF63954 Phototrab	637	15	9.4	953	6	AB068911	Ab068911 Human pro
c 581	15	9.4	686	7	ACF65977	AcF65977 Phototrab	638	15	9.4	969	7	ACF71302	AcF71302 Phototrab
c 582	15	9.4	691	7	ACF67187	AcF67187 Phototrab	639	15	9.4	993	2	AAV24131	AAV24131 Homo sap1
c 583	15	9.4	693	3	ACF47355	AcF47355 Arabidops	640	15	9.4	1002	6	AB070409	Ab070409 Streptoco
c 584	15	9.4	696	3	ACF52659	AcF52659 Arabidops	641	15	9.4	1002	6	AB067791	Ab067791 Streptoco
c 585	15	9.4	704	4	AA122125	AA122125 Human bre	642	15	9.4	1004	4	AA077074	AA077074 Streptoco
c 586	15	9.4	720	4	AA555682	AA555682 Streptoco	643	15	9.4	1004	4	AA072916	AA072916 Drosophi1
c 587	15	9.4	720	7	ACA49836	ACA49836 Prokaryot	644	15	9.4	1009	9	AD060651	AD060651 Human gen
c 588	15	9.4	727	4	AAK89198	AAK89198 Human dig	645	15	9.4	1035	2	AAK14487	AAK14487 H. pylori
c 589	15	9.4	738	4	AB049427	AB049427 Human sec	646	15	9.4	1068	7	AC028004	AC028004 Prokaryot
c 590	15	9.4	740	6	AB015471	AB015471 Oligonuc1	647	15	9.4	1092	5	ABV24326	ABV24326 Human pro
c 591	15	9.4	740	6	AB015470	AB015470 Oligonuc1	648	15	9.4	1116	8	ADA31719	ADA31719 DNA encod
c 592	15	9.4	741	5	AA580147	AA580147 DNA encod	649	15	9.4	1119	3	AA053578	AA053578 Arabidops
c 593	15	9.4	744	6	AB067508	AB067508 Streptoco	650	15	9.4	1119	7	AC054060	AC054060 Prokaryot
c 594	15	9.4	744	7	ACA37136	ACA37136 Prokaryot	651	15	9.4	1155	8	AD029444	AD029444 DNA encod
c 595	15	9.4	751	4	AA194977	AA194977 Human neu	652	15	9.4	1173	8	AA0242107	AA0242107 Human P1B
c 596	15	9.4	753	4	AAH90835	AAH90835 ZCFE 26 c	653	15	9.4	1217	4	ABL20053	ABL20053 Drosophi1
c 597	15	9.4	761	4	AA125022	AA125022 Human dre	654	15	9.4	1230	7	AC030168	AC030168 Prokaryot
c 598	15	9.4	765	4	AA124460	AA124460 Human bre	655	15	9.4	1235	3	AA252509	AA252509 Human sec
c 599	15	9.4	766	4	AA105794	AA105794 Human rep	656	15	9.4	1254	6	AB216066	AB216066 Arabidops
c 600	15	9.4	766	4	AB198358	AB198358 Human tes	657	15	9.4	1254	6	AB216319	AB216319 Arabidops
c 601	15	9.4	772	4	AAH07018	AAH07018 Human cin	658	15	9.4	1262	2	AAK13696	AAK13696 Enterococ
c 602	15	9.4	773	4	AAH08009	AAH08009 Human cin	659	15	9.4	1262	6	AB099491	AB099491 Enterococ
c 603	15	9.4	775	3	AA047164	AA047164 Arabidops	660	15	9.4	1272	6	AB092417	AB092417 Staphyloc
c 604	15	9.4	776	7	ACA32045	ACA32045 Prokaryot	661	15	9.4	1276	3	AA093902	AA093902 Human sec
c 605	15	9.4	788	6	ABV95106	ABV95106 Human pan	662	15	9.4	1278	6	AB090595	AB090595 Staphyloc
c 606	15	9.4	798	4	AAH33098	AAH33098 Human col	663	15	9.4	1301	3	AAA63930	AAA63930 DNA encod
c 607	15	9.4	800	2	AAK90757	AAK90757 Human int	664	15	9.4	1301	6	AA148386	AA148386 Human c-m
c 608	15	9.4	801	6	AB063731	AB063731 Rat seque	665	15	9.4	1303	6	AA148387	AA148387 Human c-m
c 609	15	9.4	801	9	AD0581969	AD0581969 Toxicity	666	15	9.4	1303	7	AB210096	AB210096 Haematopo
c 610	15	9.4	801	9	AD058269	AD058269 Toxicity	667	15	9.4	1303	7	AB210036	AB210036 Haematopo
c 611	15	9.4	801	9	AD052803	AD052803 Primary r	668	15	9.4	1303	7	AB210242	AB210242 Haematopo
c 612	15	9.4	802	2	AAK20466	AAK20466 Human sec	669	15	9.4	1303	7	AB210182	AB210182 Haematopo
c 613	15	9.4	802	9	AD090250	AD090250 Novel hum	670	15	9.4	1307	4	AB107035	AB107035 Drosophi1
c 614	15	9.4	804	4	AA126618	AA126618 Human bre	671	15	9.4	1308	7	AA150274	AA150274 Human nuc
c 615	15	9.4	807	6	AB067122	AB067122 Streptoco	672	15	9.4	1326	6	AB099422	AB099422 Human nuc
c 616	15	9.4	811	7	AC046087	AC046087 Human dlt	673	15	9.4	1332	8	ADA32711	ADA32711 DNA encod
c 617	15	9.4	824	6	ABQ36600	ABQ36600 Oligonuc1	674	15	9.4	1332	8	AA080507	AA080507 Gene encod
c 618	15	9.4	824	6	ABQ36601	ABQ36601 Oligonuc1	675	15	9.4	1399	1	AA080507	AA080507 Gene encod
c 619	15	9.4	845	2	AA166947	AA166947 Chicken 1	676	15	9.4	1411	4	AAH13981	AAH13981 Human cin
c 620	15	9.4	845	6	AB087700	AB087700 Human pro	677	15	9.4	1426	4	AAK74696	AAK74696 Human lim
c 621	15	9.4	861	4	AAK79732	AAK79732 Human lim	678	15	9.4	1432	6	AB134259	AB134259 Human lim
c 622	15	9.4	867	8	AD081855	AD081855 Human cin	679	15	9.4	1438	9	AD028288	AD028288 Human MDD
c 623	15	9.4	876	6	AB054672	AB054672 Human ova	680	15	9.4	1468	4	AA091700	AA091700 Mouse fat
c 624	15	9.4	876	7	ACA30332	ACA30332 Prokaryot	681	15	9.4	1480	6	AA050061	AA050061 Human fat
c 625	15	9.4	881	7	AAK56828	AAK56828 Mouse pmd	682	15	9.4	1492	5	AAH99440	AAH99440 Human foe
c 626	15	9.4	891	7	ACA22829	ACA22829 Prokaryot	683	15	9.4	1492	5	AAH94414	AAH94414 Human foe
c 627	15	9.4	892	7	AAK79612	AAK79612 Human lim	684	15	9.4	1493	4	AAK52930	AAK52930 Human pol
c 628	15	9.4	894	4	ABQ38187	ABQ38187 Oligonuc1	685	15	9.4	1496	2	AAV33362	AAV33362 Nucleotid
c 629	15	9.4	899	6	ABQ38186	ABQ38186 Oligonuc1	686	15	9.4	1496	4	AA106381	AA106381 Human rep
c 630	15	9.4	899	6	ABQ38186	ABQ38186 Oligonuc1	687	15	9.4	1502	2	AAK08689	AAK08689 Novel nuc
c 631	15	9.4	919	4	AAH06453	AAH06453 Human cin	688	15	9.4	1502	9	ADC38762	ADC38762 Human cin
c 632	15	9.4	935	4	AA106886	AA106886 Human rep	689	15	9.4	1537	6	AB097663	AB097663 Human gln
c 633	15	9.4	935	4	AB080107	AB080107 Human ova	690	15	9.4	1537	7	AD072364	AD072364 Rice gene
c 634	15	9.4	942	6	AB068221	AB068221 Listeria	691	15	9.4	1554	3	AAA49179	AAA49179 cDNA encod

c 692	15	9.4	1557	3	AA297079	AA297079 Human sec	749	15	9.4	2403	6	AA242109	AA242109 Human PIB
c 693	15	9.4	1557	8	AC66708	Ac66708 Novel hum	750	15	9.4	2408	4	AB15788	AB15788 Drosophila
c 694	15	9.4	1576	6	AB69006	Ab69006 Listeria	c 751	15	9.4	2414	4	AB127894	AB127894 Drosophila
c 695	15	9.4	1583	6	ABQ14699	Abq14699 Oligonuc	c 752	15	9.4	2460	7	ACR70439	ACR70439 Photobact
c 696	15	9.4	1583	6	ABQ14698	Abq14698 Oligonuc	753	15	9.4	2468	7	ACD19418	ACD19418 CDNA enco
c 697	15	9.4	1596	6	AA242108	AA242108 Human PIB	c 754	15	9.4	2468	7	AB556967	AB556967 CDNA enco
c 698	15	9.4	1603	3	AA598152	AA598152 Human col	c 755	15	9.4	2491	7	ACC44332	ACC44332 CDNA enco
c 699	15	9.4	1630	5	AA594470	AA594470 DNA enco	c 756	15	9.4	2506	4	AAH14282	AAH14282 Human enco
c 700	15	9.4	1631	5	AB214925	Ab214925 Arabidops	c 757	15	9.4	2506	7	AB223171	AB223171 Human cDN
c 701	15	9.4	1662	4	AAH02237	AAH02237 Tetragen	c 758	15	9.4	2506	7	AB223172	AB223172 Human cDN
c 703	15	9.4	1663	4	AAH74693	AAH74693 Human imm	c 759	15	9.4	2511	2	AAV71032	AAV71032 Grk5-gree
c 704	15	9.4	1697	4	AAH18581	AAH18581 Human EST	c 760	15	9.4	2519	9	ACN03892	ACN03892 CDNA upre
c 705	15	9.4	1729	4	AAH99095	AAH99095 Human EST	c 761	15	9.4	2529	2	AAV71024	AAV71024 Grk5-gree
c 706	15	9.4	1733	3	AA536472	AA536472 Arabidops	c 762	15	9.4	2533	2	AAQ06000	AAQ06000 Sequence
c 707	15	9.4	1733	4	AA191399	AA191399 Human pol	763	15	9.4	2541	6	AA147520	AA147520 Human rib
c 708	15	9.4	1796	5	AB21095	Ab21095 Human ner	764	15	9.4	2552	9	AD553667	AD553667 Human pro
c 709	15	9.4	1805	2	AAV52380	AAV52380 Streptoco	c 765	15	9.4	2557	4	AAH24841	AAH24841 Nucloetid
c 710	15	9.4	1815	6	ABK66231	ABK66231 CDNA enco	c 766	15	9.4	2557	6	AA236142	AA236142 Human G p
c 711	15	9.4	1817	5	AA563219	AA563219 Human pur	c 767	15	9.4	2557	6	AB249404	AB249404 CDNA enco
c 712	15	9.4	1818	5	ABV28274	ABV28274 Human pro	c 768	15	9.4	2557	7	ACA56700	ACA56700 Human sfg
c 713	15	9.4	1818	5	ABV28500	ABV28500 Human pro	c 769	15	9.4	2558	4	AB125882	AB125882 Drosophila
c 714	15	9.4	1880	6	ABD42110	ABD42110 Human PIB	c 770	15	9.4	2571	4	AAK52271	AAK52271 Human pol
c 715	15	9.4	1882	4	AB104875	AB104875 Drosophila	c 771	15	9.4	2577	7	AB223173	AB223173 Polynucle
c 716	15	9.4	1884	4	AAH99130	AAH99130 Human EST	c 772	15	9.4	2598	7	ACM27473	ACM27473 Prokaryot
c 717	15	9.4	1901	9	ADC27053	ADC27053 Human den	c 773	15	9.4	2599	6	AA235233	AA235233 Human TRN
c 718	15	9.4	1926	9	AD555611	AD555611 Human gen	c 774	15	9.4	2605	4	AAH14939	AAH14939 Human cDN
c 719	15	9.4	1926	9	AD553615	AD553615 Bacterioph	c 775	15	9.4	2627	4	AB129318	AB129318 Drosophila
c 720	15	9.4	1944	3	AA669015	AA669015 Streptoco	c 776	15	9.4	2633	6	AB261024	AB261024 FLJ10559
c 721	15	9.4	1977	6	ABN66202	ABN66202 Streptoco	c 777	15	9.4	2634	3	AAA66001	AAA66001 E. coli p
c 722	15	9.4	1984	7	AB236115	AB236115 Human sec	c 778	15	9.4	2645	4	AB127910	AB127910 Drosophila
c 723	15	9.4	1995	7	ACA30619	ACA30619 Prokaryot	c 779	15	9.4	2715	6	AA242100	AA242100 Human pro
c 724	15	9.4	1996	5	AA580696	AA580696 DNA enco	c 780	15	9.4	2716	2	AAK12939	AAK12939 Enterococ
c 725	15	9.4	1998	7	AAV78417	AAV78417 Human sec	781	15	9.4	2766	7	AB212979	AB212979 Arabidops
c 726	15	9.4	1998	7	AC50608	AC50608 Human sec	c 782	15	9.4	2766	7	AB212979	AB212979 Arabidops
c 727	15	9.4	1998	8	AD591260	AD591260 Human sec	c 783	15	9.4	2766	7	AB212979	AB212979 Arabidops
c 728	15	9.4	1998	9	ADC73677	ADC73677 Human sec	c 784	15	9.4	2791	3	AAZ52952	AAZ52952 Human NR6
c 729	15	9.4	2000	6	AB217292	AB217292 Arabidops	c 785	15	9.4	2831	4	AAK53179	AAK53179 Human pol
c 730	15	9.4	2000	6	AB216849	AB216849 Arabidops	c 786	15	9.4	2839	2	AAQ03742	AAQ03742 Human SKI
c 731	15	9.4	2000	6	AB216044	AB216044 Arabidops	787	15	9.4	2862	7	ACA45720	ACA45720 Prokaryot
c 732	15	9.4	2000	7	ADA68828	ADA68828 Arabidops	c 788	15	9.4	2887	3	AAZ294533	AAZ294533 Human cyt
c 733	15	9.4	2000	7	ADA68828	ADA68828 Arabidops	c 789	15	9.4	2887	3	AAZ294533	AAZ294533 Human cyt
c 734	15	9.4	2000	7	ADA72089	ADA72089 Rice gene	c 790	15	9.4	2916	8	AB144090	AB144090 Pasteurel
c 735	15	9.4	2000	7	ADA72251	ADA72251 Rice gene	c 791	15	9.4	2916	8	AB144090	AB144090 Pasteurel
c 736	15	9.4	2001	5	AA588985	AA588985 DNA enco	c 792	15	9.4	2937	2	AAK58857	AAK58857 Pasteurel
c 737	15	9.4	2034	6	AB61028	AB61028 Transemb	793	15	9.4	2937	2	AAK58857	AAK58857 Pasteurel
c 738	15	9.4	2055	5	AA582025	AA582025 DNA enco	794	15	9.4	2937	2	AAK58857	AAK58857 Pasteurel
c 739	15	9.4	2102	4	AA581791	AA581791 Human sec	795	15	9.4	2937	2	AAK58857	AAK58857 Pasteurel
c 740	15	9.4	2112	3	AA274468	AA274468 P. multoc	796	15	9.4	2937	2	AAK58857	AAK58857 Pasteurel
c 741	15	9.4	2220	4	AA593783	AA593783 Human sur	797	15	9.4	2937	2	AAK58857	AAK58857 Pasteurel
c 742	15	9.4	2225	4	AA513689	AA513689 Gene enco	798	15	9.4	2937	2	AAK58857	AAK58857 Pasteurel
c 743	15	9.4	2234	7	AB223174	AB223174 Polynucle	799	15	9.4	2979	3	AAA27449	AAA27449 P. multoc
c 744	15	9.4	2272	4	AB196184	AB196184 Polypepti	800	15	9.4	2979	3	AAA27449	AAA27449 P. multoc
c 745	15	9.4	2291	4	AB127734	AB127734 Drosophila	c 801	15	9.4	3024	4	AAH07569	AAH07569 Drosophila
c 746	15	9.4	2308	4	AAH18526	AAH18526 Human cDN	c 802	15	9.4	3054	4	AAH54843	AAH54843 S. epider
c 747	15	9.4	2309	4	AAH53255	AAH53255 Human pol	c 803	15	9.4	3080	4	AAH53255	AAH53255 Human sec
c 748	15	9.4	2310	2	AA23547	AA23547 Arabidops	c 804	15	9.4	3080	4	AAH53255	AAH53255 Human sec
							c 805	15	9.4	3080	6	AB190697	AB190697 Human pol

806	15	9.4	3086	6	ABN59711	Abn59711	Novel	hum	c 863	15	9.4	4308	9	ADC44175	Adc44175	Human	EST
c 807	15	9.4	3102	7	ACA30727	Ac30727	Prokaryot		c 864	15	9.4	4308	9	ADC61935	Adc61935	Human	EST
808	15	9.4	3117	7	ACF71013	Ac71013	Phototrab		c 865	15	9.4	4308	9	ADC63899	Adc63899	Human	EST
809	15	9.4	3118	4	AAK51953	AAK51953	Human	pol	c 866	15	9.4	4308	9	ADC66999	Adc66999	Human	EST
c 810	15	9.4	3132	6	ABK47581	Abk47581	DNA	enod	c 867	15	9.4	4308	9	ADC69123	Adc69123	Human	EST
c 811	15	9.4	3140	4	ADJ13390	Adj13390	Human	sec	c 868	15	9.4	4308	9	ADC69183	Adc69183	Human	EST
c 812	15	9.4	3151	6	ABO67143	Ab067143	Human	ang	c 869	15	9.4	4308	9	ADC68248	Adc68248	Human	EST
c 813	15	9.4	3192	4	ABU06428	AbU06428	Drosophill		c 870	15	9.4	4308	9	ADC41568	Adc41568	Human	EST
c 814	15	9.4	3228	4	ABU04162	AbU04162	Drosophill		c 871	15	9.4	4308	9	ADC67623	Adc67623	Human	EST
c 815	15	9.4	3242	4	ABU06414	AbU06414	Drosophill		c 872	15	9.4	4308	9	ADC62559	Adc62559	Human	EST
816	15	9.4	3275	8	ACF25333	Ac25333	Rat	cycos	c 873	15	9.4	4308	9	ADC42192	Adc42192	Human	EST
817	15	9.4	3275	9	ADBS2845	Adbs2845	Toxicity-		c 874	15	9.4	4308	9	ADE48561	AdE48561	Human	EST
818	15	9.4	3275	9	ADBS2844	Adbs2844	Primary r		c 875	15	9.4	4308	9	ADE35615	AdE35615	Human	EST
819	15	9.4	3305	5	ABY25206	AbY25206	Human	pro	c 876	15	9.4	4308	9	ADE16729	AdE16729	Human	EST
c 820	15	9.4	3387	7	ABZ36087	Abz36087	Human	sec	c 877	15	9.4	4308	9	ADD73344	AdD73344	Human	EST
821	15	9.4	3434	4	ABU19863	AbU19863	Drosophill		c 878	15	9.4	4308	9	ADD72702	AdD72702	Human	EST
822	15	9.4	3473	4	ABU17404	AbU17404	Drosophill		c 879	15	9.4	4308	9	ADE17353	AdE17353	Human	EST
c 823	15	9.4	3476	4	ABU19970	AbU19970	Drosophill		c 880	15	9.4	4308	10	ADE48861	AdE48861	Human	EST
c 824	15	9.4	3509	9	ADFS4086	Adfs4086	Human	pro	c 881	15	9.4	4308	10	ADE89962	AdE89962	Human	EST
c 825	15	9.4	3568	4	AAH17770	AaH17770	Human	CDN	c 882	15	9.4	4381	6	ABQ70889	AbQ70889	Human	EST
826	15	9.4	3586	2	AAQ56643	AaQ56643	Human	tyr	c 883	15	9.4	4394	4	AAU35762	AaU35762	Human	mus
827	15	9.4	3676	4	ABU25398	AbU25398	Drosophill		c 884	15	9.4	4394	7	AAK58750	AaK58750	Human	mus
828	15	9.4	3691	4	AAK74691	AaK74691	Human	imm	c 885	15	9.4	4400	4	AAU35763	AaU35763	Human	mus
829	15	9.4	3696	7	ACA21669	Ac21669	Prokaryot		c 886	15	9.4	4400	7	AAK58751	AaK58751	Human	mus
c 830	15	9.4	3739	4	AAH14685	AaH14685	Human	CDN	c 887	15	9.4	4449	4	ABU07034	AbU07034	Human	EST
831	15	9.4	3746	4	ABK43586	Abk43586	DNA	enod	c 888	15	9.4	4467	2	AAK19253	AaK19253	Human	EST
832	15	9.4	3772	4	ABU22533	AbU22533	Drosophill		c 889	15	9.4	4562	4	ABU05956	AbU05956	Human	EST
c 833	15	9.4	3818	4	AA259254	AA259254	Human	NR8	c 890	15	9.4	4733	5	AA570470	Aa570470	Human	EST
c 834	15	9.4	3837	4	AAH15755	AaH15755	Human	CDN	c 891	15	9.4	4735	4	ABU06622	AbU06622	Human	EST
c 835	15	9.4	3844	5	ABV23912	Abv23912	Human	pro	c 892	15	9.4	4958	4	ABU19334	AbU19334	Human	EST
c 836	15	9.4	3844	5	ABV29793	Abv29793	Human	pro	c 893	15	9.4	5005	5	AA584258	Aa584258	Human	EST
837	15	9.4	3881	3	AAA61263	Aa61263	Human	sec	c 894	15	9.4	5072	6	ABN59669	AbN59669	Human	nov
838	15	9.4	3881	7	ADMS3531	AdMS3531	Gene	enco	c 895	15	9.4	5078	9	ADC32307	AdC32307	Human	nov
839	15	9.4	3881	7	ADA39741	AdA39741	Human	sec	c 896	15	9.4	5079	4	AAK66744	AaK66744	Human	kid
c 840	15	9.4	3897	4	AAK52195	AAK52195	Human	pol	c 897	15	9.4	5126	4	AAH57506	AaH57506	Human	imm
c 841	15	9.4	3938	7	ABK11200	Abk11200	CDNA	enco	c 898	15	9.4	5133	6	ABU33913	AbU33913	Human	imm
842	15	9.4	3949	4	ABU13968	AbU13968	Drosophill		c 899	15	9.4	5142	7	ACD13398	AdC13398	Human	EST
c 843	15	9.4	3952	6	AA229901	Aa229901	Bacillus		c 900	15	9.4	5239	6	ABU43316	AbU43316	Human	DTC
844	15	9.4	4049	6	AAU42955	AaU42955	Human	cer	c 901	15	9.4	5276	4	AA546380	Aa546380	Human	nov
c 845	15	9.4	4050	4	ABU25878	AbU25878	Drosophill		c 902	15	9.4	5276	6	ABU32827	AbU32827	Human	imm
c 846	15	9.4	4130	3	AACT7406	AaCT7406	Human	ORF	c 903	15	9.4	5333	3	AAA57410	AaA57410	DNA	seque
c 847	15	9.4	4134	5	ABA19810	AbA19810	Human	ner	c 904	15	9.4	5360	6	ABU33937	AbU33937	Human	imm
848	15	9.4	4210	4	AA527090	Aa527090	CDNA	enco	c 905	15	9.4	5360	6	ABU29297	AbU29297	Human	EST
849	15	9.4	4210	9	ADBS3268	Adbs3268	Human	CDN	c 906	15	9.4	5360	6	ABU49366	AbU49366	Human	pol
c 850	15	9.4	4308	2	AAZ34327	AaZ34327	Human	EST	c 907	15	9.4	5467	6	ABU34108	AbU34108	Human	imm
c 851	15	9.4	4308	3	AACT8593	AaCT8593	Human	EST	c 908	15	9.4	5507	7	AB210057	Ab210057	Haematopo	
c 852	15	9.4	4308	7	ACD42860	Ac42860	Novel	hum	c 909	15	9.4	5507	7	AB210203	Ab210203	Haematopo	
c 853	15	9.4	4308	7	ACA63895	AcA63895	Novel	hum	c 910	15	9.4	5514	4	ABU06604	AbU06604	Drosophill	
c 854	15	9.4	4308	7	ACA72059	AcA72059	Human	PRO	c 911	15	9.4	5518	6	ABK28305	AbK28305	DNA	trans
c 855	15	9.4	4308	7	ABX92659	Abx92659	Human	PRO	c 912	15	9.4	5526	6	AA561697	Aa561697	Lung	smal
c 856	15	9.4	4308	7	ACA66440	AcA66440	Human	sec	c 913	15	9.4	5583	4	ABU15146	AbU15146	Drosophill	
c 857	15	9.4	4308	8	ADA25066	AdA25066	Novel	hum	c 914	15	9.4	5641	4	AAK51946	AaK51946	Human	pol
c 858	15	9.4	4308	8	ACD30041	AcD30041	Novel	hum	c 915	15	9.4	5768	6	ABU34163	AbU34163	Human	imm
c 859	15	9.4	4308	8	ADA12727	AdA12727	Human	sec	c 916	15	9.4	5815	6	ABK40024	AbK40024	Human	che
c 860	15	9.4	4308	8	ACD29456	AcD29456	Novel	hum	c 917	15	9.4	5828	6	AAU47247	AaU47247	Allegle	
c 861	15	9.4	4308	8	ADB74033	AdB74033	Human	PRO	c 918	15	9.4	5867	6	ABQ67151	AbQ67151	Human	ang
c 862	15	9.4	4308	9	ADB76749	AdB76749	Human	PRO	c 919	15	9.4	5869	9	AD62578	AdE62578	Human	gen

PR 02-DEC-1999; 99US-00454252.
XX (PHAG-) PHAGETECH INC.
XX
XX
PI Polletier J, Gros P, Dubow M;
XX WPI; 2000-412361/35.
DR P-PSDB; AAB15527.
XX
XX
PT Identifying a bacteriophage coding region for treating bacterial
PT infections comprises identifying a nucleic acid encoding a product that
PT inhibits bacteria when a bacteriophage infects a bacterium.
XX
XX
PS Disclosure/ Page 162; 456pp; English.
XX
XX The present invention describes a method for identifying a bacteriophage
CC coding region encoding a product active on an essential bacterial target.
CC The method comprises identifying a nucleic acid sequence encoding a gene
CC product that provides a bacteria-inhibiting function when an
CC uncharacterised bacteriophage infects a pathogenic bacterium. The
CC compound active on a target of a bacteriophage inhibitor protein in a
CC bacteria is used to treat or prevent a bacterial infection in an animal.
CC AAB6243 to AAB69442 and AAB16523 to AAB16954 represent bacteriophage
CC nucleotide and protein sequences which are used in the exemplification of
CC the present invention. (Updated on 06-AUG-2003 to correct 05 field.)
CC
XX (Updated on 15-SEP-2003 to standardise 05 field)
XX
SQ Sequence 159 BP; 58 A; 31 C; 30 G; 40 T; 0 U; 0 Other;

Query Match 100.0%; Score 159; DB 3; Length 159;
Best Local Similarity 100.0%; Pred. No. 5e-74;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTAACCAAGAAATTTTAAACTAACTGAGTTCAGATATGTAAGCTCAGAA 60
DB 1 ATGGTAACCAAGAAATTTTAAACTAACTGAGTTCAGATATGTAAGCTCAGAA 60
QY 61 CTCATGATGAGGCAAGGCGATGAAATAGGTGTGACACCTATTATCCAAAACT 120
DB 61 CTCATGATGAGGCAAGGCGATGAAATAGGTGTGACACCTATTATCCAAAACT 120
QY 121 GCAGAACGTCATACAGCCGCCCTATGTCGAATATTA 159
DB 121 GCAGAACGTCATACAGCCGCCCTATGTCGAATATTA 159

RESULT 2
AAC86107 AAC86107 standard; cDNA; 159 BP.
XX
XX AAC86107;
XX
XX 06-AUG-2003 (revised)
DT 29-AUG-2001 (first entry)
XX
XX Bacteriophage 77 ORF 104.
XX

KW DnaI, S. aureus; inhibitor; bacteriophage 77; ORF 104; phage 77ORF104;
KW screening assay; ss.
XX
XX Bacteriophage.
OS
XX W0200146383-A2.
XX
XX 28-JUN-2001.
PD
XX
XX
PF 21-DEC-2000; 2000WO-US035180.
XX
XX
XX 22-DEC-1999; 99US-00470512.
PR 12-OCT-2000; 2000US-0068952.
XX
XX (PHAG-) PHAGETECH INC.
PA (WILL/) WILLIAMS K M.
XX
XX Polletier J, Gros P, Dubow M;
PI WPI; 2001-418052/44.
DR P-PSDB; AAB47318.
XX
XX
XX Novel DnaI polypeptides useful for treating and diagnosing microbial,
PT preferably bacterial, diseases such as those caused by Staphylococcus
PT aureus.
XX
XX
XX Example 1; Fig 4; 107pp; English.
XX
XX This sequence represents open reading frame (ORF) 104 of Bacteriophage
CC 77. The growth inhibitory gene product of ORF 104 interacts with DnaI
CC derived from S. aureus, to form the basis of a screening assay. DnaI
CC polypeptides and polynucleotides are useful for treating microbial,
CC preferably bacterial, especially Staphylococcal, infections. DnaI
CC polypeptides and polynucleotides are useful for biological, diagnostic,
CC prophylactic, clinical and therapeutic use, and as components in
CC databases useful for search analyses as well as in sequence analysis
XX algorithms. (Updated on 06-AUG-2003 to correct 05 field.)
XX
SQ Sequence 159 BP; 58 A; 31 C; 30 G; 40 T; 0 U; 0 Other;

Query Match 100.0%; Score 159; DB 4; Length 159;
Best Local Similarity 100.0%; Pred. No. 5e-74;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTAACCAAGAAATTTTAAACTAACTGAGTTCAGATATGTAAGCTCAGAA 60
DB 1 ATGGTAACCAAGAAATTTTAAACTAACTGAGTTCAGATATGTAAGCTCAGAA 60
QY 61 CTCATGATGAGGCAAGGCGATGAAATAGGTGTGACACCTATTATCCAAAACT 120
DB 61 CTCATGATGAGGCAAGGCGATGAAATAGGTGTGACACCTATTATCCAAAACT 120
QY 121 GCAGAACGTCATACAGCCGCCCTATGTCGAATATTA 159
DB 121 GCAGAACGTCATACAGCCGCCCTATGTCGAATATTA 159

RESULT 3
 AA68247
 ID AAA68247 standard; DNA; 41708 BP.
 XX
 AC AAA68247;
 XX
 DT 15-SEP-2003 (revised)
 DT 06-AUG-2003 (revised)
 DT 27-OCT-2000 (first entry)
 XX
 DE Bacteriophage 77 complete genome sequence.
 XX
 KW Bacteriophage; antimicrobial; genome; identification; antibacterial;
 KW bacterial growth inhibition; bacterial infection; ds.
 XX
 OS Staphylococcus aureus; bacteriophage 77.
 XX
 PN WC000032825-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 03-DEC-1999; 99WC-1B002040.
 XX
 PR 03-DEC-1998; 98US-0110992P.
 PR 03-JUN-1999; 99US-00326144.
 PR 28-SEP-1998; 99US-00407804.
 PR 30-SEP-1999; 99US-0157218P.
 PR 01-DEC-1999; 99US-0168777P.
 PR 02-DEC-1999; 99US-00454252.
 XX
 PA (PHAG-) PHAGETECH INC.
 XX
 PI Pelletier J, Gros P, Dubow M;
 XX
 DR WPI; 2000-412361/35.
 XX
 PT Identifying a bacteriophage coding region for treating bacterial
 PT infections comprises identifying a nucleic acid encoding a product that
 PT inhibits bacteria when a bacteriophage infects a bacterium.
 XX
 PS Example 3; Page 141-151; 456pp; English.
 XX
 CC The present invention describes a method for identifying a bacteriophage
 CC coding region encoding a product active on an essential bacterial target.
 CC The method comprises identifying a nucleic acid sequence encoding a gene
 CC product that provides a bacteria-inhibiting function when an
 CC uncharacterized bacteriophage infects a pathogenic bacterium. The
 CC compound active on a target of a bacteriophage inhibitor protein in a
 CC bacteria is used to treat or prevent a bacterial infection in an animal.
 CC AAA68243 to AAA69442 and AAB16523 to AAB16954 represent bacteriophage
 CC nucleotide and protein sequences which are used in the exemplification of
 CC the present invention. (Updated on 06-AUG-2003 to correct OS field.)
 CC (Updated on 15-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 U; 0 other;
 Query Match 100.0%; Score 159; DB 3; Length 41708;

Best Local Similarity 100.0%; Pred. No. 5.7e-74;
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGTTACCAAGATTATTTTAAAACTAACTGAGTTCAGATATGTAGCTCAGAA 60
 DB 34393 ATGTTACCAAGATTATTTTAAAACTAACTGAGTTCAGATATGTAGCTCAGAA 34452
 QY 61 CTGATGATGAGGACAGGGGCAATGAAATAGGTTGTAGACCTATTTATCCAAACTT 120
 DB 34453 CTGATGATGAGGACAGGGGCAATGAAATAGGTTGTAGACCTATTTATCCAAACTT 34512
 QY 121 GCAGAACTGCTATACAGCCCGCTATGCTCAATATTA 159
 DB 34513 GCAGAACTGCTATACAGCCCGCTATGCTCAATATTA 34551
 RESULT 4
 AAC86106
 ID AAC86106 standard; cDNA; 41708 BP.
 XX
 AC AAC86106;
 XX
 DT 06-AUG-2003 (revised)
 DT 29-AUG-2001 (first entry)
 XX
 DE Complete genome of bacteriophage 77.
 XX
 KW DnaI; S. aureus; inhibitor; bacteriophage 77; ORF 104; phage 77ORF104;
 KW screening assay; ss.
 XX
 OS Bacteriophage.
 XX
 EN WC000146383-A2.
 XX
 PD 28-JUN-2001.
 XX
 PF 21-DEC-2000; 2000MO-US035180.
 XX
 PR 22-DEC-1999; 99US-00470512.
 PR 12-OCT-2000; 2000US-00689952.
 XX
 PA (PHAG-) PHAGETECH INC.
 PA (WILL/) WILLIAMS K M.
 XX
 PI Pelletier J, Gros P, Dubow M;
 XX
 DR WPI; 2001-418052/44.
 XX
 CC Novel DnaI polypeptides useful for treating and diagnosing microbial,
 CC preferably bacterial, diseases such as those caused by Staphylococcus
 CC aureus.
 XX
 PS Disclosure; Fig 2; 107pp; English.
 XX
 CC This sequence represents the genome of Bacteriophage 77. The growth
 CC inhibitory gene product of ORF 104 interacts with DnaI derived from S.
 CC aureus, to form the basis of a screening assay. DnaI polypeptides and

Sequence 41708 BP, 15607 A, 5898 C, 8088 G, 12115 T, 0 U, 0 Other;

Matches 15

Db 34393

Db 34453

Db 34513

AAAT83989

ID AAT83989 standard; DNA; 1134 BP.

AC MAT83989,

DT 27-AUG-1998 (first entry)

DE DNA encoding a Staphylococcus aureus protein of unknown function

Staphylococcus aureus protein; ribozyme; antisense sequence; control;

KW vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;

2 x 2

OS Staphylococcus aureus.

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
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96	96	96
97	97	97
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99	99	99
100	100	100

13

PN W09730070-A1.

PD 21-AUG-1997

PF 19-FEB-1997; 97WO-US002318.

PR 20-FEB-1996; 96US-0011888P.

PA (SMIK) SMITHKLINE BEECHAM CORP.

XX

PI Black MT, Burnham MK, Hodgson JE, Knowles DJC, Nicholas RO;
PI Pratt JM, Reichard RW, Rosenburt M, Ward JM.

Platt JM, Reichard RW, Rosenberg M, Ward JM;
XX

DR WP1: 199/-424969/39
DB P-PSDB: AAW2B036

Novel polymeride

PT Isolate antimicrobial compounds, and in vaccines against *S. aureus* infection.

PS Claim 9; Page 797; 989pp; English.

CC The present sequence encodes a *Staphylococcus aureus* protein of unknown
CC function. The present sequence was isolated from a library of clones of
CC *S. aureus* WCUH 29 in *Escherichia coli*. The DNA sequence can be used in
CC the construction of ribozymes and antisense sequences to control the
CC expression of *Staphylococcus* genes. The DNA sequence is also useful as a
CC source of regulatory elements for the control of bacterial gene
CC expression. The encoded protein may be used to produce vaccines to enable
CC a host to produce specific antibodies with antibacterial action. These
CC vaccines and antibodies would protect a host against invasion by *S.*
CC aureus, and conditions relating to *Staphylococcus* infection, e.g.,
CC *Staphylococcus* food poisoning, scaled skin syndrome, and toxic shock
CC syndrome

SQ Sequence 1134 BP; 407 A; 179 C; 247 G; 290 T; 0 U; 11 other;

Query Match	Score	DB 2	Length
28.36	45	1134	

Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 ATGCTAACCAAGATTTTAAAACTAACTTGAGTGTCAGAT 45
        |||||
        5 ATGCTAACCAAGATTTTAAAACTAACTTGAGTGTCAGAT 49
Db
```

Search completed: October 15, 2004, 00:17:33
Job time : 134.071 secs

OK nucleole - nucleole search, using SW model

Run on: October 14, 2004, 22:42:59 ; Search time 743.134 Seconds

(without alignments)
6389.277 Million cell updates/sec

SUMMARIES

28: gb_gsa1:.*
29: gb_gsa2:.*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Title: US-09-407-804A-8
Perfect score: 159
Sequence: 1 atggttaaccaagaattttt.....ccgctatcgctgaattctaa 159
Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0
Searched: 27513289 seqs, 14931090276 residues
Word size : 0
Total number of hits satisfying chosen parameters: 53026578
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Listing first 1000 summaries
Database : ESI:.*
1: em_gstba:.*
2: em_gsthum:.*
3: em_gstlin:.*
4: em_gstmu:.*
5: em_gstov:.*
6: em_gstpl:.*
7: em_gstro:.*
8: em_hrc:.*
9: gb_gst1:.*
10: gb_gst2:.*
11: gb_hrc:.*
12: gb_gst3:.*
13: gb_gst4:.*
14: gb_gst5:.*
15: em_gstfun:.*
16: em_gstom:.*
17: em_gst_hum:.*
18: em_gst_inv:.*
19: em_gst_pln:.*
20: em_gst_vrt:.*
21: em_gst_fun:.*
22: em_gst_man:.*
23: em_gst_mus:.*
24: em_gst_pro:.*
25: em_gst_rnd:.*
26: em_gst_phg:.*
27: em_gst_vrt:.*

Result		Query		DB		ID	Description
No.	Score	Match	Length	DB	ID		
1	21	13.2	270	29	CE255312		CE255312 tigr-gsa-
2	21	13.2	357	29	CE691097		CE691097 tigr-gsa-
3	21	13.2	697	29	CE423104		CE423104 tigr-gsa-
4	20	12.6	342	9	AV858453		AV858453 tigr-gsa-
5	20	12.6	456	28	AZ232968		AZ232968 RPT-23-9
6	20	12.6	546	12	B1610223		B1610223 RH5267.5
7	20	12.6	719	29	CC622177		CC622177 OGMA708TV
8	20	12.6	724	12	BG705867		BG705867 602669359
9	20	12.6	781	29	CC622172		CC622172 OGMA708TV
10	20	12.6	1179	28	CC264106		CC264106 CH261-57C
11	19	11.9	287	10	AM905496		AM905496 RC4-NN108
12	19	11.9	475	29	CE660226		CE660226 tigr-gsa-
13	19	11.9	561	28	AZ424688		AZ424688 tigr-gsa-
14	19	11.9	569	28	AQ420952		AQ420952 RPT-11-2
15	19	11.9	579	14	CB935098		CB935098 RU03a11.Y
16	19	11.9	595	28	AQ368393		AQ368393 HS 5039.A
17	19	11.9	596	9	AL041452		AL041452 DKF2p434E
18	19	11.9	639	12	B1106130		B1106130 602892014
19	19	11.9	685	29	CE297788		CE297788 tigr-gsa-
20	19	11.9	693	29	CE429047		CE429047 tigr-gsa-
21	19	11.9	701	29	AG088522		AG088522 Pan treg1
22	19	11.9	734	28	AZ200805		AZ200805 SP.1011.A
23	19	11.9	854	28	AZ190550		AZ190550 SP.1017.B
24	19	11.9	885	28	CC117791		CC117791 NDL-5L7.T
25	19	11.9	1016	29	CNS06YMW		AL421590 T3 end of
26	18	11.3	165	10	BE841808		BE841808 MRI-SN006
27	18	11.3	168	28	CC170087		CC170087 1194h08.g
28	18	11.3	172	28	CC170085		CC170085 1194h08.g
29	18	11.3	181	29	CNS07FJ2		AL608561 Anopheles
30	18	11.3	199	14	CA812153		CA812153 CA411N021
31	18	11.3	250	9	AA251660		AA251660 z811f05.-9
32	18	11.3	260	29	CG668289		CG668289 OS7464103
33	18	11.3	263	10	AW832582		AW832582 PM4-CT024
34	18	11.3	265	28	AZ912465		AZ912465 RPT-24-1
35	18	11.3	316	10	BB395991		BB395991 BB395991
36	18	11.3	317	14	CD587746		CD587746 RK043A160
37	18	11.3	320	10	BB255119		BB255119 BB255119
38	18	11.3	341	13	BU360800		BU360800 603786155
39	18	11.3	362	28	BH373111		BH373111 AG-ND-137
40	18	11.3	367	14	CB088393		CB088393 1699f12.b
41	18	11.3	369	14	R99699		R99699 YG72606.r1
42	18	11.3	370	28	AQ513966		AQ513966 HS-5179.B
43	18	11.3	383	10	BF012226		BF012226 US95g03.Y
44	18	11.3	390	10	BF012250		BF012250 US40a06.Y
45	18	11.3	391	28	AZ342125		AZ342125 IM0075H01

46	18	11.3	392	12	B0167771	B0167771	103	18	11.3	699	29	AG215096
47	18	11.3	396	12	B0685591	B0685591	104	18	11.3	701	28	BH322345
48	18	11.3	407	28	A2512143	A2512143	105	18	11.3	704	28	BH971448
49	18	11.3	408	28	AQ104107	AQ104107	106	18	11.3	704	28	BH397547
50	18	11.3	438	28	AQ602863	AQ602863	107	18	11.3	710	28	BH992062
51	18	11.3	443	28	CC170086	CC170086	108	18	11.3	714	12	BG695502
52	18	11.3	451	10	BB679871	BB679871	109	18	11.3	715	14	BG695502
53	18	11.3	465	28	AQ441657	AQ441657	110	18	11.3	720	18	CB266873
54	18	11.3	481	12	B1741223	B1741223	111	18	11.3	723	28	A2854721
55	18	11.3	481	12	CA682350	CA682350	112	18	11.3	728	12	B3585672
56	18	11.3	485	29	CE726036	CE726036	113	18	11.3	733	29	BX244581
57	18	11.3	497	14	CD565756	CD565756	114	18	11.3	741	12	B3605840
58	18	11.3	500	12	BP109214	BP109214	115	18	11.3	744	29	BN501790
59	18	11.3	500	12	BP186540	BP186540	116	18	11.3	746	14	CF408079
60	18	11.3	504	14	CD538790	CD538790	117	18	11.3	761	14	CF747486
61	18	11.3	516	14	CD548998	CD548998	118	18	11.3	763	14	CD299599
62	18	11.3	523	14	CD547227	CD547227	119	18	11.3	766	29	CE021679
63	18	11.3	529	28	A2765927	A2765927	120	18	11.3	771	13	BU455066
64	18	11.3	534	9	AV960850	AV960850	121	18	11.3	776	28	BH545670
65	18	11.3	553	13	BQ394219	BQ394219	122	18	11.3	786	14	CF747503
66	18	11.3	554	28	BH378082	BH378082	123	18	11.3	790	29	CC527885
67	18	11.3	555	14	CD561729	CD561729	124	18	11.3	808	13	BU454610
68	18	11.3	560	29	CE653603	CE653603	125	18	11.3	823	14	CE662123
69	18	11.3	571	9	AV701220	AV701220	126	18	11.3	826	28	BH262136
70	18	11.3	578	14	CA396589	CA396589	127	18	11.3	826	28	BH355686
71	18	11.3	578	28	BH059617	BH059617	128	18	11.3	830	28	AQ750378
72	18	11.3	588	28	AQ624968	AQ624968	129	18	11.3	835	14	CD644235
73	18	11.3	592	14	CD546392	CD546392	130	18	11.3	840	28	AQ892977
74	18	11.3	592	28	BH317476	BH317476	131	18	11.3	853	28	B2841480
75	18	11.3	594	9	AL595905	AL595905	132	18	11.3	860	29	CG117558
76	18	11.3	597	28	BH264109	BH264109	133	18	11.3	862	13	BU322661
77	18	11.3	602	13	BQ396416	BQ396416	134	18	11.3	875	11	CF239298
78	18	11.3	604	9	AL595165	AL595165	135	18	11.3	876	11	CF239298
79	18	11.3	607	9	AL850869	AL850869	136	18	11.3	889	28	B2252751
80	18	11.3	610	29	CC767439	CC767439	137	18	11.3	892	12	B1648511
81	18	11.3	614	12	BM940643	BM940643	138	18	11.3	908	29	CC653519
82	18	11.3	615	13	BQ526286	BQ526286	139	18	11.3	913	13	EX743864
83	18	11.3	618	9	AV845559	AV845559	140	18	11.3	927	14	CA472543
84	18	11.3	624	9	AL871043	AL871043	141	18	11.3	936	12	BG423519
85	18	11.3	625	9	AL683050	AL683050	142	18	11.3	960	14	CF782339
86	18	11.3	634	29	CC736161	CC736161	143	18	11.3	972	14	CF591419
87	18	11.3	642	9	AL899906	AL899906	144	18	11.3	988	29	CNS066HF
88	18	11.3	646	9	AL876497	AL876497	145	18	11.3	1027	28	CC203152
89	18	11.3	647	9	AL877431	AL877431	146	18	11.3	1047	29	CNS0530N
90	18	11.3	650	14	CD599680	CD599680	147	18	11.3	1055	29	CNS0530N
91	18	11.3	652	12	BG907416	BG907416	148	18	11.3	1118	28	B09876
92	18	11.3	663	10	BH452472	BH452472	149	18	11.3	1124	14	CF994239
93	18	11.3	663	28	BH208660	BH208660	150	18	11.3	1163	28	CC186610
94	18	11.3	667	28	A2436122	A2436122	151	18	11.3	1201	9	AL534838
95	18	11.3	669	28	BH265963	BH265963	152	18	11.3	1209	11	AK083395
96	18	11.3	671	9	AL645123	AL645123	153	18	11.3	1322	28	A2561648
97	18	11.3	672	29	AG149254	AG149254	154	18	11.3	1322	28	A2561648
98	18	11.3	683	28	BH266872	BH266872	155	18	11.3	150	13	BU578780
99	18	11.3	683	29	AG059187	AG059187	156	18	11.3	150	28	A2774120
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101	18	11.3	689	11	CNS09127	CNS09127	158	18	11.3	166	9	AV266112
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c 160	17	10.7	207	10	BB200265	BB200265	c 217	17	10.7	404	13	BY523913	BY523913
c 161	17	10.7	218	10	BB013168	BB013168	c 218	17	10.7	406	10	BG044050	BG044050
c 162	17	10.7	219	9	AU071473	AU071473	c 219	17	10.7	406	13	BY533393	BY533393
c 163	17	10.7	224	10	BB037237	BB037237	c 220	17	10.7	409	29	CE712808	CE712808
c 164	17	10.7	236	9	AV236694	AV236694	c 221	17	10.7	410	9	AV976542	AV976542
c 165	17	10.7	236	10	BF333693	BF333693	c 222	17	10.7	410	13	BY521034	BY521034
c 166	17	10.7	236	28	AA539449	AA539449	c 223	17	10.7	414	12	BI815478	BI815478
c 167	17	10.7	240	28	BB772326	BB772326	c 224	17	10.7	417	12	BQ342006	BQ342006
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c 171	17	10.7	263	28	AQ524888	AQ524888	c 228	17	10.7	423	28	AZ299013	AZ299013
c 172	17	10.7	268	9	AL598037	AL598037	c 229	17	10.7	423	28	AQ203215	AQ203215
c 173	17	10.7	269	9	AV277144	AV277144	c 230	17	10.7	424	28	AQ596662	AQ596662
c 174	17	10.7	272	10	BB412255	BB412255	c 231	17	10.7	427	12	BI245048	BI245048
c 175	17	10.7	272	10	BB577721	BB577721	c 232	17	10.7	431	10	BE580829	BE580829
c 176	17	10.7	275	10	BB128300	BB128300	c 233	17	10.7	434	10	BF986122	BF986122
c 177	17	10.7	276	10	BB456442	BB456442	c 234	17	10.7	435	28	AQ556737	AQ556737
c 178	17	10.7	277	10	BB434280	BB434280	c 235	17	10.7	438	12	BI18987	BI18987
c 179	17	10.7	282	9	AL639159	AL639159	c 236	17	10.7	439	12	BQ341202	BQ341202
c 180	17	10.7	283	28	AQ999053	AQ999053	c 237	17	10.7	440	13	BY531602	BY531602
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c 183	17	10.7	312	28	AZ589032	AZ589032	c 240	17	10.7	442	28	AQ813262	AQ813262
c 184	17	10.7	318	13	BBW139793	BBW139793	c 241	17	10.7	442	28	AZ818168	AZ818168
c 185	17	10.7	321	10	BB313457	BB313457	c 242	17	10.7	443	28	AQ388029	AQ388029
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c 190	17	10.7	344	10	BB131569	BB131569	c 247	17	10.7	454	29	CE533929	CE533929
c 191	17	10.7	344	13	BY602850	BY602850	c 248	17	10.7	455	10	BE223544	BE223544
c 192	17	10.7	346	9	AV732005	AV732005	c 249	17	10.7	459	12	BI244916	BI244916
c 193	17	10.7	349	9	AW022843	AW022843	c 250	17	10.7	460	9	AI550436	AI550436
c 194	17	10.7	349	12	BQ343683	BQ343683	c 251	17	10.7	467	28	AZ061189	AZ061189
c 195	17	10.7	352	9	AW103146	AW103146	c 252	17	10.7	470	12	BQ388733	BQ388733
c 196	17	10.7	355	12	BQ435375	BQ435375	c 253	17	10.7	471	28	AZ389317	AZ389317
c 197	17	10.7	360	28	AQ000938	AQ000938	c 254	17	10.7	473	14	CA576019	CA576019
c 198	17	10.7	363	9	AA083840	AA083840	c 255	17	10.7	475	9	AI619574	AI619574
c 199	17	10.7	369	12	BQ430127	BQ430127	c 256	17	10.7	476	12	BI324501	BI324501
c 200	17	10.7	371	9	AA303096	AA303096	c 257	17	10.7	477	9	AI552896	AI552896
c 201	17	10.7	372	14	R31632	R31632	c 258	17	10.7	479	28	AQ959902	AQ959902
c 202	17	10.7	374	9	AV678271	AV678271	c 259	17	10.7	480	9	AL597343	AL597343
c 203	17	10.7	375	14	CB691517	CB691517	c 260	17	10.7	482	28	AZ887273	AZ887273
c 204	17	10.7	378	12	BI245004	BI245004	c 261	17	10.7	483	13	BY533608	BY533608
c 205	17	10.7	378	13	BY543189	BY543189	c 262	17	10.7	487	12	BM539027	BM539027
c 206	17	10.7	378	29	CS597432	CS597432	c 263	17	10.7	488	9	AV645834	AV645834
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c 208	17	10.7	383	12	BQ431652	BQ431652	c 265	17	10.7	491	12	BI314919	BI314919
c 209	17	10.7	387	9	AI955613	AI955613	c 266	17	10.7	491	28	CC092816	CC092816
c 210	17	10.7	389	10	BB551454	BB551454	c 267	17	10.7	492	10	BF548989	BF548989
c 211	17	10.7	390	28	AQ326526	AQ326526	c 268	17	10.7	492	28	AZ813586	AZ813586
c 212	17	10.7	393	14	CB774189	CB774189	c 269	17	10.7	493	28	AQ165956	AQ165956
c 213	17	10.7	396	10	BB644309	BB644309	c 270	17	10.7	495	10	AAW90042	AAW90042
c 214	17	10.7	399	10	BE456611	BE456611	c 271	17	10.7	501	29	CC968714	CC968714
c 215	17	10.7	399	12	BI293288	BI293288	c 272	17	10.7	503	28	AQ424830	AQ424830
c 216	17	10.7	404	10	BB544025	BB544025	c 273	17	10.7	504	28	AZ909615	AZ909615

BY533913	BY523913	BG044050	aa223g12.	BY533393	CE712808	tl4r-gs-	AV976542	BY521034	BI815478	BQ342006	AQ262207	CITBI-EI-	AA067007	mm5a02..r	CE300383	tl4r-gs-	AZ299013	RPCT-23-9	AQ203215	AQ596662	HS_5192.B	BI245048	AR057D05L	BE580829	KPB2501.Y	BF986122	CM4-GN008	AQ556737	HS_5331.A	BI18987	AR21CS_Po	BY531602	AA183097	mt8b03..r	AL931574	AL931574	AQ813262	HS_5112.A	AZ818168	ZM008B106	HS_5017.A	AQ275872	CITBI-EI-	AI145286	UI-R-BFO-	BG078258	tl02G603-	CE703758	tl4r-gs-	CE533929	tl4r-gs-	BE223544	KPB2501.Y	BI244916	AR055E11L	AI550436	vx16f09..x	AZ061189	RPCT-23-4	BQ388733	BQ398733	AZ389317	IM0149G13	CA576019	K0638G11-	AI619574	ty50c09..x	BI324501	FX80F07.Y	AI552896	vg67606.Y	AQ959902	LEHE021TF	AL597343	DKEP313H	AZ887273	RPCT-24-1	BY533608	BY593608	BM539027	hD03h05..g	AV645834	AV645834	AA217066	mu93c10..r	BI314919	daa56c12.	CC092816	CSU-R34.1	BF548989	UI-R-A0-a	AZ813586	ZM008B122	AQ165956	HS_3066.A	AAW90042	utF3412.Y	CC968714	BOEN93TR	AQ424830	CITBI-EI-	AZ909615	RPCT-24-1
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[illegible]

c 388	17	10.7	636	12	B3429018	B3429018	B3429018	445	17	10.7	674	14	CB448101	CB448101 702161 MA
c 389	17	10.7	637	29	CB441600	c19t-799-	AG130526	c 446	17	10.7	674	29	AG130526	AG130526 Pan treg1
c 390	17	10.7	638	10	BF295849	029B504	BB031133	c 447	17	10.7	675	10	BB031133	BB031133
c 391	17	10.7	638	13	BK846326	BK846326	B3429473	c 448	17	10.7	675	12	B3429473	B3429473
c 392	17	10.7	639	10	BB657037	BB657037	AO288036	c 449	17	10.7	675	28	AO288036	AO288036 rnhb0030
c 393	17	10.7	639	28	A2507265	1M0348M17	BK131355	c 450	17	10.7	676	29	BK131355	BK131355 Dario for
c 394	17	10.7	640	12	BQ042168	BQ042168	BP316683	c 451	17	10.7	678	12	BP316683	BP316683
c 395	17	10.7	641	28	A2590598	1M0400114	BM250504	c 452	17	10.7	678	13	BM250504	BM250504 BM250504
c 396	17	10.7	642	10	BB652597	BB652597	AV731320	c 453	17	10.7	680	9	AV731320	AV731320 AV731320
c 397	17	10.7	643	29	CC966741	CC966741	BB227725	c 454	17	10.7	680	10	BB227725	BB227725
c 398	17	10.7	643	12	B372517	B372517	B2028531	c 455	17	10.7	680	28	B2028531	B2028531
c 399	17	10.7	644	10	BB457204	BB457204	CB556703	c 456	17	10.7	681	14	CB556703	CB556703
c 400	17	10.7	644	12	BM939750	BM939750	AQ780105	c 457	17	10.7	681	28	AQ780105	AQ780105
c 401	17	10.7	645	12	B3399763	B3399763	A2534508	c 458	17	10.7	681	28	A2534508	A2534508
c 402	17	10.7	645	12	B3401764	B3401764	CG415709	c 459	17	10.7	681	29	CG415709	CG415709
c 403	17	10.7	646	12	B342632	B342632	B3402996	c 460	17	10.7	682	12	B3402996	B3402996
c 404	17	10.7	646	14	CF359600	CF359600	BG506881	c 461	17	10.7	683	12	BG506881	BG506881
c 405	17	10.7	647	12	B343157	B343157	B3399165	c 462	17	10.7	683	12	B3399165	B3399165
c 406	17	10.7	649	13	BU775320	BU775320	B335043	c 463	17	10.7	684	12	B335043	B335043
c 407	17	10.7	649	13	BM032128	BM032128	B3343473	c 464	17	10.7	685	12	B3343473	B3343473
c 408	17	10.7	650	9	AV711848	AV711848	CF789112	c 465	17	10.7	685	14	CF789112	CF789112
c 409	17	10.7	650	12	B344094	B344094	AG099358	c 466	17	10.7	685	28	AG099358	AG099358
c 410	17	10.7	651	10	BB445269	BB445269	BM227725	c 467	17	10.7	685	12	BM227725	BM227725
c 411	17	10.7	652	28	B2499384	B2499384	BM227725	c 468	17	10.7	687	29	BM227725	BM227725
c 412	17	10.7	653	10	BB259184	BB259184	BM227725	c 469	17	10.7	688	12	BM227725	BM227725
c 413	17	10.7	654	14	CF911383	CF911383	BM227725	c 470	17	10.7	688	12	BM227725	BM227725
c 414	17	10.7	655	12	B3344261	B3344261	BM227725	c 471	17	10.7	688	28	BM227725	BM227725
c 415	17	10.7	656	12	B3347001	B3347001	BM227725	c 472	17	10.7	689	12	BM227725	BM227725
c 416	17	10.7	656	14	CD2402905	CD2402905	BM227725	c 473	17	10.7	689	12	BM227725	BM227725
c 417	17	10.7	657	10	BB246599	BB246599	BM227725	c 474	17	10.7	690	10	BM227725	BM227725
c 418	17	10.7	657	10	BB246599	BB246599	BM227725	c 475	17	10.7	690	12	BM227725	BM227725
c 419	17	10.7	658	12	B3344967	B3344967	BM227725	c 476	17	10.7	692	12	BM227725	BM227725
c 420	17	10.7	658	12	B3432168	B3432168	BM227725	c 477	17	10.7	693	12	BM227725	BM227725
c 421	17	10.7	659	13	BM244120	BM244120	BM227725	c 478	17	10.7	693	12	BM227725	BM227725
c 422	17	10.7	659	12	B3342501	B3342501	BM227725	c 479	17	10.7	693	12	BM227725	BM227725
c 423	17	10.7	660	9	AV990367	AV990367	BM227725	c 480	17	10.7	693	12	BM227725	BM227725
c 424	17	10.7	661	28	BM035204	BM035204	BM227725	c 481	17	10.7	694	12	BM227725	BM227725
c 425	17	10.7	662	12	B3345464	B3345464	BM227725	c 482	17	10.7	694	12	BM227725	BM227725
c 426	17	10.7	662	12	B3435959	B3435959	BM227725	c 483	17	10.7	695	12	BM227725	BM227725
c 427	17	10.7	663	10	BB435790	BB435790	BM227725	c 484	17	10.7	695	12	BM227725	BM227725
c 428	17	10.7	663	13	BM077377	BM077377	BM227725	c 485	17	10.7	695	12	BM227725	BM227725
c 429	17	10.7	665	12	B3398569	B3398569	BM227725	c 486	17	10.7	696	12	BM227725	BM227725
c 430	17	10.7	666	12	B3344068	B3344068	BM227725	c 487	17	10.7	697	12	BM227725	BM227725
c 431	17	10.7	666	12	B3345547	B3345547	BM227725	c 488	17	10.7	697	12	BM227725	BM227725
c 432	17	10.7	666	12	B3428278	B3428278	BM227725	c 489	17	10.7	698	12	BM227725	BM227725
c 433	17	10.7	667	12	B3343483	B3343483	BM227725	c 490	17	10.7	699	12	BM227725	BM227725
c 434	17	10.7	667	28	B2017640	B2017640	BM227725	c 491	17	10.7	700	13	BM227725	BM227725
c 435	17	10.7	668	14	CB456866	CB456866	BM227725	c 492	17	10.7	702	12	BM227725	BM227725
c 436	17	10.7	670	12	B3347463	B3347463	BM227725	c 493	17	10.7	702	12	BM227725	BM227725
c 437	17	10.7	670	29	CG942657	CG942657	BM227725	c 494	17	10.7	703	28	BM227725	BM227725
c 438	17	10.7	671	12	B3346734	B3346734	BM227725	c 495	17	10.7	705	28	BM227725	BM227725
c 439	17	10.7	671	28	AQ428230	AQ428230	BM227725	c 496	17	10.7	707	28	BM227725	BM227725
c 440	17	10.7	672	9	AU200398	AU200398	BM227725	c 497	17	10.7	708	28	BM227725	BM227725
c 441	17	10.7	673	9	AU270319	AU270319	BM227725	c 498	17	10.7	708	28	BM227725	BM227725
c 442	17	10.7	673	28	BH883813	BH883813	BM227725	c 499	17	10.7	713	29	BM227725	BM227725
c 443	17	10.7	673	29	AG149990	AG149990	BM227725	c 500	17	10.7	714	12	BM227725	BM227725
c 444	17	10.7	674	14	CB265472	CB265472	BM227725	c 501	17	10.7	716	9	BM227725	BM227725

502	17	10.7	716	28	BH944479	BH944479	chub8308.
c 503	17	10.7	717	12	BH946332	BH946332	
c 504	17	10.7	719	12	BH941872	BH941872	
c 505	17	10.7	720	12	BH947039	BH947039	
c 506	17	10.7	720	12	BH939414	BH939414	
507	17	10.7	722	29	CE114816	CE114816	tiqr-gss-
c 508	17	10.7	723	12	BH346049	BH346049	
c 509	17	10.7	723	12	BH341083	BH341083	
510	17	10.7	725	13	BH048011	BH048011	
c 511	17	10.7	726	28	BZ830052	BZ830052	PUECL37TD
c 512	17	10.7	727	29	CC475914	CC475914	CH240_301
c 513	17	10.7	727	29	BK164609	BK164609	Danilo rer
c 514	17	10.7	728	28	AQ482048	AQ482048	RPT-11-2
c 515	17	10.7	729	12	BH433480	BH433480	
c 516	17	10.7	731	12	BH402546	BH402546	
c 517	17	10.7	731	28	BH673789	BH673789	BOHFD0TF
c 518	17	10.7	735	28	BH957419	BH957419	cdg69408-
519	17	10.7	735	28	BZ003100	BZ003100	oeh85608.
520	17	10.7	736	13	BH048210	BH048210	
c 521	17	10.7	737	12	BH400601	BH400601	
522	17	10.7	740	10	AW914299	AW914299	ESTJ45603
523	17	10.7	740	12	BH245277	BH245277	602357394
524	17	10.7	740	28	BH266860	BH266860	CH230-162
c 525	17	10.7	740	29	CC649144	CC649144	OGWI239TV
c 526	17	10.7	741	29	CC920401	CC920401	EO33113ba
c 527	17	10.7	744	28	BH505544	BH505544	BOHJ196TR
c 528	17	10.7	744	28	BZ053906	BZ053906	1kx42a12.
529	17	10.7	745	12	BG862096	BG862096	602795634
c 530	17	10.7	745	29	CG958540	CG958540	MHEEP7TF
c 531	17	10.7	745	29	AG163909	AG163909	Pan trogl
c 532	17	10.7	746	12	BH345981	BH345981	
c 533	17	10.7	747	12	BH344432	BH344432	
c 534	17	10.7	749	13	BH131573	BH131573	
c 535	17	10.7	750	14	CD250829	CD250829	AGENCOURT
536	17	10.7	750	28	BZ359435	BZ359435	1d73d12.b
c 537	17	10.7	750	28	BZ518021	BZ518021	BOHQZ77TR
538	17	10.7	751	28	BH455324	BH455324	BOHVS0TR
c 539	17	10.7	751	28	BZ444039	BZ444039	BONGE07TF
c 540	17	10.7	753	12	BH340949	BH340949	
c 541	17	10.7	753	13	BH144797	BH144797	
c 542	17	10.7	755	14	CA195930	CA195930	SCEZAD108
c 543	17	10.7	756	12	BH347212	BH347212	
c 544	17	10.7	756	13	BH038600	BH038600	DH01D02.H
545	17	10.7	756	28	BH447128	BH447128	BOGPD8TF
c 546	17	10.7	757	13	BH142553	BH142553	
c 547	17	10.7	757	14	CD675133	CD675133	fa19d08.y
548	17	10.7	758	29	BH133682	BH133682	Danilo rer
549	17	10.7	761	29	CE660294	CE660294	tiqr-gss-
550	17	10.7	761	28	BZ431152	BZ431152	BOHVS6TF
c 551	17	10.7	766	28	BZ015134	BZ015134	oa106b09.
c 552	17	10.7	767	14	CD250754	CD250754	AGENCOURT
553	17	10.7	767	14	CK129219	CK129219	AGENCOURT
c 554	17	10.7	767	28	AF010827	AF010827	
555	17	10.7	768	28	AQ745892	AQ745892	HS_2275.A
556	17	10.7	768	28	BZ061232	BZ061232	1kF38605.
557	17	10.7	770	13	BH097318	BH097318	
558	17	10.7	771	28	BZ320729	BZ320729	hz12d12.g

559	17	10.7	771	29	CC559013	CC559013	CH240_467
c 560	17	10.7	775	12	BH345183	BH345183	
561	17	10.7	782	28	BH681474	BH681474	BOHUR19TR
c 562	17	10.7	785	29	CC925589	CC925589	t064d21ba
563	17	10.7	787	29	CC9862041	CC9862041	
564	17	10.7	788	12	BH560821	BH560821	ZMBMB027
c 565	17	10.7	789	28	BZ439893	BZ439893	BONDE65TR
566	17	10.7	790	13	BH748838	BH748838	CH3#023.B
c 567	17	10.7	792	28	BZ462127	BZ462127	BONIVU4TF
568	17	10.7	793	29	CC643807	CC643807	BOH1236TH
569	17	10.7	800	28	BH552315	BH552315	
570	17	10.7	800	29	AG216474	AG216474	
571	17	10.7	803	13	BH058042	BH058042	DroepoPh11
572	17	10.7	806	14	CF444853	CF444853	AGENCOURT
573	17	10.7	807	28	BH719903	BH719903	BOMWV22TR
c 574	17	10.7	811	28	BH586401	BH586401	
c 575	17	10.7	811	28	BZ188329	BZ188329	BOHJ52TR
576	17	10.7	816	13	BH910378	BH910378	CH230-378
c 577	17	10.7	817	29	CH119726	CH119726	AGENCOURT
c 578	17	10.7	820	11	CH508012	CH508012	tefreedon
c 579	17	10.7	821	14	CF207942	CF207942	Single re
580	17	10.7	821	29	CC916032	CC916032	CAB20002.
581	17	10.7	822	14	CA329159	CA329159	t090b12ba
582	17	10.7	822	29	CG119726	CG119726	UI-M-FV0-
583	17	10.7	823	10	BF161090	BF161090	PUIAV32TR
584	17	10.7	823	29	CH500ADW	CH500ADW	601768030
c 585	17	10.7	824	28	BZ437619	BZ437619	BOHRT74TR
c 586	17	10.7	824	28	CC0005340	CC0005340	PUDH822TD
587	17	10.7	826	29	CG846307	CG846307	OGAAB61TV
c 588	17	10.7	827	29	CG209453	CG209453	OGB087TV
589	17	10.7	828	29	CG868816	CG868816	ZMBMB036
c 590	17	10.7	832	28	BZ458977	BZ458977	BOMLX4TR
c 591	17	10.7	833	28	BH584551	BH584551	BOHKB58TF
c 592	17	10.7	835	13	BH111622	BH111622	603128064
593	17	10.7	835	13	BH537583	BH537583	AGENCOURT
c 594	17	10.7	837	28	BH704423	BH704423	BONTIS9TF
595	17	10.7	837	13	BH106004	BH106004	603116014
596	17	10.7	839	13	BH600088	BH600088	OGZAW63TR
c 597	17	10.7	840	29	CG324061	CG324061	OGZAW63TR
c 598	17	10.7	841	29	CC673686	CC673686	OGUJ009TV
c 599	17	10.7	843	11	CH508014	CH508014	Single re
600	17	10.7	845	29	CG933666	CG933666	MEBNA88TF
601	17	10.7	846	14	CB204606	CB204606	AGENCOURT
602	17	10.7	846	29	BX246490	BX246490	Danilo rer
603	17	10.7	848	13	EU927730	EU927730	AGENCOURT
c 604	17	10.7	849	28	AZ669753	AZ669753	ENT193TF
605	17	10.7	855	28	AZ674251	AZ674251	ENT124TR
c 606	17	10.7	855	28	BH688369	BH688369	BOMEB03TR
607	17	10.7	860	28	CC096281	CC096281	CSU-R34.1
608	17	10.7	863	28	AZ667582	AZ667582	ENTHA69TR
609	17	10.7	866	14	CF224086	CF224086	AGENCOURT
610	17	10.7	867	28	AZ532968	AZ532968	ENTC889TR
c 611	17	10.7	873	28	CC102268	CC102268	CH230-238
c 612	17	10.7	882	28	CC102169	CC102169	CSU-R34.1
613	17	10.7	887	29	CC504836	CC504836	CH240_345
c 614	17	10.7	898	28	AZ673635	AZ673635	ENTH667TF
c 615	17	10.7	913	10	BF694306	BF694306	602082946

616	17	10.7	913	28	A0748999	HS_5575_A	673	16	10.1	167	12	BI131490	BI131490 dan98c-09.
c 617	17	10.7	927	29	CC233141	CC2ADT1TV	c 674	16	10.1	168	9	A1866547	A1866547 wmb62b06.x
c 618	17	10.7	931	28	CC237558	CH261-75E	c 675	16	10.1	178	10	BF317792	BF317792 OVI_9_E08
c 619	17	10.7	931	29	CG966260	MBENT25TF	c 676	16	10.1	178	28	BH901284	BH901284 SALX_0742
c 620	17	10.7	936	29	CG324071	OGZAM63TV	c 677	16	10.1	184	13	CO1402	CO1402 HMG500838
c 621	17	10.7	939	29	CG339707	CG339707 OG3AMT4TH	c 678	16	10.1	184	14	F28634	F28634 HSPD17902 H
c 622	17	10.7	941	29	CG312010	OG3AM61TV	c 679	16	10.1	185	14	F34756	F34756 HSPD00057 H
c 623	17	10.7	941	29	CNS02G2G		c 680	16	10.1	185	14	N74083	N74083 HSPD14842 H
c 624	17	10.7	948	28	A25341020		c 681	16	10.1	186	14	F27085	F27085 HSPD14842 H
c 625	17	10.7	963	11	BC040740	Homo sap1	c 682	16	10.1	188	29	CE050730	CE050730 t1gr-gs-s
c 626	17	10.7	964	13	BUI59269		c 683	16	10.1	189	14	F36413	F36413 HSPD14024 H
c 627	17	10.7	986	29	CNS04K48		c 684	16	10.1	191	9	AV107802	AV107802 AV107802
c 628	17	10.7	990	29	CNS04KWL		c 685	16	10.1	192	10	BE116158	BE116158 UI-R-B51-
c 629	17	10.7	996	23	BY711106		c 686	16	10.1	192	10	BF081768	BF081768 PM2-AN008
c 630	17	10.7	996	29	CNS03D7H		c 687	16	10.1	194	9	AA771809	AA771809 a134f06.s
c 631	17	10.7	1001	28	CC283474		c 688	16	10.1	194	13	BU8889904	BU8889904 P027D04_P
c 632	17	10.7	1020	12	BM472044	AGENCOURT	c 689	16	10.1	194	29	CG817985	CG817985 SOYFHO7TH
c 633	17	10.7	1021	29	CNS05BNC		c 690	16	10.1	199	12	BG355027	BG355027 91703 MKR
c 634	17	10.7	1051	29	CNS02OHV		c 691	16	10.1	205	10	BB065169	BB065169 BB065169
c 635	17	10.7	1058	28	CC245840		c 692	16	10.1	205	28	B2117988	B2117988 CH230-523
c 636	17	10.7	1063	28	CC215169		c 693	16	10.1	208	10	AM576285	AM576285 UI-HF-BNO
c 637	17	10.7	1076	28	CC208627	CH261-126	c 694	16	10.1	208	14	W38801	W38801 zb27f03.f1
c 638	17	10.7	1082	12	BM557847		c 695	16	10.1	209	13	CO4293	CO4293 CO4293 Huma
c 639	17	10.7	1088	12	BM450763	AGENCOURT	c 696	16	10.1	210	9	AA094524	AA094524 cp0620.-se
c 640	17	10.7	1091	12	BM477620		c 697	16	10.1	211	10	BB025218	BB025218 BB025218
c 641	17	10.7	1099	14	CDM98364		c 698	16	10.1	212	9	AA093757	AA093757 zn51a02.r
c 642	17	10.7	1101	29	CNS00528		c 699	16	10.1	212	10	BE087679	BE087679 QV1-BT068
c 643	17	10.7	1123	29	CG684199	Drcsoeph11	c 700	16	10.1	212	12	BM898269	BM898269 ph62d12.y
c 644	17	10.7	1124	28	B2219909		c 701	16	10.1	215	10	BE181363	BE181363 CMO-HT063
c 645	17	10.7	1125	28	CC294226	CH230-518	c 702	16	10.1	215	13	BO310475	BO310475 MKR-BT300
c 646	17	10.7	1137	29	CNS04LAB		c 703	16	10.1	215	29	CE029001	CE029001 t1gr-gs-s
c 647	17	10.7	1155	28	CC252734		c 704	16	10.1	218	9	AA137647	AA137647 UI-R-C0-h
c 648	17	10.7	1198	29	AY411728		c 705	16	10.1	218	29	CE376323	CE376323 t1gr-gs-s
c 649	17	10.7	1201	9	AL523872		c 706	16	10.1	219	10	BB060670	BB060670 BB060670
c 650	17	10.7	1458	28	B2574818	meb2_3888	c 707	16	10.1	220	10	BE630035	BE630035 uis9a12.x
c 651	17	10.7	1574	12	BM542661		c 708	16	10.1	221	9	AY232898	AY232898 AV222898
c 652	17	10.7	1799	11	AK011899		c 709	16	10.1	222	14	F23378	F23378 HSPD12394 H
c 653	17	10.7	1853	11	AK082940		c 710	16	10.1	222	28	CC089474	CC089474 CSU-K33f.
c 654	17	10.7	1915	11	AK039342		c 711	16	10.1	226	9	AA107123	AA107123 EST7a_JL
c 655	17	10.7	2362	11	AK041400		c 712	16	10.1	226	13	BU674857	BU674857 UI-CF-ID0
c 656	17	10.7	2595	28	BH770927		c 713	16	10.1	226	14	F30054	F30054 HSPD0306 H
c 657	17	10.7	2735	11	AK016540		c 714	16	10.1	228	9	AA093466	AA093466 KK4677.se
c 658	17	10.7	2936	11	BC034963		c 715	16	10.1	234	9	AA283274	AA283274 TH700 HTC
c 659	17	10.7	3019	11	AK030928		c 716	16	10.1	234	14	F29762	F29762 HSPD19832 H
c 660	17	10.7	3114	11	AK051372		c 717	16	10.1	235	9	AA585361	AA585361 ZTH63 HT
c 661	17	10.7	3241	11	AK051462		c 718	16	10.1	235	28	BH478281	BH478281 BORNKX1TF
c 662	17	10.7	3659	11	AK053093		c 719	16	10.1	236	9	AA190233	AA190233 TH671 HTC
c 663	17	10.7	4301	11	AK030745		c 720	16	10.1	237	9	AA216324	AA216324 hp1119.-se
c 664	16	10.1	97	10	AM198775		c 721	16	10.1	238	10	BE691822	BE691822 uc06c03.x
c 665	16	10.1	107	28	A2217492		c 722	16	10.1	238	28	B2594262	B2594262 SALK_0837
c 666	16	10.1	116	12	BP510848		c 723	16	10.1	239	9	A1802949	A1802949 c158c11.x
c 667	16	10.1	125	14	CM645152		c 724	16	10.1	239	9	AA190222	AA190222 TH53 HTC
c 668	16	10.1	125	14	CF330892		c 725	16	10.1	239	13	CO4671	CO4671 CO4671 Huma
c 669	16	10.1	139	14	CA340996		c 726	16	10.1	240	9	AA224570	AA224570 zt17b09.s
c 670	16	10.1	145	14	F26021		c 727	16	10.1	241	14	N92024	N92024 zt24e11.f1
c 671	16	10.1	150	9	AA190211		c 728	16	10.1	242	9	A1602370	A1602370 UI-R-AA0-
c 672	16	10.1	161	14	N85619		c 729	16	10.1	242	10	BE996179	BE996179 UI-M-BZ1-

730	c	729	16	10.1	243	14	F29289	H	787	16	10.1	284	9	AU275389	AU275389	
731	c	730	16	10.1	243	14	N87284	Huma	c	788	16	10.1	284	10	BB479082	BB479082
732	c	731	16	10.1	245	9	AA190224	THS63	c	789	16	10.1	284	10	BB719469	BB719469
733	c	732	16	10.1	245	14	F22682	HSPD07552	c	790	16	10.1	284	10	BE116685	BE116685
734	c	733	16	10.1	246	9	AA408063	AV408063	c	791	16	10.1	285	9	AI872815	AI872815
735	c	734	16	10.1	246	10	AA316018	AV316018	c	792	16	10.1	286	10	BB024114	BB024114
736	c	735	16	10.1	250	10	AA811071	MR2-ST013	c	793	16	10.1	286	14	N48648	N48648
737	c	736	16	10.1	251	9	AU259063	AU259063	c	794	16	10.1	287	9	AV014782	AV014782
738	c	737	16	10.1	251	10	BB452103	BB452103	c	795	16	10.1	287	10	BB380261	BB380261
739	c	738	16	10.1	251	10	BE222136	BE222136	c	796	16	10.1	287	14	H51387	H51387
740	c	739	16	10.1	252	9	AA725493	AA725493	c	797	16	10.1	288	14	F26057	F26057
741	c	740	16	10.1	252	9	AI225002	AI225002	c	798	16	10.1	289	14	F28844	F28844
742	c	741	16	10.1	252	14	F26301	HSPD13733	c	799	16	10.1	289	29	CE058018	CE058018
743	c	742	16	10.1	252	28	BE222199	BE222199	c	800	16	10.1	291	10	BB351418	BB351418
744	c	743	16	10.1	253	9	AA035493	AA035493	c	801	16	10.1	291	10	F15685	F15685
745	c	744	16	10.1	253	9	AA114712	AA114712	c	802	16	10.1	292	9	AI476147	AI476147
746	c	745	16	10.1	254	10	BB253566	BB253566	c	803	16	10.1	292	9	AJ572039	AJ572039
747	c	746	16	10.1	255	14	N84748	J0759F	c	804	16	10.1	292	10	BB065938	BB065938
748	c	747	16	10.1	257	14	F35135	F35135	c	805	16	10.1	293	10	BB509277	BB509277
749	c	748	16	10.1	259	9	AA093732	AA093732	c	806	16	10.1	293	10	BE934647	BE934647
750	c	749	16	10.1	259	9	AI683803	AI683803	c	807	16	10.1	293	14	F15746	F15746
751	c	750	16	10.1	259	9	AA249667	AA249667	c	808	16	10.1	293	14	F25270	F25270
752	c	751	16	10.1	260	13	C05545	C05545	c	809	16	10.1	293	14	N48853	N48853
753	c	752	16	10.1	262	9	AI383627	AI383627	c	810	16	10.1	294	29	CNS00N7E	CNS00N7E
754	c	753	16	10.1	264	28	AZ820012	AZ820012	c	811	16	10.1	295	9	AJ574500	AJ574500
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756	c	755	16	10.1	265	9	AA912311	AA912311	c	813	16	10.1	295	10	BB245931	BB245931
757	c	756	16	10.1	265	14	CD667588	CD667588	c	814	16	10.1	295	14	F33624	F33624
758	c	757	16	10.1	266	10	BB288358	BB288358	c	815	16	10.1	296	10	BB477900	BB477900
759	c	758	16	10.1	266	10	BB352159	BB352159	c	816	16	10.1	296	14	F33068	F33068
760	c	759	16	10.1	266	12	B0022638	B0022638	c	817	16	10.1	297	9	AA216058	AA216058
761	c	760	16	10.1	268	9	AI967804	AI967804	c	818	16	10.1	298	12	BI044585	BI044585
762	c	761	16	10.1	268	10	BB578655	BB578655	c	819	16	10.1	298	14	F34763	F34763
763	c	762	16	10.1	269	14	N83966	N83966	c	820	16	10.1	299	9	AA256960	AA256960
764	c	763	16	10.1	270	10	AA188720	AA188720	c	821	16	10.1	300	13	C38332	C38332
765	c	764	16	10.1	271	14	F34627	F34627	c	822	16	10.1	300	29	AB082333	AB082333
766	c	765	16	10.1	272	13	C05377	C05377	c	823	16	10.1	301	10	BE715375	BE715375
767	c	766	16	10.1	273	10	BF912336	BF912336	c	824	16	10.1	302	28	AQ094817	AQ094817
768	c	767	16	10.1	273	10	BB288338	BB288338	c	825	16	10.1	303	9	AI863759	AI863759
769	c	768	16	10.1	274	9	AI832283	AI832283	c	826	16	10.1	303	14	F22525	F22525
770	c	769	16	10.1	274	9	AV068342	AV068342	c	827	16	10.1	303	14	N85087	N85087
771	c	770	16	10.1	274	14	F29010	F29010	c	828	16	10.1	303	14	N89723	N89723
772	c	771	16	10.1	275	28	A0543863	A0543863	c	829	16	10.1	304	10	BB256995	BB256995
773	c	772	16	10.1	276	9	AU267574	AU267574	c	830	16	10.1	304	14	F36042	F36042
774	c	773	16	10.1	277	9	AV267719	AV267719	c	831	16	10.1	304	14	F37465	F37465
775	c	774	16	10.1	278	9	AA387665	AA387665	c	832	16	10.1	305	9	AI666365	AI666365
776	c	775	16	10.1	279	10	BB373448	BB373448	c	833	16	10.1	305	9	AV104290	AV104290
777	c	776	16	10.1	280	14	D61811	D61811	c	834	16	10.1	305	10	BF709641	BF709641
778	c	777	16	10.1	281	13	C05528	C05528	c	835	16	10.1	306	9	AV014254	AV014254
779	c	778	16	10.1	281	14	F31107	F31107	c	836	16	10.1	307	9	AI819876	AI819876
780	c	779	16	10.1	281	14	N86266	N86266	c	837	16	10.1	307	10	BB394191	BB394191
781	c	780	16	10.1	281	28	AQ097603	AQ097603	c	838	16	10.1	307	10	BE934598	BE934598
782	c	781	16	10.1	282	9	AI197903	AI197903	c	839	16	10.1	307	12	BC358566	BC358566
783	c	782	16	10.1	282	13	BK082301	BK082301	c	840	16	10.1	307	14	F32154	F32154
784	c	783	16	10.1	282	28	B2186197	B2186197	c	841	16	10.1	307	14	N84876	N84876
785	c	784	16	10.1	283	9	AA093117	AA093117	c	842	16	10.1	309	10	AA517949	AA517949
786	c	785	16	10.1	283	10	AA977710	AA977710	c	843	16	10.1	309	29	CE700415	CE700415

C 844	16	10.1	310	9	AA194302	AA194302 zq04e10.s	C 901	16	10.1	329	13	BY371962	BY371962 BY371962
C 845	16	10.1	310	10	BF092443	BF092443 MR0-TN010	C 902	16	10.1	329	29	CE719358	CE719358 t1gr-gsa-
C 846	16	10.1	311	9	A1077805	A1077805 oy35d02.s	C 903	16	10.1	329	29	CG382997	CG382997 CGC6227H
C 847	16	10.1	311	13	B0536548	B0536548 AGNCCOURT	C 904	16	10.1	329	29	CG383005	CG383005 OGCGE2TV
C 848	16	10.1	312	9	A115590	A115590 ub87d11.r	C 905	16	10.1	330	9	AA1401457	AA1401457 t6q6e10.x
C 849	16	10.1	312	9	AA144499	AA144499 m76e05.r	C 906	16	10.1	330	14	F26664	F26664 HSPD14223.H
C 850	16	10.1	312	9	A165870	A165870 m76e05.y	C 907	16	10.1	331	9	A1264052	A1264052 q105f07.x
C 851	16	10.1	312	10	BB104144	BB104144 BB104144	C 908	16	10.1	331	9	AU276995	AU276995 UI-CF-FNO
C 852	16	10.1	312	12	BI043590	BI043590 PMO-OT021	C 909	16	10.1	331	14	CA314429	CA314429 UI-CF-FNO
C 853	16	10.1	312	13	BQ940185	BQ940185 AGNCCOURT	C 910	16	10.1	333	14	HA61503	HA61503 y660d02.r1
C 854	16	10.1	312	14	F19143	F19143 HSPD03741.H	C 911	16	10.1	334	9	AA129597	AA129597 z112b09.s
C 855	16	10.1	313	14	F27527	F27527 HSPD55500.H	C 912	16	10.1	334	14	T47249	T47249 y664d01.r1
C 856	16	10.1	314	9	AU259559	AU259559 AU259559	C 913	16	10.1	335	12	BG958655	BG958655 PM4-CF080
C 857	16	10.1	314	13	CO3748	CO3748 CO3748.Huma	C 914	16	10.1	335	12	BG955665	BG955665 PM4-CF065
C 858	16	10.1	315	10	AA181377	AA181377 zp42d12.s	C 915	16	10.1	337	9	AA004597	AA004597 z8t7a08.s
C 859	16	10.1	315	10	BB375776	BB375776 BB375776	C 916	16	10.1	337	9	AA004597	AA004597 z8t7a08.s
C 860	16	10.1	315	29	CE792824	CE792824 t1gr-gsa-	C 917	16	10.1	337	10	AA570098	AA570098 n67a08.s
C 861	16	10.1	316	9	AA767883	AA767883 o830h07.s	C 918	16	10.1	337	10	BB137033	BB137033 BB137033
C 862	16	10.1	316	10	BB257391	BB257391 BB257391	C 919	16	10.1	339	9	AA093917	AA093917 c11392.se
C 863	16	10.1	316	10	BB802674	BB802674 BB802674	C 920	16	10.1	339	10	BB085107	BB085107 BB085107
C 864	16	10.1	316	12	BP512976	BP512976 BP512976	C 921	16	10.1	339	10	BB251395	BB251395 BB251395
C 865	16	10.1	316	12	BP513021	BP513021 BP513021	C 922	16	10.1	339	28	AQ070375	AQ070375 HS_3035.B
C 866	16	10.1	316	12	BP513231	BP513231 BP513231	C 923	16	10.1	339	29	BX532507	BX532507 A7rdb1dops
C 867	16	10.1	316	14	R28472	R28472 v950f12.r1	C 924	16	10.1	340	9	AA859365	AA859365 UI-R-EO-c
C 868	16	10.1	316	14	R28472	R28472 v950f12.r1	C 925	16	10.1	340	9	AA092298	AA092298 z1r82f02.r
C 869	16	10.1	317	10	AA820506	AA820506 QV2-ST029	C 926	16	10.1	340	9	AA255766	AA255766 z1r82f02.r
C 870	16	10.1	317	14	F37090	F37090 HSPD53132.H	C 927	16	10.1	340	10	BF360021	BF360021 PM2-MT010
C 871	16	10.1	318	9	A1056346	A1056346 oy46a06.x	C 928	16	10.1	340	10	BG055929	BG055929 n67a08.s
C 872	16	10.1	318	9	AA058311	AA058311 wM18g02.x	C 929	16	10.1	340	10	BE770937	BE770937 RCO-FT007
C 873	16	10.1	318	13	BQ091347	BQ091347 ku16c01.y	C 930	16	10.1	340	13	BY085504	BY085504 B1085504
C 874	16	10.1	318	14	F00187	F00187 HSB67H081.S	C 931	16	10.1	341	14	F21748	F21748 HSPD06337.H
C 875	16	10.1	318	28	BB366406	BB366406 t696g06.b	C 932	16	10.1	342	14	CA930245	CA930245 EST643753
C 876	16	10.1	319	10	BE770923	BE770923 RCO-FT007	C 933	16	10.1	342	28	AQ923423	AQ923423 RPT-23-2
C 877	16	10.1	319	12	BI043561	BI043561 PMO-OT021	C 934	16	10.1	343	12	BI016052	BI016052 PMO-ET025
C 878	16	10.1	319	14	F28646	F28646 HSPD17919.H	C 935	16	10.1	344	10	BF871137	BF871137 CMO-ET012
C 879	16	10.1	320	13	BU717944	BU717944 SUM2BUA04	C 936	16	10.1	344	10	AA561866	AA561866 KOTM13524
C 880	16	10.1	320	14	F29030	F29030 HSPD18718.H	C 937	16	10.1	344	14	F31243	F31243 HSPD22246.H
C 881	16	10.1	321	9	AA211591	AA211591 zn556c04.s	C 938	16	10.1	346	10	BE714899	BE714899 I15-HT073
C 882	16	10.1	321	10	BB098654	BB098654 BB098654	C 939	16	10.1	347	9	AJ572947	AJ572947 PM2-MT010
C 883	16	10.1	321	14	F26467	F26467 HSPD13956.H	C 940	16	10.1	347	10	BF360027	BF360027 PM2-MT010
C 884	16	10.1	322	9	A1420607	A1420607 tF08d12.x	C 941	16	10.1	347	10	BE714925	BE714925 I15-HT073
C 885	16	10.1	322	9	AA176458	AA176458 zp33b06.s	C 942	16	10.1	348	9	AA213908	AA213908 zn57h09.s
C 886	16	10.1	322	10	AA427027	AA427027 62120.MAR	C 943	16	10.1	349	9	AA1742923	AA1742923 n339g03.r
C 887	16	10.1	324	9	AL653369	AL653369 AL653369	C 944	16	10.1	349	9	AA899344	AA899344 UI-R-EO-c
C 888	16	10.1	324	14	CE922451	CE922451 gm7hmw24	C 945	16	10.1	350	10	AA605883	AA605883 MR0-HT024
C 889	16	10.1	324	14	DE0080	DE0080 HUM084F12A	C 946	16	10.1	350	14	CB844639	CB844639 M2PM-0187
C 890	16	10.1	325	10	AAW275645	AAW275645 xp39b08.x	C 947	16	10.1	351	14	T29701	T29701 EST90491.Hu
C 891	16	10.1	325	10	BB101918	BB101918 BB101918	C 948	16	10.1	352	13	BQ668531	BQ668531 Q6014E10.
C 892	16	10.1	325	14	F21882	F21882 HSPD06478.H	C 949	16	10.1	352	28	BZ351429	BZ351429 hm01a11.g
C 893	16	10.1	325	14	F37981	F37981 HSPD07589.H	C 950	16	10.1	353	13	BG810902	BG810902 dm632h11.
C 894	16	10.1	326	10	BB388324	BB388324 BB388324	C 951	16	10.1	353	13	BY632966	BY632966 BY632966
C 895	16	10.1	327	9	AA213317	AA213317 zF92a12.r	C 952	16	10.1	353	14	F24165	F24165 HSPD10239.H
C 896	16	10.1	328	13	CO4265	CO4265 CO4265.x	C 953	16	10.1	354	9	AU039063	AU039063 AU039063
C 897	16	10.1	328	13	CO4265	CO4265 CO4265.Huma	C 954	16	10.1	355	9	AA437904	AA437904 vdz2907.s
C 898	16	10.1	329	9	AA413115	AA413115 v697d04.r	C 955	16	10.1	356	9	AJ572577	AJ572577 AJ572577
C 899	16	10.1	329	10	BB221788	BB221788 7o62f11.x	C 956	16	10.1	356	9	AA184300	AA184300 mt30d01.r
C 900	16	10.1	329	10	BB221788	BB221788 7o62f11.x	C 957	16	10.1	356	9	AA184300	AA184300 mt30d01.r

958	16	10.1	356	9	AV817582	AV817582
959	16	10.1	356	13	BY474878	BY474878
960	16	10.1	356	14	F22132	F22132 HSPD06815 H
961	16	10.1	356	14	F25805	F25805 HSPD13021 H
962	16	10.1	357	9	AA193172	AA193172 zp94q01.s
963	16	10.1	357	12	BM659243	BM659243 RMX602767
964	16	10.1	358	9	AI073804	AI073804 oy69c08.x
965	16	10.1	358	9	AI480855	AI480855 v061911.x
966	16	10.1	358	9	AA192104	AA192104 zq02f09.s
967	16	10.1	358	9	AA194326	AA194326 zq04e10.f
968	16	10.1	358	9	AV648037	AV648037 AV648037
969	16	10.1	359	9	AA501555	AA501555 ne68h02.s
970	16	10.1	359	14	F21208	F21208 HSPD05692.s
971	16	10.1	359	28	AA098517	AA098517 HS_3046.B
972	16	10.1	359	28	AA560854	AA560854 RPCI-23-2
973	16	10.1	360	9	AJ572851	AJ572851 AJ572851
974	16	10.1	361	9	AA482822	AA482822 n748b10.s
975	16	10.1	361	14	F33470	F33470 HSPD26923 H
976	16	10.1	361	14	F33845	F33845 HSPD28150 H
977	16	10.1	362	13	BQ410205	BQ410205 GA_E34002
978	16	10.1	362	14	F24271	F24271 HSPD10416 H
979	16	10.1	363	9	AU257485	AU257485 AU257485
980	16	10.1	363	10	AW379899	AW379899 RC4-HT025
981	16	10.1	363	10	AW658504	AW658504 94572 MAR
982	16	10.1	363	12	BM659309	BM659309 RMX602767
983	16	10.1	363	14	F21375	F21375 HSPD05894 H
984	16	10.1	364	10	BE668328	BE668328 137017 MA
985	16	10.1	364	10	BE770063	BE770063 CM1-FT005
986	16	10.1	364	12	BM273376	BM273376 PFESt0a4
987	16	10.1	364	12	BM659358	BM659358 RMX602767
988	16	10.1	365	9	AI675540	AI675540 wC01507.x
989	16	10.1	365	13	BQ539975	BQ539975 PTM0290
990	16	10.1	367	9	AA873455	AA873455 o169g08.s
991	16	10.1	367	10	BF897149	BF897149 ILO-MT021
992	16	10.1	367	10	BF919308	BF919308 ILO-MT017
993	16	10.1	367	12	BM659313	BM659313 RMX602767
994	16	10.1	368	10	BF575892	BF575892 602132752
995	16	10.1	368	10	BF925591	BF925591 MR2-MT013
996	16	10.1	368	13	BQ334613	BQ334613 ILO-MT021
997	16	10.1	368	13	BQ344283	BQ344283 ILO-MT017
998	16	10.1	368	28	B2116067	B2116067 CH230-460
999	16	10.1	369	9	AJ572211	AJ572211 AJ572211
1000	16	10.1	369	10	BE770071	BE770071 CM1-FT005

Search completed: October 15, 2004, 06:28:09
Job time : 801.134 secs

OM nucleic - nucleic search, using SW model

Run on: October 14, 2004, 09:12:14 ; Search time 816.186 Seconds
(without alignments)
8443.595 Million cell updates/sec

Title: US-09-407-804A-8

Perfect score: 159
Sequence: 1 atggtaaccagaagaattttt.....ccgcatacgcgcgaattata 159

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: +
1: gb_ba: +
2: gb_htg: +
3: gb_in: +
4: gb_cm: +
5: gb_ov: +
6: gb_pat: +
7: gb_ph: +
8: gb_pl: +
9: gb_pr: +
10: gb_ro: +
11: gb_sta: +
12: gb_sy: +
13: gb_un: +
14: gb_vt: +
15: em_da: +
16: em_fun: +
17: em_hum: +
18: em_in: +
19: em_mu: +
20: em_om: +
21: em_or: +
22: em_ov: +
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25: em_pl: +
26: em_ro: +
27: em_sta: +

28: em_un: +
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30: em_htg_hum: +
31: em_htg_inv: +
32: em_htg_other: +
33: em_htg_mus: +
34: em_htg_pin: +
35: em_htg_rnd: +
36: em_htg_mam: +
37: em_htg_vrt: +
38: em_sy: +
39: em_htgo_hum: +
40: em_htgo_mus: +
41: em_htgo_other: +

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	159	100.0	159	6	BD245279
2	159	100.0	159	6	AR368771
3	159	100.0	41708	6	BD245281
4	159	100.0	41708	6	AR368770
5	149.4	94.0	42942	7	AB045978
6	146.2	91.9	42722	7	AF424783
7	143	89.9	346527	1	AF003360
8	52.6	33.1	43081	7	AP001553
9	41.2	25.9	234864	5	BX004819
10	40	25.2	45636	7	AB044554
11	36.8	23.1	3824	6	BD243849
12	36.8	23.1	3824	6	AR435602
13	36.8	23.1	4620	6	AB037782
14	36.8	23.1	4972	6	AX405735
15	36.8	23.1	23943	3	CEC38C6
16	36.8	23.1	87790	9	AC090698
17	36.8	23.1	161198	2	AC015867
18	36.8	23.1	188346	2	AC010189
19	35.8	22.5	149109	2	AC023181
20	35.8	22.5	149252	9	AC066580
21	35.8	22.5	183120	2	AC109770
22	35.8	22.5	207606	9	AC024910
23	35.8	22.5	222542	9	AC022379
24	35.6	22.4	110352	8	AC006220
25	35.2	22.1	60645	2	AC105228
26	35.2	22.1	159874	2	AC113867
27	35.2	22.1	171206	9	AC090946
28	35.2	22.1	179723	9	AC087858
29	35.2	22.1	196519	2	AC133761
30	34.8	21.9	155290	2	AL359175
31	34.8	21.9	166055	2	AC013552
32	34.8	21.9	174646	5	AL929151
33	34.6	21.8	105842	9	AC107387

34 34.4 21.6 162413 9 AC091530 AC091530 Papiu anu
35 34.4 21.6 182069 10 AL662829 AL662829 Mouse DNA
36 34.4 21.6 261322 2 AC095985 AC095985 Mus muscu
37 34.2 21.5 230603 2 AC120635 AC120635 Rattus no
38 34.2 21.5 246778 2 AC097961 AC097961 Rattus no
39 34 21.4 11622 6 AX345576 AX345576 Sequence
40 34 21.4 259474 2 AC095692 AC095692 Rattus no
41 33.8 21.3 106100 2 AC138099 AC138099 Mus muscu
42 33.8 21.3 176201 2 AC095629 AC095629 Mus muscu
43 33.8 21.3 196140 10 AL672150 AL672150 Mouse DNA
44 33.6 21.1 64799 5 AL732411 AL732411 Zebrafish
45 33.6 21.1 87235 2 AC022963 AC022963 Homo sapi

ALIGNMENTS

RESULT 1
BD245279 159 bp DNA linear PAT 17-JUL-2003
LOCUS BD245279
DEFINITION Development of novel antibiotics based on bacteriophage genomics.
ACCESSION BD245279.1 GI:33055049
VERSION JP 2002531107-A/14.
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 159)
AUTHORS Polletier,J., Gros,P. and Dubow,M.
TITLE Development of novel antibiotics based on bacteriophage genomics
JOURNAL Patent: JP 2002531107-A 14 24-SEP-2002;
PUBTECH INC
OS Staphylococcus aureus bacteriophage 77
PN JP 2002531107-A/14
PD 24-SEP-2002
PR 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR
01-DEC-1999 US 60/168777,02-DEC-1999 US 09/434252 P1 JERRY
PELLETIER,PHILIPPE GROS,MICHAEL DUBOW
PC C12N15/09,A01N63/00,A61K45/00,A61P31/04,C07K14/005,
PC C12N15/00,
PC C12N15/21,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/566, PC
C12N15/00,
PC A61K37/02
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FT aureus bacteriophage 77',
FT Location/Qualifiers
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source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.8e-38;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 CTGATGATGAGGACAGGGGATGAATAGTTGTACAGCTATTATCCAAAACTT 120
DB 61 CTGATGATGAGGACAGGGGATGAATAGTTGTACAGCTATTATCCAAAACTT 120
QY 121 GCAGAACGTGATACAGCCCGCTATGTCGAAATATTA 159
DB 121 GCAGAACGTGATACAGCCCGCTATGTCGAAATATTA 159

RESULT 2
AR368771 159 bp DNA linear PAT 12-SEP-2003
LOCUS AR368771
DEFINITION Sequence 4 from patent US 6376652.
ACCESSION AR368771
VERSION AR368771.1 GI:34603078
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 159)
AUTHORS Polletier,J., Gros,P. and Dubow,M.
TITLE Compositions and methods involving an essential Staphylococcus
JOURNAL aureus gene and its encoded protein
Patent: US 6376652-A 4 23-Apr-2002;
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source Location/Qualifiers
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/organism="unknown"
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ORIGIN
Query Match 100.0%; Score 159; DB 6; Length 159;
Best Local Similarity 100.0%; Pred. No. 2.8e-38;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 ATGGTACCAAGATTTTAAAACTGAAGTTCAGATATGTAAGCTCAGAA 60
QY 61 CTGATGATGAGGACAGGGGATGAATAGTTGTACAGCTATTATCCAAAACTT 120
DB 61 CTGATGATGAGGACAGGGGATGAATAGTTGTACAGCTATTATCCAAAACTT 120
QY 121 GCAGAACGTGATACAGCCCGCTATGTCGAAATATTA 159
DB 121 GCAGAACGTGATACAGCCCGCTATGTCGAAATATTA 159

RESULT 3

BD245281 41708 bp DNA linear PAT 17-JUL-2003
LOCUS BD245281
DEFINITION Development of novel antibiotics based on bacteriophage genomics.
ACCESSION BD245281
VERSION BD245281.1 GI:33055051
KEYWORDS JP 2002531107-A/16.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 41708)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Development of novel antibiotics based on bacteriophage genomics
JOURNAL Patent: JP 2002531107-A 16 24-SEP-2002;
PHARTECH INC
COMMENT OS Staphylococcus aureus bacteriophage 77
PN JP 2002531107-A/16
PD 24-SEP-2002
PF 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR
01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454252 P1 JERRY
PELLETIER,PHILLIPE GROS,MICHAEL DUBOW
PC C12N15/09,A01N63/00,A61K45/00,A61P31/04,C07K14/005,
PC C12N1/00,
PC C12N1/21,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/566, PC
C12N15/00,
PC A61K37/02
CC Genome Sequence
FH Key Location/Qualifiers
FT source 1..41708
FT aureus bacteriophage 77' /organism='Staphylococcus
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source Location/Qualifiers
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/organism="unidentified"
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/db_xref="taxon:32644"
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Best Local Similarity 100.0%; Pred. No. 5e-38;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 34393 ATGGTAAACCAAGAAATTTTAAAACTAACTTGAGGTTCAGATATGTAAGCTCAGAAA 34452
QY 61 CTCATGATGAGGACGAGGCGCATGAATAATAGGTTGTACGACCTATTATCAAAAAAATT 120
DB 34453 CTCATGATGAGGACGAGGCGCATGAATAATAGGTTGTACGACCTATTATCAAAAAAATT 34512
QY 121 GCAGAACGTCTATACACGCCGCCCTATGTCGAATATTAA 159
DB 34513 GCAGAACGTCTATACACGCCGCCCTATGTCGAATATTAA 34551

RESULT 4
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LOCUS AR368770
DEFINITION Sequence 3 from patent US 6376652.
ACCESSION AR368770
VERSION AR368770.1 GI:34603077
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 41708)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Compositions and methods involving an essential Staphylococcus
aureus gene and its encoded protein
JOURNAL Patent: US 6376652-A 3 23-Apr-2002;
FEATURES
source Location/Qualifiers
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/organism="unknown"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 5e-38;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTAAACCAAGAAATTTTAAAACTAACTTGAGGTTCAGATATGTAAGCTCAGAAA 60
DB 34393 ATGGTAAACCAAGAAATTTTAAAACTAACTTGAGGTTCAGATATGTAAGCTCAGAAA 34452
QY 61 CTCATGATGAGGACGAGGCGCATGAATAATAGGTTGTACGACCTATTATCAAAAAAATT 120
DB 34453 CTCATGATGAGGACGAGGCGCATGAATAATAGGTTGTACGACCTATTATCAAAAAAATT 34512
QY 121 GCAGAACGTCTATACACGCCGCCCTATGTCGAATATTAA 159
DB 34513 GCAGAACGTCTATACACGCCGCCCTATGTCGAATATTAA 34551
RESULT 5
AB045978 42942 bp DNA linear PHG 26-MAY-2001
LOCUS AB045978
DEFINITION Staphylococcus aureus temperate phage phIS1T genomic DNA, complete
sequence.
ACCESSION AB045978
VERSION AB045978.1 GI:12697822
KEYWORDS
SOURCE Staphylococcus aureus temperate phage phIS1T
ORGANISM Staphylococcus aureus temperate phage phIS1T
REFERENCE 1 (sites)
AUTHORS Naito,S., Kaneko,J., Chiba,J., Plémont,Y., Jarraud,S., Etienne,J.
and Kamio,Y.
TITLE Phage conversion of Pantone-Valentine leukocidin in Staphylococcus
aureus: molecular analysis of a PVL-converting phage, phIS1T
JOURNAL Gene 268 (1-2), 195-206 (2001)
MEDLINE 21261956
PUBMED 11368915

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Best Local Similarity 96.2%; Pred. No. 4,66-35;
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QY 61 CTCATAGTAGGACGACGAGGCGATGAATAAGTTGTACGACCTATTATCCAAAACTT 120
DB 11958 CTCATAGTAGGACGACGAGGCGATGAATAAGTTATAGACTATTATCCAAAACTT 12017
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DB 12018 GCAGAACTCATACACGCCCGCTATGTCGAAATATA 12056

Search completed: October 14, 2004, 16:00:35
Job time : 819.186 secs

OM nucleic - nucleic search, using aw model

Run on: October 14, 2004, 07:30:59 / Search time 106 Seconds
(without alignments)
6372.297 Million cell updates/sec

Title: US-09-407-804A-8

Perfect score: 159
Sequence: 1 atgttaacacaaagaattttt.....ccgcatacgcgaattttta 159

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

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7:	geneeqn2003as:*
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10:	geneeqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	159	100.0	159	AAA68252	Aa68252 Bacterioph
2	159	100.0	159	AAC86107	Aa86107 Bacterioph
3	159	100.0	41708	AAA68247	Aa68247 Bacterioph
4	159	100.0	41708	AAC86106	Aa86106 Complete
5	144.6	90.9	1134	2 AAT83989	Aa83989 DNA encod
6	36.8	23.1	1401	5 ABA19641	Ab19641 Human ner
7	36.8	23.1	1401	5 ABA19640	Ab19640 Human ner

8	36.8	23.1	1401	5	ABA19639	Ab19639 Human ner
9	36.8	23.1	2023	3	AAC76979	Aa76979 Human ORF
10	36.8	23.1	3824	2	AA240489	Aa240489 Human SUL
11	36.8	23.1	4535	8	AA162250	AA162250 Human TAO
12	36.8	23.1	4536	8	AA162249	AA162249 Human TAO
13	36.8	23.1	4620	7	ACC50205	Acc50205 Breast ca
14	36.8	23.1	4620	8	AA162248	AA162248 Human TAO
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17	35.2	22.1	290	2	AA606038	AA606038 Human e11
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20	33.4	21.0	2946	2	AAV34005	Aav34005 Human Rab
21	33.4	21.0	3389	4	AAH17587	Aah17587 Human c1N
22	33.4	21.0	3635	6	AB164076	Ab164076 Breast ca
23	33.4	21.0	4455	4	AAH99544	Aah99544 Human pro
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25	33.4	21.0	7327	5	ABV21859	Abv21859 Human pro
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27	33	20.8	110000	7	ABQ84281_1	Abq84281_1 of
28	32	20.1	110000	2	AAV21209_04	AAV21209_04 of
29	31.8	20.0	18888	6	ABQ75562	Abq75562 Human rel
30	31.6	19.9	1835	3	AA63914	Aa63914 Cucumbe
31	31.4	19.7	199377	9	ADC35071	Adc35071 Mouse gen
32	31.2	19.6	21580	8	ABT44140	Abt44140 Human nuc
33	30.6	19.2	948	7	ACF68708	Acf68708 Phototrab
34	30.6	19.2	110000	7	ACF67367_14	ACF67367_14 of
35	30.6	19.2	249878	7	ACF65381_1	ACF65381 Phototrab
36	30.4	19.1	3150	2	AAV74654	Aav74654 Stephyloc
37	30.4	19.1	3730	7	ADH89879	Adh89879 Stephyloc
38	30.2	19.0	3570	9	ADC35141	Adc35141 Human bre
39	30.2	19.0	3872	2	AAK39630	Aak39630 Breast ca
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44	29.8	18.7	8603	6	AB132534	Ab132534 Human imm
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ALIGNMENTS

RESULT 1
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ID AAA68252 standard; DNA; 159 BP.
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XX AC AAA68252;
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DT 15-SEP-2003 (revised)
DT 06-AUG-2003 (revised)
DT 27-OCT-2000 (first entry)
DE
DE Bacteriophage 77 770RF104 nucleotide sequence.
XX
XX Bacteriophage; antimicrobial; genome; identification; antibacterial;
RW Bacterial growth inhibition; bacterial infection; ds.
RW

XX Staphylococcus aureus; bacteriophage 77.
 OS WO200032825-A2.
 PN 08-JUN-2000.
 PD 03-DEC-1999; 99WO-1B002040.
 PF 03-DEC-1998; 98US-0110992P.
 PR 03-JUN-1999; 99US-00326144.
 PR 28-SEP-1999; 99US-00407804.
 PR 30-SEP-1999; 99US-0157218P.
 PR 01-DEC-1999; 99US-0168777P.
 PR 02-DEC-1999; 99US-00454252.
 XX (PHAG-) PHAGETECH INC.
 PA Polletier J, Gros P, Dubow M;
 PI WPI, 2000-412361/35.
 DR P-PSDB; AAB16527.
 XX
 XX Identifying a bacteriophage coding region for treating bacterial
 PT infections comprises identifying a nucleic acid encoding a product that
 PT inhibits bacteria when a bacteriophage infects a bacterium.
 XX
 PS Diagnostics; Page 162; 456pp; English.
 XX
 CC The present invention describes a method for identifying a bacteriophage
 CC coding region encoding a product active on an essential bacterial target.
 CC The method comprises identifying a nucleic acid sequence encoding a gene
 CC product that provides a bacteria-inhibiting function when an
 CC uncharacterised bacteriophage infects a pathogenic bacterium. The
 CC compound active on a target of a bacteriophage inhibitor protein in a
 CC bacteria is used to treat or prevent a bacterial infection in an animal.
 CC AAB6243 to AAB69442 and AAB16523 to AAB16954 represent bacteriophage
 CC nucleotide and protein sequences which are used in the exemplification of
 CC the present invention. (Updated on 06-AUG-2003 to correct OS field.)
 CC (Updated on 13-SEP-2003 to standardise OS field)
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 Best Local Similarity 100.0%; Pred. No. 1.2e-41;
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 61 CTGATAGATGAGGCACAGGCGCATGAAATAGGTGTGACGACTATTATCAAAAACTT 120
 QY 121 GCAGAACTCATACAGCCCGCGCTATGCTGAATATTAA 159
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 ID AAC86107 standard; cDNA; 159 BP.
 AC AAC86107;
 AC 06-AUG-2003 (revised)
 DT 29-AUG-2001 (first entry)
 XX
 DE Bacteriophage 77 ORF 104.
 XX
 KW DnaI; S. aureus; inhibitor; bacteriophage 77; ORF 104; phage 77ORF104;
 KW screening assay; ss.
 XX
 OS Bacteriophage.
 PN WO200146383-A2.
 PD 28-JUN-2001.
 PF 21-DEC-2000; 2000WO-US035180.
 PR 22-DEC-1999; 99US-00470512.
 PR 12-OCT-2000; 2000US-00689952.
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 PA (PHAG-) PHAGETECH INC.
 PA (WILLIAMS K M.
 PI Polletier J, Gros P, Dubow M;
 DR WPI; 2001-418052/44.
 DR P-PSDB; AAB47318.
 XX
 PT Novel DnaI polypeptides useful for treating and diagnosing microbial,
 PT preferably bacterial, diseases such as those caused by Staphylococcus
 PT aureus.
 XX
 PS Example 1; Fig 4; 107pp; English.
 XX
 CC This sequence represents open reading frame (ORF) 104 of Bacteriophage
 CC 77. The growth inhibitory gene product of ORF 104 interacts with DnaI
 CC derived from S. aureus, to form the basis of a screening assay. DnaI
 CC polypeptides and polynucleotides are useful for treating microbial,
 CC preferably bacterial, especially staphylococcal, infections. DnaI
 CC polypeptides and polynucleotides are useful for biological, diagnostic,
 CC prophylactic, clinical and therapeutic use, and as components in
 CC databases useful for search analyses as well as in sequence analysis
 CC algorithms. (Updated on 06-AUG-2003 to correct OS field.)
 CC
 XX Sequence 159 BP; 58 A; 31 C; 30 G; 40 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 159; DB 4; Length 159;
 Best Local Similarity 100.0%; Pred. No. 1.2e-41;
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTAACCAAGATTTTAAAACTTGTGATGTGATATGTACCTCAGAA 60
DB 1 ATGTTAACCAAGATTTTAAAACTTGTGATGTGATATGTACCTCAGAA 60
QY 61 CTCTATGATGAGGACAGGGCGATGAAATAGTTGTAGACCTATTATCCAAAACCT 120
DB 61 CTCTATGATGAGGACAGGGCGATGAAATAGTTGTAGACCTATTATCCAAAACCT 120
QY 121 GCAGAACGTCTATACAGCCGCCCTATCGTCGAAATTTAA 159
DB 121 GCAGAACGTCTATACAGCCGCCCTATCGTCGAAATTTAA 159
RESULT 3
AAA68247
ID AAA68247 standard; DNA; 41708 BP.
XX
AC AAA68247;
XX
DT 15-SEP-2003 (revised)
DT 06-AUG-2003 (revised)
DT 27-OCT-2000 (first entry)
XX
DE Bacteriophage 77 complete genome sequence.
XX
KW Bacteriophage; antimicrobial; genome; identification; antibacterial;
KW bacterial growth inhibition; bacterial infection; ds.
XX
OS Stephylococcus aureus; bacteriophage 77.
XX
PN WO200032825-A2.
XX
PD 08-JUN-2000.
XX
PF 03-DEC-1999; 99WC-1B002040.
XX
PR 03-DEC-1998; 98US-0110992P.
PR 03-JUN-1999; 99US-00326144.
PR 28-SEP-1999; 99US-00407804.
PR 30-SEP-1999; 99US-0157218P.
PR 01-DEC-1999; 99US-0168777P.
PR 02-DEC-1999; 99US-00454252.
XX
PA (PHAG-) PHAGETECH INC.
XX
PI Pelletier J, Gros P, Dubow M;
XX
DR WPI; 2000-412361/35.
XX
PT Identifying a bacteriophage coding region for treating bacterial
PT infections comprises identifying a nucleic acid encoding a product that
PT inhibits bacteria when a bacteriophage infects a bacterium.
XX
PS Example 3; Page 141-151; 456pp; English.
XX
CC The present invention describes a method for identifying a bacteriophage

CC coding region encoding a product active on an essential bacterial target.
CC The method comprises identifying a nucleic acid sequence encoding a gene
CC product that provides a bacteria-inhibiting function when an
CC uncharacterised bacteriophage infects a pathogenic bacterium. The
CC compound active on a target of a bacteriophage inhibitor protein in a
CC bacteria is used to treat or prevent a bacterial infection in an animal.
CC AAA68243 to AAA69442 and ABB16923 to ABB16994 represent bacteriophage
CC nucleotide and protein sequences which are used in the exemplification of
CC the present invention. (Updated on 06-AUG-2003 to correct OS field.)
CC (Updated on 15-SEP-2003 to standardise OS field)
XX
SQ Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 U; 0 Other;
Query Match 100.0%; Score 159; DB 3; Length 41708;
Best Local Similarity 100.0%; Pred. No. 6, 6e-41;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTTAACCAAGATTTTAAAACTTGTGATGTGATATGTACCTCAGAA 60
DB 34393 ATGTTAACCAAGATTTTAAAACTTGTGATGTGATATGTACCTCAGAA 34452
QY 61 CTCTATGATGAGGACAGGGCGATGAAATAGTTGTAGACCTATTATCCAAAACCT 120
DB 34453 CTCTATGATGAGGACAGGGCGATGAAATAGTTGTAGACCTATTATCCAAAACCT 34512
QY 121 GCAGAACGTCTATACAGCCGCCCTATCGTCGAAATTTAA 159
DB 34513 GCAGAACGTCTATACAGCCGCCCTATCGTCGAAATTTAA 34551
RESULT 4
AAC86106
ID AAC86106 standard; cDNA; 41708 BP.
XX
AC AAC86106;
XX
DT 06-AUG-2003 (revised)
DT 29-AUG-2001 (first entry)
XX
DE Complete genome of bacteriophage 77.
XX
KW Draft S. aureus; inhibitor; bacteriophage 77; ORF 104; phage 77ORF104;
KW screening assay; ss.
XX
OS Bacteriophage.
XX
OS
XX
PN WO200146383-A2.
XX
PD 28-JUN-2001.
XX
PF 21-DEC-2000; 2000WO-US035180.
PF 22-DEC-1999; 99US-00470512.
PR 12-OCT-2000; 2000US-00689952.
XX
PA (PHAG-) PHAGETECH INC.
PA (WILLI) WILLIAMS K M.

XX Polletier J, Groe P, Dubow M;
XX WPI; 2001-418052/44.
XX Novel DnaI polypeptides useful for treating and diagnosing microbial,
XX preferably bacterial, diseases such as those caused by Staphylococcus
XX aureus.
XX Disclosure; Fig 2; 107pp; English.
XX This sequence represents the genome of Bacteriophage 77. The growth
XX inhibitory gene product of ORF 104 interacts with DnaI derived from S.
XX aureus, to form the basis of a screening assay. DnaI polypeptides and
XX polynucleotides are useful for treating microbial, preferably bacterial,
XX especially Staphylococcal, infections. DnaI polypeptides and
XX polynucleotides are useful for biological, diagnostic, prophylactic,
XX clinical and therapeutic use, and as components in databases useful for
XX search analyses as well as in sequence analysis algorithms. (updated on
XX 06-AUG-2003 to correct OS field.)
SQ Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 U; 0 Other;
Query Match 100.0%; Score 159; DB 4; Length 41708;
Best Local Similarity 100.0%; Pred. No. 6, 6e-41;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTAACCAAGATTATTTAACTAACTGAGTGTGAGATATGTAGCTCAGAA 60
DB 34393 ATGGTAACCAAGATTATTTAACTAACTGAGTGTGAGATATGTAGCTCAGAA 34452
QY 61 CTCATGATGAGGCGACAGGCGCATGAAATAGTGTGACACCTATTATCCAAAACCT 120
DB 34453 CTCATGATGAGGCGACAGGCGCATGAAATAGTGTGACACCTATTATCCAAAACCT 34512
QY 121 GCAGAACTCATACACGCCCGCTATGTCGAATATTAA 159
DB 34513 GCAGAACTCATACACGCCCGCTATGTCGAATATTAA 34551
RESULT 5
AAT83989
ID AAT83989 standard; DNA; 1134 BP.
XX
AC AAT83989;
DT 27-AUG-1998 (first entry)
XX
XX DNA encoding a Staphylococcus aureus protein of unknown function.
XX
XX Staphylococcus aureus protein; ribozyme; antisense sequence; control;
XX Staphylococcal gene; regulatory element; bacterial gene expression;
XX Staphylococcal infection; food poisoning; scaled skin syndrome;
XX toxic shock syndrome; ss.
XX
XX Staphylococcus aureus.
XX

FH Key Location/Qualifiers
FT CDS 593..946
FT /*tag= a
XX
XX WO9730070-A1.
XX
XX 21-AUG-1997.
XX
XX 19-FEB-1997; 97WO-US002318.
XX
XX 20-FEB-1996; 96US-001188BP.
XX
XX (SMK) SMITHKLINE BEECHAM CORP.
XX
XX Black MT, Burnham MK, Hodgson JE, Knowles DJC, Nicholas RO;
XX Platt JM, Reichard RW, Rosenberg M, Ward JW;
XX WPI; 1997-424969/39.
XX P-PSDB; AAW28036.
XX
XX Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 - used to
XX isolate antimicrobial compounds, and in vaccines against S. aureus
XX infection.
XX
XX Claim 9; Page 797; 989pp; English.
XX
XX The present sequence encodes a Staphylococcus aureus protein of unknown
XX function. The present sequence was isolated from a library of clones of
XX S. aureus WCUH 29 in Escherichia coli. The DNA sequence can be used in
XX the construction of ribozymes and antisense sequences to control the
XX expression of Staphylococcal genes. The DNA sequence is also useful as a
XX source of regulatory elements for the control of bacterial gene
XX expression. The encoded protein may be used to produce vaccines to enable
XX a host to produce specific antibodies with antibacterial action. These
XX vaccines and antibodies would protect a host against invasion by S.
XX Staphylococcal food poisoning, scaled skin syndrome, and toxic shock
XX syndrome
XX
SQ Sequence 1134 BP; 407 A; 179 C; 247 G; 290 T; 0 U; 11 Other;
Query Match 90.9%; Score 144.6; DB 2; Length 1134;
Best Local Similarity 94.3%; Pred. No. 1e-36; 9; Indels 0; Gaps 0;
Matches 150; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 ATGGTAACCAAGATTATTTAACTAACTGAGTGTGAGATATGTAGCTCAGAA 60
DB 5 ATGGTAACCAAGATTATTTAACTAACTGAGTGTGAGATATGTAGCTCAGAA 64
QY 61 CTCATGATGAGGCGACAGGCGCATGAAATAGTGTGACACCTATTATCCAAAACCT 120
DB 65 CTCATGATGAGGCGACAGGCGCATGAAATAGTGTGACACCTATTATCCAAAACCT 124
QY 121 GCAGAACTCATACACGCCCGCTATGTCGAATATTAA 159
DB 125 GCAGAACTCATACACGCCCGCTATGTCGAATATTAA 163

Search completed: October 14, 2004, 12:48:19
Job time : 108 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 14, 2004, 12:03:47 ; Search time 742.638 Seconds
(without alignments)
6393.544 Million cell updates/sec

Title: US-09-407-804A-8

Perfect score: 139
Sequence: 1 atggtaccacaaagaatttt.....ccgcatacgcgaataataa 139

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : ESR:*

1:	em_estba:*
2:	em_esthum:*
3:	em_estlin:*
4:	em_estnu:*
5:	em_estov:*
6:	em_estpl:*
7:	em_estro:*
8:	em_hnc:*
9:	gb_est1:*
10:	gb_est2:*
11:	gb_hic:*
12:	gb_est3:*
13:	gb_est4:*
14:	gb_est5:*
15:	em_estfun:*
16:	em_estcom:*
17:	em_gss_hum:*
18:	em_gss_inv:*
19:	em_gss_pin:*
20:	em_gss_vrt:*
21:	em_gss_fun:*
22:	em_gss_mam:*
23:	em_gss_nus:*
24:	em_gss_pro:*
25:	em_gss_rtd:*
26:	em_gss_phg:*
27:	em_gss_vpl:*

28: gb_ges1:++
29: gb_ges2:++

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
c 1	38	23.9	913	29	CG112425	CG112425 PUPV31TD
c 2	36.8	23.1	398	9	AA812069	AA812069 ob75b07.s
c 3	36.8	23.1	399	9	AA426563	AA426563 zw02904.s
c 4	36.8	23.1	545	13	BUS32303	BUS32303 AGENCOURT
c 5	36.8	23.1	628	12	BG938678	BG938678 cn27f10.x
c 6	36.8	23.1	974	10	BF794164	BF794164 602255543
c 7	35.6	22.4	704	12	BG169535	BG169535 602321355
c 8	35.2	22.1	290	14	M86125	M86125 EST02651 Fe
c 9	35.2	22.1	564	28	AQ372904	AQ372904 RPrC11-15
c 10	35.2	22.1	708	11	AY067269	AY067269 Schmidttea
c 11	35.2	22.1	716	14	CB172558	CB172558 UMJ603014
c 12	35	22.0	418	13	BQ457264	BQ457264 ke37a01.Y
c 13	34.4	21.6	937	11	AK039507	AK039507 Mus muscu
c 14	34.4	21.6	979	28	CC190084	CC190084 CH261-958
c 15	34.4	21.6	1051	28	CC243328	CC243328 CH261-120
c 16	34.2	21.5	277	9	AA684791	AA684791 EST105419
c 17	33.8	21.3	1128	9	AL514043	AL514043 AL514043
c 18	33.6	21.1	535	28	B2187708	B2187708 CH230-435
c 19	33.4	21.1	792	28	BH980133	BH980133 odg45a04
c 20	33.4	21.0	328	10	AW903175	AW903175 CM4-NN102
c 21	33.4	21.0	346	10	BE812146	BE812146 RCO-AM004
c 22	33.4	21.0	352	29	CE699981	CE699981 t1gr-9s-
c 23	33.4	21.0	364	9	AJ430442	AJ430442 AJ430442
c 24	33.4	21.0	510	9	AI940791	AI940791 CM0-ST005
c 25	33.4	21.0	572	9	AI940804	AI940804 CM0-ST005
c 26	33.4	21.0	659	9	AU137533	AU137533 AU137533
c 27	33.4	21.0	684	12	BH015272	BH015272 603641411
c 28	33.4	21.0	869	13	BUI54160	BUI54160 AGENCOURT
c 29	33.4	21.0	881	28	B2068209	B2068209 1kh85d09.
c 30	33.4	21.0	969	28	CC239125	CC239125 CH261-664
c 31	33.4	21.0	1038	28	CC215035	CC215035 CH261-189
c 32	33.4	21.0	1090	28	CC218385	CC218385 CH261-371
c 33	33.4	21.0	1094	12	BH465386	BH465386 AGENCOURT
c 34	33.4	21.0	2868	29	AY412813	AY412813 Pan trogl
c 35	33.4	21.0	2928	29	AY412812	AY412812 Homo sapi
c 36	33.2	20.9	856	29	CNS02PPI	AL208287 Tetrarodon
c 37	33.2	20.9	989	28	CC392353	CC392353 PUNRKS6TB
c 38	32.8	20.6	602	14	CH105217	CH105217 I077P84.5
c 39	32.8	20.6	633	28	BH081489	BH081489 RPrC1-24-3
c 40	32.8	20.6	661	10	BB626448	BB626448 BB626448
c 41	32.8	20.6	686	10	BB189020	BB189020 BB189020
c 42	32.8	20.6	711	28	B2686533	B2686533 PUBCA42TD
c 43	32.8	20.6	853	28	CC378784	CC378784 PUNNDB2TD
c 44	32.8	20.6	2976	11	AK079101	AK079101 Mus muscu
c 45	32.6	20.5	518	28	AQ251087	AQ251087 F18F12-SP

Search completed: October 14, 2004, 18:55:20
Job time : 746.638 secs

OM nucleic - nucleic search, using sw model

Run on: October 14, 2004, 19:00:14 / Search time 1524.71 Seconds

(without alignments)
8442.862 Million cell updates/sec

Title: US-09-407-804A-9

Perfect score: 297
Sequence: 1 atgttcacatataaacgaaa.....actatgcacgaatgtag 297

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 2167151695 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenBdl: +
1: gb_ba: +
2: gb_hg: +
3: gb_lm: +
4: gb_cm: +
5: gb_ov: +
6: gb_pat: +
7: gb_ph: +
8: gb_pl: +
9: gb_pr: +
10: gb_ro: +
11: gb_sy: +
12: gb_vl: +
13: gb_un: +
14: gb_vt: +
15: em_da: +
16: em_fun: +
17: em_hum: +
18: em_lm: +
19: em_mu: +
20: em_ov: +
21: em_or: +
22: em_ov: +
23: em_pat: +
24: em_ph: +
25: em_pl: +
26: em_ro: +
27: em_sy: +

28: em_un: +
29: em_vl: +
30: em_hg_hum: +
31: em_hg_inv: +
32: em_hg_other: +
33: em_hg_mus: +
34: em_hg_pln: +
35: em_hg_rod: +
36: em_hg_mam: +
37: em_hg_vrt: +
38: em_sy: +
39: em_hgco_hum: +
40: em_hgco_mus: +
41: em_hgco_other: +

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	297	100.0	297	6	BD245280
2	297	100.0	41708	6	BD245281
3	297	100.0	41708	6	AR368770
4	261	87.9	261	6	BD245277
5	183	61.6	45636	7	AB044554
6	181	60.9	348527	1	AP003360
7	172	57.9	41401	7	AB009866
8	161	54.2	42942	7	AB045978
9	133	44.8	43081	7	AP001553
10	39	13.1	291150	1	AP003135
11	29	9.8	267	6	AX618246
12	29	9.8	42722	7	AF424783
13	29	9.8	272850	1	AP004828
14	28	9.4	580	6	AR355085
15	28	9.4	43594	6	BD245634
16	28	9.4	43604	7	AF424781
17	27	9.1	348650	1	AP003364
18	25	8.4	258	6	AX618548
19	21	7.1	190220	5	AL935305
20	20	6.7	163899	2	AC073060
21	20	6.7	168459	5	AL772289
22	20	6.7	177517	2	AC140389
23	20	6.7	241347	2	AC096352
24	20	6.7	241679	2	AC020861
25	20	6.7	257471	2	AC139675
26	20	6.7	267943	2	AC136702
27	19	6.4	237	6	AR383649
28	19	6.4	480	8	RID428847
29	19	6.4	991	6	A26050
30	19	6.4	991	6	166499
31	19	6.4	7037	6	AX346653
32	19	6.4	10408	6	166486
33	19	6.4	10408	6	166487

34	19	6.4	17309	9	AC130709	Homo sapi	c	91	18	6.1	836	11	EV051957	EV051957 S21296049
35	19	6.4	46024	2	AC100659	Mus muscu	c	92	18	6.1	1880	5	BC052972	BC052972 Dantio rer
36	19	6.4	64167	9	HSBA89B2	Al080245 Human DNA	c	93	18	6.1	2000	6	AX510142	AX510142 Sequence
37	19	6.4	82700	2	AC015635	Al015635 Homo sapi	c	94	18	6.1	2000	6	AX596276	AX596276 Sequence
38	19	6.4	93476	2	AC112352_3	Continuation (4 of	c	95	18	6.1	2000	6	AX820574	AX820574 Sequence
39	19	6.4	93476	2	AC112352_3	Continuation (4 of	c	96	18	6.1	2000	6	AX831604	AX831604 Sequence
40	19	6.4	106253	8	AP003815	Oryza sat	c	97	18	6.1	3486	8	AK121411	AK121411 Oryza sat
41	19	6.4	110000	2	AC096457_1	Continuation (2 of	c	98	18	6.1	3542	8	SCYDL149W	SCYDL149W
42	19	6.4	110000	2	AC096457_2	Continuation (3 of	c	99	18	6.1	4307	9	HSTYL	HSTYL
43	19	6.4	134308	9	AC011488	Al121959 Human DNA	c	100	18	6.1	5958	6	AX797908	AX797908
44	19	6.4	136377	9	HSBJ76N10	Al121959 Human DNA	c	101	18	6.1	7699	6	AL603626	AL603626
45	19	6.4	139629	2	AP003809	Oryza sat	c	102	18	6.1	11859	4	AC144695	AC144695
46	19	6.4	139648	2	AP004335	Oryza sat	c	103	18	6.1	23096	8	SCIV23	SCIV23
47	19	6.4	145476	2	AC044911	AP004335 Oryza sat	c	104	18	6.1	29885	8	AC093679	AC093679
48	19	6.4	147638	8	AP003303	AP003303 Oryza sat	c	105	18	6.1	33099	6	AX059508	AX059508
49	19	6.4	152046	2	AC101763	AP005204 Homo sapi	c	106	18	6.1	37991	9	AP000565	AP000565
50	19	6.4	157244	9	AP005204	AP005204 Homo sapi	c	107	18	6.1	44583	6	AX059545	AX059545
51	19	6.4	158432	2	AC105438	AC105438 Sus scrofa	c	108	18	6.1	58608	2	AC100499	AC100499
52	19	6.4	158577	9	AP001485	AP001485 Homo sapi	c	109	18	6.1	64426	2	AC014778	AC014778
53	19	6.4	159674	2	AC113867	AC113867 Rattus no	c	110	18	6.1	70626	9	AL356274	AL356274
54	19	6.4	165761	2	AC145750	AC145750 Homo sapi	c	111	18	6.1	72590	5	AL603744	AL603744
55	19	6.4	167280	2	AC102825	AC102825 Mus muscu	c	112	18	6.1	74589	8	AB010068	AB010068
56	19	6.4	169116	5	BX324202	BX324202 Zebrafish	c	113	18	6.1	82596	8	FGH8	FGH8
57	19	6.4	169682	9	AC010854	AC010854 Homo sapi	c	114	18	6.1	83594	8	AB008268	AB008268
58	19	6.4	170123	9	AC018371	AC018371 Homo sapi	c	115	18	6.1	86004	9	HSI1023	HSI1023
59	19	6.4	172113	2	AP001176	AP001176 Homo sapi	c	116	18	6.1	87726	2	AC014337	AC014337
60	19	6.4	175802	10	AL805929	AL805929 Homo sapi	c	117	18	6.1	90425	2	AC138337	AC138337
61	19	6.4	177379	10	AC140212	AC140212 Mus muscu	c	118	18	6.1	93276	9	AL139124	AL139124
62	19	6.4	178239	2	AC011968	AC011968 Homo sapi	c	119	18	6.1	103920	2	AC014955	AC014955
63	19	6.4	178469	2	BX248504	BX248504 Dantio rer	c	120	18	6.1	109491	9	AC022224	AC022224
64	19	6.4	179941	2	BX664752	BX664752 Dantio rer	c	121	18	6.1	110000	2	AC098244_1	AC098244_1
65	19	6.4	181170	2	AC109244	AC109244 Mus muscu	c	122	18	6.1	110000	2	AL359032_0	AL359032_0
66	19	6.4	186394	2	BX330068	BX330068 Dantio rer	c	123	18	6.1	110000	2	AL360016_2	AL360016_2
67	19	6.4	194578	2	AC007832	AC007832 Homo sapi	c	124	18	6.1	110000	2	AL928982_1	AL928982_1
68	19	6.4	194604	2	AP001275	AP001275 Homo sapi	c	125	18	6.1	111692	9	AL161783	AL161783
69	19	6.4	201182	9	AC069540	AC069540 Homo sapi	c	126	18	6.1	112886	9	AL590726	AL590726
70	19	6.4	202205	2	AC068895	AC068895 Homo sapi	c	127	18	6.1	118473	10	AL671969	AL671969
71	19	6.4	206675	2	AC133827	AC133827 Rattus no	c	128	18	6.1	123576	9	AC015969	AC015969
72	19	6.4	208363	10	AL691416	AL691416 Mouse DNA	c	129	18	6.1	125502	8	ATT4120	ATT4120
73	19	6.4	209335	2	BX346476	BX346476 Dantio rer	c	130	18	6.1	126807	9	HS391022	HS391022
74	19	6.4	210617	2	AC034201	AC034201 Homo sapi	c	131	18	6.1	128765	3	AC010053	AC010053
75	19	6.4	212643	2	BX311103	BX311103 Dantio rer	c	132	18	6.1	129722	9	HS15005	HS15005
76	19	6.4	223808	2	AC114139	AC114139 Rattus no	c	133	18	6.1	13263	2	AC126235	AC126235
77	19	6.4	226147	9	AP002478	AP002478 Homo sapi	c	134	18	6.1	137043	9	AC068794	AC068794
78	19	6.4	231946	2	AC115544	AC115544 Rattus no	c	135	18	6.1	138350	2	AC010801	AC010801
79	19	6.4	244739	2	AC112042	AC112042 Rattus no	c	136	18	6.1	140212	2	AC016730	AC016730
80	19	6.4	245090	2	BX890597	BX890597 Dantio rer	c	137	18	6.1	140987	9	AC099061	AC099061
81	19	6.4	278299	2	AC129681	AC129681 Rattus no	c	138	18	6.1	141742	9	AC092621	AC092621
82	19	6.4	288339	14	AF198100	AF198100 Fowlpox v	c	139	18	6.1	141915	2	AC096636	AC096636
83	19	6.4	288888	9	HSN310932	HSN310932 Homo sapi	c	140	18	6.1	143220	9	AL389887	AL389887
84	19	6.4	324399	2	AC098418	AC098418 Rattus no	c	141	18	6.1	145763	2	AC064809	AC064809
85	19	6.4	329181	2	AC094238	AC094238 Rattus no	c	142	18	6.1	146248	2	AC013677	AC013677
86	18	6.1	249	11	G21301	G21301 human STR W	c	143	18	6.1	146843	9	AC096761	AC096761
87	18	6.1	480	6	AR388675	AR388675 Sequence	c	144	18	6.1	146921	9	AC007992	AC007992
88	18	6.1	520	6	AR424133	AR424133 Sequence	c	145	18	6.1	147114	9	AP001939	AP001939
89	18	6.1	520	6	BD119686	BD119686 EST and e	c	146	18	6.1	147419	9	HS738P11	HS738P11
90	18	6.1	597	6	AR388671	AR388671 Sequence	c	146	18	6.1	147419	9	HS738P11	HS738P11

147	18	6.1 148282	9	AC024649	AC024649 Homo sapi	204	18	6.1 181725	2	AC102430	AC102430 Mus muscu
148	18	6.1 149907	4	AC091436	AC091436 fells cat	205	18	6.1 181864	9	AL353743	AL353743 Human DNA
149	18	6.1 150242	9	AC006195	AC006195 Homo sapi	206	18	6.1 182240	2	AC074201	AC074201 Homo sapi
150	18	6.1 152022	9	AC094081	AC094081 Homo sapi	207	18	6.1 182504	2	AC146660	AC146660 Ootolemur
151	18	6.1 152324	2	AC136938	AC136938 Homo sapi	208	18	6.1 182925	2	AC128749	AC128749 Rattus no
152	18	6.1 153099	9	CNS057CE	AL355095 Human chr	209	18	6.1 183462	5	BX571976	BX571976 Zebrafish
153	18	6.1 153439	8	AP003113	AP003113 Oryza sat	210	18	6.1 183706	2	BK470078	BK470078 Danio rer
154	18	6.1 153440	2	AC105263	AC105263 Drosophill	211	18	6.1 183925	2	AC078870	AC078870 Homo sapi
155	18	6.1 153028	2	BX347940	BX347940 Danio rer	212	18	6.1 184317	10	AL606494	AL606494 Mouse DNA
156	18	6.1 155039	2	AC012548	AC012548 Homo sapi	213	18	6.1 184433	2	AC108479	AC108479 Homo sapi
157	18	6.1 155475	5	BX321885	BX321885 Zebrafish	214	18	6.1 184600	2	AC117347	AC117347 Rattus no
158	18	6.1 156873	9	AC015998	AC015998 Homo sapi	215	18	6.1 184706	9	AC004782	AC004782 Homo sapi
159	18	6.1 157088	5	AL335300	AL335300 Zebrafish	216	18	6.1 186117	9	AC072046	AC072046 Homo sapi
160	18	6.1 157494	10	AL605512	AL605512 Mouse DNA	217	18	6.1 186322	2	BX294389	BX294389 Danio rer
161	18	6.1 159231	2	AC116499	AC116499 Mus muscu	218	18	6.1 187684	2	AC016008	AC016008 Homo sapi
162	18	6.1 159670	2	AC027626	AC027626 Homo sapi	219	18	6.1 189386	2	AP001456	AP001456 Homo sapi
163	18	6.1 159806	2	AC024340	AC024340 Homo sapi	220	18	6.1 189579	9	AL354733	AL354733 Human DNA
164	18	6.1 161001	9	AC068775	AC068775 Homo sapi	221	18	6.1 190506	2	AC096890	AC096890 Homo sapi
165	18	6.1 161104	9	AL732499	AL732499 Zebrafish	222	18	6.1 190520	2	AC138271	AC138271 Homo sapi
166	18	6.1 161402	9	AP003113	AP003113 Homo sapi	223	18	6.1 192332	10	AL606745	AL606745 Mouse DNA
167	18	6.1 161660	2	AC115920	AC115920 Mus muscu	224	18	6.1 192437	5	BX322665	BX322665 Zebrafish
168	18	6.1 162386	9	AC113397	AC113397 Homo sapi	225	18	6.1 192673	2	AC018870	AC018870 Homo sapi
169	18	6.1 162428	2	BX005112	BX005112 Danio rer	226	18	6.1 193147	2	AC097960	AC097960 Rattus no
170	18	6.1 163209	2	AC007949	AC007949 Homo sapi	227	18	6.1 193553	9	AC097634	AC097634 Homo sapi
171	18	6.1 163353	10	AL627076	AL627076 Mouse DNA	228	18	6.1 194091	9	AP003534	AP003534 Homo sapi
172	18	6.1 163551	2	AC015777	AC015777 Homo sapi	229	18	6.1 194813	2	AC100723	AC100723 Mus muscu
173	18	6.1 163741	3	AC007821	AC007821 Drosophill	230	18	6.1 195031	2	AC141325	AC141325 Pen trogl
174	18	6.1 163942	9	AC034207	AC034207 Homo sapi	231	18	6.1 195323	2	AP003459	AP003459 Homo sapi
175	18	6.1 163966	5	AL954708	AL954708 Zebrafish	232	18	6.1 195592	8	ATC090982	ATC090982 Homo sapi
176	18	6.1 164763	2	BK470262	BK470262 Danio rer	233	18	6.1 195921	8	ATC091981	ATC091981 Homo sapi
177	18	6.1 164806	10	AC138715	AC138715 Mus muscu	234	18	6.1 196044	2	AC102296	AC102296 Mus muscu
178	18	6.1 165006	8	AP003791	AP003791 Oryza sat	235	18	6.1 196602	2	AC114248	AC114248 Homo sapi
179	18	6.1 165617	9	AF165926	AF165926 Homo sapi	236	18	6.1 196766	8	ATC091916	ATC091916 Homo sapi
180	18	6.1 167015	9	BX649387	BX649387 Mus muscu	237	18	6.1 197159	3	AC009340	AC009340 Homo sapi
181	18	6.1 167237	9	AC007938	AC007938 Homo sapi	238	18	6.1 198281	10	AC122254	AC122254 Mus muscu
182	18	6.1 168124	2	AC021971	AC021971 Homo sapi	239	18	6.1 198734	3	AC007820	AC007820 Drosophill
183	18	6.1 168544	2	AC024334	AC024334 Homo sapi	240	18	6.1 198911	2	AC111975	AC111975 Rattus no
184	18	6.1 168866	8	OSJN00023	AL606588 Oryza sat	241	18	6.1 199036	9	AC025449	AC025449 Homo sapi
185	18	6.1 169162	9	AL138926	AL138926 Human DNA	242	18	6.1 199566	2	AC103676	AC103676 Homo sapi
186	18	6.1 170116	9	AC087257	AC087257 Homo sapi	243	18	6.1 200689	2	AC067865	AC067865 Homo sapi
187	18	6.1 170247	2	AC110896	AC110896 Mus muscu	244	18	6.1 200841	10	AC108830	AC108830 Mus muscu
188	18	6.1 172036	9	AC046181	AC046181 Homo sapi	245	18	6.1 202843	2	CNS01DWM	AL135961 Human chr
189	18	6.1 172494	2	BX572089	BX572089 Danio rer	246	18	6.1 203178	2	AC114678	AC114678 Mus muscu
190	18	6.1 173226	10	AC132120	AC132120 Mus muscu	247	18	6.1 203317	2	AC021062	AC021062 Mus muscu
191	18	6.1 174074	2	BX842671	BX842671 Mus muscu	248	18	6.1 205475	2	AC130033	AC130033 Rattus no
192	18	6.1 174138	5	AC008871	AC008871 Homo sapi	249	18	6.1 206093	2	BK571844	BK571844 Danio rer
193	18	6.1 174646	5	AL929151	AL929151 Zebrafish	250	18	6.1 206222	2	AC108891	AC108891 Bos tauru
194	18	6.1 177020	2	AC091326	AC091326 Homo sapi	251	18	6.1 206291	10	AL672091	AL672091 Mouse DNA
195	18	6.1 177087	2	AC093687	AC093687 Homo sapi	252	18	6.1 207365	2	AC093653	AC093653 Homo sapi
196	18	6.1 177734	9	AC073569	AC073569 Homo sapi	253	18	6.1 207695	2	AC097190	AC097190 Rattus no
197	18	6.1 178455	2	AC137969	AC137969 Mus muscu	254	18	6.1 210057	10	AC124501	AC124501 Mus muscu
198	18	6.1 179497	2	BX663521	BX663521 Danio rer	255	18	6.1 212892	2	AC132420	AC132420 Mus muscu
199	18	6.1 180486	2	AC118051	AC118051 Mus muscu	256	18	6.1 214146	2	AC096822	AC096822 Rattus no
200	18	6.1 180555	9	AC079384	AC079384 Homo sapi	257	18	6.1 221070	10	AC026949	AC026949 Mus muscu
201	18	6.1 180962	2	AC068917	AC068917 Homo sapi	258	18	6.1 223465	2	AC098603	AC098603 Rattus no
202	18	6.1 181315	2	AC147271	AC147271 Pen trogl	259	18	6.1 223678	2	AC130000	AC130000 Rattus no
203	18	6.1 181460	9	AC090877	AC090877 Homo sapi	260	18	6.1 225379	2	AC121485	AC121485 Rattus no

c 261	18	6.1 225538	2	AC108577	AC108577 Rattus no	c 318	17	5.7 1146	10	MREDA	X12801 Murline mRNA
c 262	18	6.1 226637	2	AC124613	AC124613 Mus muscu	c 319	17	5.7 1284	5	XEHAND	Z95080 X.laevis mR
c 263	18	6.1 227182	2	AC099283	AC099283 Rattus no	c 320	17	5.7 1515	8	AF227978	AF227978 Brassica
c 264	18	6.1 227411	10	AC130821	AC130821 Mus muscu	c 321	17	5.7 1593	8	AK070418	AK070418 Oryza sat
c 265	18	6.1 228693	2	AC111848	AC111848 Rattus no	c 322	17	5.7 1597	5	BC049424	BC049424 Danto rer
c 266	18	6.1 229082	2	AC111600	AC111600 Rattus no	c 323	17	5.7 1597	5	BC053150	BC053150 Danto rer
c 267	18	6.1 229606	2	AC105519	AC105519 Rattus no	c 324	17	5.7 1781	9	HSN805147	HSN805147 Homo sapi
c 268	18	6.1 230155	2	AC114073	AC114073 Rattus no	c 325	17	5.7 1837	5	AF22388253	AF22388253 Homo sapi
c 269	18	6.1 230444	2	AC117368	AC117368 Rattus no	c 326	17	5.7 1838	5	AF22381953	AF22381953 Oncorhyn
c 270	18	6.1 230449	2	AC105504	AC105504 Rattus no	c 327	17	5.7 1838	5	AF22382553	AF22382553 Oncorhyn
c 271	18	6.1 230940	10	AC123043	AC123043 Mus muscu	c 328	17	5.7 1838	5	AF22382553	AF22382553 Oncorhyn
c 272	18	6.1 231746	9	AC011389	AC011389 Homo sapi	c 329	17	5.7 1838	5	AF22382553	AF22382553 Oncorhyn
c 273	18	6.1 232190	2	AC123645	AC123645 Mus muscu	c 330	17	5.7 1838	5	AF22382553	AF22382553 Oncorhyn
c 274	18	6.1 232223	2	AC132892	AC132892 Rattus no	c 331	17	5.7 1838	5	AF22383153	AF22383153 Oncorhyn
c 275	18	6.1 232251	2	AC093690	AC093690 Rattus no	c 332	17	5.7 1838	5	AF22383453	AF22383453 Oncorhyn
c 276	18	6.1 232610	2	AC123157	AC123157 Rattus no	c 333	17	5.7 1838	5	AF22383753	AF22383753 Oncorhyn
c 277	18	6.1 233274	2	AC098636	AC098636 Rattus no	c 334	17	5.7 1838	5	AF22384053	AF22384053 Oncorhyn
c 278	18	6.1 236096	3	AE003775	AE003775 Drosophi	c 335	17	5.7 1838	5	AF22384453	AF22384453 Oncorhyn
c 279	18	6.1 237067	2	AC118339	AC118339 Rattus no	c 336	17	5.7 1838	5	AF22384653	AF22384653 Oncorhyn
c 280	18	6.1 237712	9	AC012634	AC012634 Homo sapi	c 337	17	5.7 1838	5	AF22384953	AF22384953 Oncorhyn
c 281	18	6.1 239623	2	AC121220	AC121220 Rattus no	c 338	17	5.7 1838	5	AF22385253	AF22385253 Oncorhyn
c 282	18	6.1 240255	2	BX37326	BX37326 Danto rer	c 339	17	5.7 1838	5	AF22385553	AF22385553 Oncorhyn
c 283	18	6.1 242384	2	AC105847	AC105847 Rattus no	c 340	17	5.7 1838	5	AF22385653	AF22385653 Oncorhyn
c 284	18	6.1 242743	2	AC137367	AC137367 Rattus no	c 341	17	5.7 1838	5	AF22386153	AF22386153 Oncorhyn
c 285	18	6.1 242907	2	AC106660	AC106660 Rattus no	c 342	17	5.7 1838	5	AF22386453	AF22386453 Oncorhyn
c 286	18	6.1 243768	2	AC125725	AC125725 Rattus no	c 343	17	5.7 1838	5	AF22386753	AF22386753 Oncorhyn
c 287	18	6.1 244974	2	AC111249	AC111249 Rattus no	c 344	17	5.7 1838	5	AF22387053	AF22387053 Oncorhyn
c 288	18	6.1 250087	2	AC096931	AC096931 Rattus no	c 345	17	5.7 1838	5	AF22387353	AF22387353 Oncorhyn
c 289	18	6.1 250937	2	AC098144	AC098144 Rattus no	c 346	17	5.7 1838	5	AF22387653	AF22387653 Oncorhyn
c 290	18	6.1 251852	2	AC114625	AC114625 Mus muscu	c 347	17	5.7 1838	5	AF22387953	AF22387953 Oncorhyn
c 291	18	6.1 252129	2	AC133975	AC133975 Rattus no	c 348	17	5.7 1838	5	AF22388553	AF22388553 Oncorhyn
c 292	18	6.1 261775	3	AE003639	AE003639 Drosophi	c 349	17	5.7 1838	5	AF22388853	AF22388853 Oncorhyn
c 293	18	6.1 261938	2	AC103891	AC103891 Rattus no	c 350	17	5.7 1879	8	BT000241	BT000241
c 294	18	6.1 263855	2	AC127197	AC127197 Rattus no	c 351	17	5.7 1947	6	AR321206	AR321206 Sequence
c 295	18	6.1 265977	2	AC134623	AC134623 Mus muscu	c 352	17	5.7 2002	8	AY009806	AY009806 Sequence
c 296	18	6.1 266574	2	AC087129	AC087129 Mus muscu	c 353	17	5.7 2109	8	BT003163	BT003163 Arabidops
c 297	18	6.1 267326	2	AC110972	AC110972 Rattus no	c 354	17	5.7 2159	9	HSU26396	HSU26396 Human fetal
c 298	18	6.1 269296	2	AC107602	AC107602 Rattus no	c 355	17	5.7 2247	3	DMU66460	DMU66460 Human fetal
c 299	18	6.1 271788	2	AC110973	AC110973 Rattus no	c 356	17	5.7 2318	5	ONHP6460	ONHP6460 Human fetal
c 300	18	6.1 276372	2	AC123569	AC123569 Rattus no	c 357	17	5.7 2534	1	ECRCB	ECRCB Human fetal
c 301	18	6.1 278227	2	AC128099	AC128099 Rattus no	c 358	17	5.7 2551	8	SCRCB	SCRCB Human fetal
c 302	18	6.1 279666	2	AC130931	AC130931 Rattus no	c 359	17	5.7 2552	2	AC020498	AC020498 Drosophi
c 303	18	6.1 280394	3	AE003544	AE003544 Drosophi	c 360	17	5.7 2625	8	AK070975	AK070975 Oryza sat
c 304	18	6.1 333192	2	AC113779	AC113779 Rattus no	c 361	17	5.7 2671	5	DI06363	DI06363 Oncorhyn
c 305	18	6.1 340000	9	AP001718	AP001718 Homo sapi	c 362	17	5.7 2760	9	HUMALP6D	HUMALP6D Human alpha
c 306	18	6.1 349505	2	AC130443	AC130443 Rattus no	c 363	17	5.7 2760	9	HUMEDRINA	HUMEDRINA Human alpha
c 307	18	6.1 349505	2	AC130443	AC130443 Rattus no	c 364	17	5.7 2875	8	AY383719	AY383719 Human alpha
c 308	17	5.7 232	6	AR251699	AR251699 Sequence	c 365	17	5.7 3024	10	BC057064	BC057064 Mus muscu
c 309	17	5.7 401	6	AX321179	AX321179 Sequence	c 366	17	5.7 3105	6	AX794253	AX794253 Sequence
c 310	17	5.7 441	6	AX570166	AX570166 Sequence	c 367	17	5.7 3452	3	AT128432	AT128432 Sequence
c 311	17	5.7 607	11	BY040243	BY040243 S208P6811	c 368	17	5.7 3476	3	BT009955	BT009955 Drosophi
c 312	17	5.7 647	8	AJ060065	AJ060065 Arabidops	c 369	17	5.7 3577	3	DMROSA	DMROSA Arabidops
c 313	17	5.7 785	6	BD019595	BD019595 Novel gen	c 370	17	5.7 3618	8	HUMTYRP	HUMTYRP Homo sapi
c 314	17	5.7 785	6	BD095933	BD095933 Novel gen	c 371	17	5.7 3935	8	SCYK127W	SCYK127W Homo sapi
c 315	17	5.7 785	6	BD186809	BD186809 Nucleic a	c 372	17	5.7 4077	10	BC064438	BC064438 Rattus no
c 316	17	5.7 786	11	BY038169	BY038169 S212P6629	c 373	17	5.7 4513	10	BC027791	BC027791 Mus muscu
c 317	17	5.7 1021	8	GAN251559	AJ251559 Genetum gn	c 374	17	5.7 4734	9	HSN800826	HSN800826

375	17	5.7	5355	6	E30079	E30079 Novel prote	432	17	5.7	45014	2	AC147003	AC147003 Homo sapi
c 376	17	5.7	5355	6	E30080	E30080 Novel prote	c 433	17	5.7	45472	3	CEY59A8A	AL132895 Caenorhab
377	17	5.7	5377	8	AB011422	AB011422 Homo sapi	c 434	17	5.7	46826	3	AC084155	AC084155 Caenorhab
378	17	5.7	5777	8	AT133743	AT133743 Arabidops	c 435	17	5.7	51648	2	AC015434	AC015434 Drosophill
379	17	5.7	5830	9	HSMB07900	BX647754 Homo sapi	c 436	17	5.7	51860	10	ALB080109	ALB080109 Mouse DNA
c 380	17	5.7	6177	6	AX281402	AX281402 Sequence	c 437	17	5.7	52417	9	AC114777	AC114777 Homo sapi
c 381	17	5.7	6177	6	AX319151	AX319151 Sequence	c 438	17	5.7	53411	2	AC087287	AC087287 Homo sapi
c 382	17	5.7	6207	6	AX251536	AX251536 Sequence	c 439	17	5.7	55343	9	AL139152	AL139152 Human DNA
c 383	17	5.7	6497	8	AF159061	AF159061 Oryza sat	c 440	17	5.7	55687	9	AC079464	AC079464 Homo sapi
c 384	17	5.7	6514	9	AF148808	AF148808 Homo sapi	c 441	17	5.7	57198	2	AL590046	AL590046 Homo sapi
c 385	17	5.7	7172	6	AR218888	AR218888 Sequence	c 442	17	5.7	58190	2	AL590046	AL590046 Homo sapi
c 386	17	5.7	7172	6	BD003800	BD003800 Polynucle	c 443	17	5.7	58449	10	HS498124	HS498124 Homo sapi
387	17	5.7	7499	1	EC81DMR	X13145 Escherichia	c 444	17	5.7	59219	2	AC090585	AC090585 Homo sapi
388	17	5.7	7672	6	AR274887	AR274887 Sequence	c 445	17	5.7	59303	8	AP004955	AP004955 Lotus cor
389	17	5.7	7672	6	AX180070	AX180070 Sequence	c 446	17	5.7	61150	2	AC100284	AC100284 Homo sapi
390	17	5.7	7672	6	HS083667	HS083667 Human alpha	c 447	17	5.7	61267	3	AC004336	AC004336 Drosophill
391	17	5.7	7787	6	AX334524	AX334524 Sequence	c 448	17	5.7	61725	2	AC100105	AC100105 Mus muscu
392	17	5.7	7787	6	HUMASPX	J05243 Human noner	c 449	17	5.7	62219	2	AC120844	AC120844 Mus muscu
393	17	5.7	7827	9	BC053521	BC053521 Homo sapi	c 450	17	5.7	63268	2	AC103683	AC103683 Homo sapi
c 394	17	5.7	8303	6	AX345324	AX345324 Sequence	c 451	17	5.7	63268	2	AC103683	AC103683 Homo sapi
c 395	17	5.7	10029	1	AE007457	AE007457 Streptococ	c 452	17	5.7	64139	9	AC069064	AC069064 Homo sapi
c 396	17	5.7	10189	1	AE005549	AE005549 Escherich	c 453	17	5.7	64208	2	AL929000	AL929000 Human DNA
c 397	17	5.7	10189	1	AE015336	AE015336 Shigella	c 454	17	5.7	64786	2	AC017805	AC017805 Homo sapi
c 398	17	5.7	10382	1	AE008517	AE008517 Streptococ	c 455	17	5.7	64849	2	AC113037	AC113037 Mus muscu
c 399	17	5.7	10710	6	AX344589	AX344589 Sequence	c 456	17	5.7	65014	2	AC100176	AC100176 Mus muscu
c 400	17	5.7	10846	1	AE013594	AE013594 Methanosa	c 457	17	5.7	66137	2	AC101526	AC101526 Mus muscu
c 401	17	5.7	11857	2	AC018299	AC018299 Drosophill	c 458	17	5.7	66310	2	AC135728	AC135728 Homo sapi
c 402	17	5.7	13460	8	SPBC685	AE000400 Escherich	c 459	17	5.7	66668	2	AC134694	AC134694 Homo sapi
c 403	17	5.7	14295	1	AE000400	AE000400 Escherich	c 460	17	5.7	69514	9	AY129465	AY129465 Homo sapi
c 404	17	5.7	14764	10	AL974311	AL974311 Mouse DNA	c 461	17	5.7	71380	9	AC092605	AC092605 Homo sapi
c 405	17	5.7	16697	9	AL591687	AL591687 Human DNA	c 462	17	5.7	72591	2	AC080137	AC080137 Homo sapi
c 406	17	5.7	18556	2	AC017481	AC017481 Drosophill	c 463	17	5.7	73184	2	AC090864	AC090864 Homo sapi
c 407	17	5.7	19814	6	AX349041	AX349041 Sequence	c 464	17	5.7	78054	3	AC004296	AC004296 Drosophill
c 408	17	5.7	21011	8	AB025627	AB025627 Arabidops	c 465	17	5.7	78643	3	AC004352	AC004352 Drosophill
c 409	17	5.7	24139	10	AF463765	AF463765 Mus muscu	c 466	17	5.7	81147	9	AL606504	AL606504 Human DNA
c 410	17	5.7	24667	9	AF001295	AF001295 Homo sapi	c 467	17	5.7	81476	10	EX004788	EX004788 Mouse DNA
c 411	17	5.7	25464	6	A91686	A91686 Sequence 4	c 468	17	5.7	82064	2	AC006937	AC006937 Drosophill
c 412	17	5.7	25464	6	AR307527	AR307527 Sequence	c 469	17	5.7	83490	8	AP004039	AP004039 Oryza sat
c 413	17	5.7	25464	6	BD023435	BD023435 Nucleotid	c 470	17	5.7	83511	8	AB013389	AB013389 Arabidops
c 414	17	5.7	26514	2	AC005649	AC005649 Drosophill	c 471	17	5.7	83557	9	AL138735	AL138735 Human DNA
c 415	17	5.7	27503	9	AL160404	AL160404 Human DNA	c 472	17	5.7	84551	3	AC004295	AC004295 Drosophill
c 416	17	5.7	28716	10	AL928795	AL928795 Mouse DNA	c 473	17	5.7	85785	8	ATF21P8	ATF21P8 Homo sapi
c 417	17	5.7	30985	8	SPAC961	298763 S.pombe chr	c 474	17	5.7	87256	9	AC091865	AC091865 Homo sapi
c 418	17	5.7	31151	2	AC107201_8	Continuation (9 of	c 475	17	5.7	90463	8	AP003810	AP003810 Oryza sat
c 419	17	5.7	31557	3	AC00467	AC00467 Drosophill	c 476	17	5.7	90875	5	AL672192	AL672192 Zebrafish
c 420	17	5.7	31737	3	U50072	U50072 Caenorhabd	c 477	17	5.7	91025	9	AL359270	AL359270 Homo sapi
c 421	17	5.7	32479	2	AC090240	AC090240 Homo sapi	c 478	17	5.7	91059	9	AP003463	AP003463 Homo sapi
c 422	17	5.7	32703	3	CEFI4D1	292967 Caenorhabd	c 479	17	5.7	93217	2	AC023171	AC023171 Homo sapi
c 423	17	5.7	33156	3	CERT25612	282055 Caenorhabd	c 480	17	5.7	93586	9	AL590487	AL590487 Homo sapi
c 424	17	5.7	37386	3	LMFL8806	LMFL8806 Sequence	c 481	17	5.7	94802	2	SPNE01913	SPNE01913 Homo sapi
c 425	17	5.7	38475	8	SPCC350	AL596286 Lelishmani	c 482	17	5.7	94924	2	AC087108	AC087108 Homo sapi
c 426	17	5.7	38692	3	AC116919	AC116919 Dicycoste	c 483	17	5.7	99878	2	AC087108	AC087108 Homo sapi
c 427	17	5.7	39013	1	AF088896	AF088896 Zymomonas	c 484	17	5.7	101029	9	AC026954	AC026954 Homo sapi
c 428	17	5.7	39338	1	AL590456	AL590456 Human DNA	c 485	17	5.7	101333	8	AP004030	AP004030 Oryza sat
c 429	17	5.7	40699	8	SPBC119	AL022117 S.pombe c	c 486	17	5.7	101882	9	AC021089	AC021089 Homo sapi
c 430	17	5.7	40753	8	BFY18967	Y18367 Branchiosto	c 487	17	5.7	101923	10	AC138172	AC138172 Mus muscu
c 431	17	5.7	44326	2	AC025719	AC025719 Caenorhab	c 488	17	5.7	102282	9	AL158033	AL158033 Human DNA

c 489	17	5.7 102965	2	AC146727	Orcolenur
c 490	17	5.7 103390	9	AL358533	Human DNA
c 491	17	5.7 103479	9	AC140059	Homo sapi
c 492	17	5.7 103523	9	AL390408	Human DNA
c 493	17	5.7 105070	8	AP006352	Lotus cor
c 494	17	5.7 105247	9	AL356266	Human DNA
c 495	17	5.7 105600	8	AP005173	Oryza sat
c 496	17	5.7 105695	2	BX571758	Danio rer
c 497	17	5.7 106961	2	AC119411	Medicago
c 498	17	5.7 106975	8	OSJN00045	Oryza sat
c 499	17	5.7 107025	2	AL139235_3	Continuation (4 of
c 500	17	5.7 109685	9	AC024578	Homo sapi
c 501	17	5.7 110000	1	EC0067_1	Continuation (2 of
c 502	17	5.7 110000	2	AC101676_2	Continuation (3 of
c 503	17	5.7 110000	2	AC107201_7	Continuation (8 of
c 504	17	5.7 110000	2	AC112133_0	Continuation (3 of
c 505	17	5.7 110000	2	AC113868_2	Continuation (3 of
c 506	17	5.7 110000	2	AC116279_0	Continuation (3 of
c 507	17	5.7 110000	2	AC116411_0	Rattus no
c 508	17	5.7 110000	2	AC120762_2	Continuation (3 of
c 509	17	5.7 110000	2	AC123241_1	Continuation (2 of
c 510	17	5.7 110000	2	AC132794_2	Continuation (3 of
c 511	17	5.7 110000	2	AC141403_1	Continuation (2 of
c 512	17	5.7 110000	2	AL139235_2	Continuation (3 of
c 513	17	5.7 110000	2	BX294176_1	Continuation (2 of
c 514	17	5.7 110000	2	BX23020_2	Continuation (3 of
c 515	17	5.7 110000	2	PFMAL3_01	Continuation (2 of
c 516	17	5.7 110901	9	AL359675	Human DNA
c 517	17	5.7 110999	9	AC091983	Homo sapi
c 518	17	5.7 110999	9	AC091983	Homo sapi
c 519	17	5.7 114026	5	AL165501	Human DNA
c 520	17	5.7 114626	4	AC138157	Carollia
c 521	17	5.7 115040	8	AC124954	Medicago
c 522	17	5.7 115424	2	AC146806	Medicago
c 523	17	5.7 117217	9	AP002076	Homo sapi
c 524	17	5.7 117911	9	HS117919	Human DNA
c 525	17	5.7 118755	9	AC090152	Homo sapi
c 526	17	5.7 118669	9	AC004903	Homo sapi
c 527	17	5.7 119491	9	AC098860	Homo sapi
c 528	17	5.7 119875	8	AC108051	Homo sapi
c 529	17	5.7 120562	8	AY268139	Hordeum v
c 530	17	5.7 120625	2	AC017563	Human DNA
c 531	17	5.7 121141	10	AC125314	Drosophila
c 532	17	5.7 122681	9	AC006062	Mus muscu
c 533	17	5.7 123386	8	F12F1	Homo sapi
c 534	17	5.7 124214	9	AL807246	Arabidops
c 535	17	5.7 125439	9	AC138990	Human DNA
c 536	17	5.7 125527	9	AL353133	Human DNA
c 537	17	5.7 125760	2	AC080122	Human DNA
c 538	17	5.7 125785	2	AC107393	Homo sapi
c 539	17	5.7 125973	2	AC010353	Homo sapi
c 540	17	5.7 127178	9	AC005160	Homo sapi
c 541	17	5.7 127472	2	AC124962	Medicago
c 542	17	5.7 127506	8	OSJN00096	Oryza sat
c 543	17	5.7 128016	2	AC138131	Medicago
c 544	17	5.7 128218	2	AC121096	Mus muscu
c 545	17	5.7 128751	5	BX649386	Zebrafish
c 546	17	5.7 128965	9	AL357562	Human DNA
c 547	17	5.7 129083	2	AC096853	Sus scrofa
c 548	17	5.7 129984	9	AC115620	Homo sapi
c 549	17	5.7 130361	10	AL929546	Mouse DNA
c 550	17	5.7 130586	2	AC073238	Homo sapi
c 551	17	5.7 130632	9	AC004547	Homo sapi
c 552	17	5.7 131704	2	AP004313	Homo sapi
c 553	17	5.7 132200	2	AL161619	Oryza sat
c 554	17	5.7 132782	8	AC120983	Oryza sat
c 555	17	5.7 132927	8	AC078890	Oryza sat
c 556	17	5.7 133157	9	AC109351	Homo sapi
c 557	17	5.7 133330	10	AL928871	Mouse DNA
c 558	17	5.7 135513	3	BS000023	Pan trogl
c 559	17	5.7 136164	3	AC099006	Medicago
c 560	17	5.7 136551	9	AC123786	Homo sapi
c 561	17	5.7 136901	9	AC073626	Homo sapi
c 562	17	5.7 136906	2	RN86120	Rattus no
c 563	17	5.7 137289	9	AC022828	Homo sapi
c 564	17	5.7 137441	5	AL928712	Zebrafish
c 565	17	5.7 137445	2	AP004780	Oryza sat
c 566	17	5.7 137985	2	AP005634	Oryza sat
c 567	17	5.7 138419	9	AL137793	Human DNA
c 568	17	5.7 138769	2	BX571896	Danio rer
c 569	17	5.7 139033	8	HS038084	Human DNA
c 570	17	5.7 139330	8	AC119415	Medicago
c 571	17	5.7 140606	2	AL353761	Homo sapi
c 572	17	5.7 140680	2	BX510917	Danio rer
c 573	17	5.7 141889	2	AC032006	Homo sapi
c 574	17	5.7 142021	10	AL645843	Mouse DNA
c 575	17	5.7 142123	2	AC068890	Homo sapi
c 576	17	5.7 142353	2	AC073286	Homo sapi
c 577	17	5.7 142911	2	BX835398	Danio rer
c 578	17	5.7 142959	2	AC025453	Homo sapi
c 579	17	5.7 143146	9	AC073855	Homo sapi
c 580	17	5.7 143687	9	AC016572	Homo sapi
c 581	17	5.7 144062	5	AL954190	Zebrafish
c 582	17	5.7 144631	9	AC069027	Homo sapi
c 583	17	5.7 144649	2	AC145841	Macropus
c 584	17	5.7 144979	2	AC138597	Homo sapi
c 585	17	5.7 145085	2	AC090261	Homo sapi
c 586	17	5.7 145173	9	AC005599	Homo sapi
c 587	17	5.7 145629	2	BX322794	Danio rer
c 588	17	5.7 145829	2	BX571953	Danio rer
c 589	17	5.7 145913	2	AP005821	Oryza sat
c 590	17	5.7 145947	9	AL353588	Human DNA
c 591	17	5.7 146170	2	AC073224	Homo sapi
c 592	17	5.7 146275	2	AC080119	Homo sapi
c 593	17	5.7 146396	10	AL929449	Mouse DNA
c 594	17	5.7 146468	2	AC118126	Rattus no
c 595	17	5.7 146690	2	AC102254	Mus muscu
c 596	17	5.7 146810	9	AC084706	Homo sapi
c 597	17	5.7 146952	9	AC068522	Homo sapi
c 598	17	5.7 147008	2	AC138980	Homo sapi
c 599	17	5.7 147177	2	AC138981	Homo sapi
c 600	17	5.7 148003	2	BX537320	Danio rer
c 601	17	5.7 149085	2	AC123364	Rattus no
c 602	17	5.7 149143	2	AC092974	Homo sapi

c 603	17	5.7	148428	2	ACO10264	ACO10264 Homo sapi	660	17	5.7	159735	10	AL672101	AL672101 Mouse DNA
604	17	5.7	148559	9	AL139327	AL139327 Human DNA	661	17	5.7	160002	5	BX000446	BX000446 Zebrafish
605	17	5.7	149901	2	ACO22243	ACO22243 Homo sapi	662	17	5.7	160069	2	ACO64867	ACO64867 Homo sapi
c 606	17	5.7	150026	2	AL589868	AL589868 Homo sapi	663	17	5.7	160197	2	AC115700	AC115700 Mus muscu
607	17	5.7	150096	2	AC117562	AC117562 Mus muscu	c 664	17	5.7	160302	9	ACO10685	ACO10685 Homo sapi
608	17	5.7	150162	9	ACO26722	ACO26722 Homo sapi	c 665	17	5.7	160624	2	AC144418	AC144418 Rattus no
c 609	17	5.7	150350	9	CNS01DMW	AL138539 Human chr	666	17	5.7	161054	2	AC123744	AC123744 Mus muscu
c 610	17	5.7	150355	9	HS3364H10	AL078603 Human DNA	c 667	17	5.7	161364	2	AC068637	AC068637 Homo sapi
c 611	17	5.7	150399	9	AC093680	AC093680 Homo sapi	668	17	5.7	161638	9	AC107934	AC107934 Homo sapi
c 612	17	5.7	150400	10	AC122911	AC122911 Mus muscu	669	17	5.7	161672	2	AC136667	AC136667 Rattus no
613	17	5.7	150887	2	ACO18580	ACO18580 Homo sapi	670	17	5.7	162046	2	AC127375	AC127375 Mus muscu
c 614	17	5.7	151203	8	CNS09S4W	BX558075 Oryza sat	c 671	17	5.7	162075	9	HS12723	HS12723 Homo sapi
615	17	5.7	151319	9	AC108036	AC108036 Homo sapi	c 672	17	5.7	162151	9	AL138753	AL138753 Human DNA
616	17	5.7	151540	2	AL772252	AL772252 Homo sapi	c 673	17	5.7	162411	2	AC147061	AC147061 Pan trogl
617	17	5.7	151696	2	AP001768	AP001768 Homo sapi	c 674	17	5.7	162492	3	AC099039	AC099039 Drosophi
618	17	5.7	151761	9	HS493D19	AL096868 Human DNA	675	17	5.7	162880	2	AC120363	AC120363 Mus muscu
619	17	5.7	151822	9	AC004478	AC004478 Homo sapi	676	17	5.7	162922	2	ACO11281	ACO11281 Homo sapi
620	17	5.7	152081	9	AC007381	AC007381 Homo sapi	c 677	17	5.7	162995	10	AL663032	AL663032 Mouse DNA
c 621	17	5.7	152246	9	ACO23473	ACO23473 Homo sapi	678	17	5.7	163066	2	AC116506	AC116506 Mus muscu
622	17	5.7	152454	2	AC067909	AC067909 Homo sapi	c 679	17	5.7	163110	2	AC068705	AC068705 Homo sapi
623	17	5.7	153064	8	CNS08CAL	AL831808 Oryza sat	680	17	5.7	163231	9	AL162575	AL162575 Human DNA
c 624	17	5.7	153155	2	AC060783	AC060783 Homo sapi	c 681	17	5.7	163357	2	ACO23276	ACO23276 Homo sapi
625	17	5.7	153319	2	AC136027	AC136027 Mus muscu	682	17	5.7	163404	2	AC118883	AC118883 Rattus no
c 626	17	5.7	153402	9	HS247E2	AL773569 Homo sapi	683	17	5.7	163443	5	AL773542	AL773542 Zebrafish
c 627	17	5.7	153553	2	AC124338	AC124338 Mus muscu	684	17	5.7	163706	2	AL354927	AL354927 Homo sapi
628	17	5.7	153716	9	AL590631	AL590631 Human DNA	c 685	17	5.7	163712	9	AC004065	AC004065 Homo sapi
629	17	5.7	154016	2	ACO91311	ACO91311 Mus muscu	c 686	17	5.7	164007	2	AC069218	AC069218 Homo sapi
c 630	17	5.7	154323	2	ACO25831	ACO25831 Homo sapi	687	17	5.7	164118	2	ACO23184	ACO23184 Homo sapi
c 631	17	5.7	154417	2	AC102530	AC102530 Mus muscu	688	17	5.7	164278	2	AC073126	AC073126 Homo sapi
c 632	17	5.7	154455	2	ACO21844	ACO21844 Homo sapi	689	17	5.7	164799	2	BX511121	BX511121 Drosophi
633	17	5.7	154604	5	AL954739	AL954739 Zebrafish	c 690	17	5.7	165011	9	AL445255	AL445255 Human DNA
c 634	17	5.7	154753	2	ACO20605	ACO20605 Homo sapi	691	17	5.7	165089	9	ACO21646	ACO21646 Homo sapi
635	17	5.7	154758	9	AC112491	AC112491 Homo sapi	c 692	17	5.7	165768	2	ACO23517	ACO23517 Homo sapi
c 636	17	5.7	155326	9	CNS07EF2	AL512311 Human chr	693	17	5.7	165798	2	AC117794	AC117794 Mus muscu
637	17	5.7	155394	2	AC092328	AC092328 Homo sapi	694	17	5.7	166007	9	CNS01DRC	CNS01DRC Homo chr
c 638	17	5.7	156008	9	AL353093	AL353093 Human DNA	695	17	5.7	166071	2	ACO22336	ACO22336 Homo sapi
c 639	17	5.7	156142	3	ACO91228	ACO91228 Homo sapi	c 696	17	5.7	166168	2	AC115193	AC115193 Rattus no
c 640	17	5.7	156190	2	AC097651	AC097651 Homo sapi	697	17	5.7	166174	2	ACO09633	ACO09633 Homo sapi
c 641	17	5.7	156232	8	AC108084	AC108084 Oryza sat	698	17	5.7	166231	9	AL773537	AL773537 Human DNA
c 642	17	5.7	156332	10	AC116581	AC116581 Mus muscu	c 699	17	5.7	166525	9	ACO22413	ACO22413 Homo sapi
c 643	17	5.7	156392	9	AC026341	AC026341 Homo sapi	700	17	5.7	166531	2	BX890591	BX890591 Drosophi
644	17	5.7	157067	2	AC137265	AC137265 Rattus no	c 701	17	5.7	166651	4	ACO87160	ACO87160 Sus scrof
c 645	17	5.7	157393	2	ACO36212	ACO36212 Homo sapi	702	17	5.7	166716	9	AC108482	AC108482 Homo sapi
c 646	17	5.7	157591	2	BX323068	BX323068 Drosophi	c 703	17	5.7	167162	2	AC139872	AC139872 Rattus no
c 647	17	5.7	157747	2	AC067915	AC067915 Homo sapi	c 704	17	5.7	167214	2	AC096202	AC096202 Homo sapi
c 648	17	5.7	157816	9	AC093666	AC093666 Homo sapi	705	17	5.7	167853	2	AP001798	AP001798 Homo sapi
649	17	5.7	157949	9	AL355578	AL355578 Human DNA	706	17	5.7	167974	9	AL591073	AL591073 Homo sapi
c 650	17	5.7	158549	9	HS796C4	297200 Human DNA	707	17	5.7	168043	2	ACO11935	ACO11935 Homo sapi
651	17	5.7	158600	2	BX296541	BX296541 Drosophi	c 708	17	5.7	168108	9	AL445687	AL445687 Human DNA
652	17	5.7	158684	2	AC079493	AC079493 Mus muscu	c 709	17	5.7	168197	9	ACO23307	ACO23307 Homo sapi
653	17	5.7	158830	10	AC131740	AC131740 Mus muscu	710	17	5.7	168306	3	ACO08135	ACO08135 Drosophi
c 654	17	5.7	159013	2	BX323995	BX323995 Drosophi	711	17	5.7	168331	2	BX470138	BX470138 Homo sapi
655	17	5.7	159024	2	AC025495	AC025495 Homo sapi	c 712	17	5.7	168843	2	ACO91711	ACO91711 Rattus no
c 656	17	5.7	159188	2	AC037432	AC037432 Homo sapi	713	17	5.7	168996	2	ACO15785	ACO15785 Homo sapi
c 657	17	5.7	159242	2	AC078800	AC078800 Homo sapi	c 714	17	5.7	169083	2	AL355346	AL355346 Homo sapi
c 658	17	5.7	159300	9	HS279E22	AL662879 Homo sapi	c 715	17	5.7	169479	2	BX890540	BX890540 Drosophi
c 659	17	5.7	159331	9	AL589741	AL589741 Human DNA	716	17	5.7	169557	9	ACO24706	ACO24706 Homo sapi

717	17	5.7 169570	5	AL928989	AL928989 Zebrafish	774	17	5.7 177083	3	AC008285	AC008285 Drosophila
718	17	5.7 169628	5	BK322567	BK322567 Zebrafish	775	17	5.7 177112	9	AC002452	AC002452 Homo sapi
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LOCUS Development of novel antibiotics based on bacteriophage genomics.
ACCESSION BD245277
VERSION BD245277.1 GI:33055047
KEYWORDS JP 2002531107-A/12.
SOURCE unidentified
ORGANISM unidentified

REFERENCE 1 (bases 1 to 261)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Development of novel antibiotics based on bacteriophage genomics
JOURNAL Patent: JP 2002531107-A 12 24-SEP-2002;
PHARTECH INC
COMMENT OS Staphylococcus aureus bacteriophage 77
PN JP 2002531107-A/12
PD 24-SEP-2002
PF 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR
01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454252 PI JERRY
PELLETIER,PHILIPPE GROS,MICHAEL DUBOW
PC C12N15/09,A01N63/00,A61K45/00,A61P31/04,C07K14/005,
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VERSION AB044554.1 GI:8918747
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SOURCE Staphylococcus aureus prophage phiPV83
ORGANISM Staphylococcus aureus prophage phiPV83
REFERENCE 1 (sites)
AUTHORS Virtuesi,daDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
TITLE 2 (sites)
Kaneko,J., Kimura,T., Kawakami,Y., Tomita,T. and Kamio,Y.
JOURNAL Pantom-valentine leukocidin genes in a phage-like particle isolated
Biosci. Biotechnol. Biochem. 61 (11), 1960-1962 (1997)
MEDLINE 94067870
PUBMED 9404084

REFERENCE 2 (sites)
AUTHORS Zou,D., Kaneko,J., Narita,S. and Kamio,Y.
TITLE Complete nucleotide sequence and molecular characterization of
prophage PV83pro carrying lukM-lukF-PV(p83) gene cluster in
Staphylococcus aureus strain p83
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 45636)
AUTHORS Kaneko,J., Zou,D. and Kamio,Y.
TITLE Direct Submission
JOURNAL Submitted (09-JUN-2000) Jun Kaneko, Tohoku University, Graduate
school of Agricultural Sciences; 1-1 Tsurumi-dori Aomiyamachi,
Aoba-ku, Sendai, Miyagi 981-8555, Japan
(E-mail: j.kaneko@biochem.tohoku.ac.jp, Tel: 81-22-717-8781,
Fax: 81-22-717-8780)

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 Db 7148 AGA 7150

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 sequence, section 3/9.
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 AP003360.2 GI:14246388
 KEYWORDS
 SOURCE
 ORGANISM
 Staphylococcus aureus subsp. aureus Mu50
 Staphylococcus aureus subsp. aureus Mu50
 Bacteria; Firmicutes; Bacillales; Staphylococcus.

REFERENCE
 AUTHORS
 Kuroda, M., Ohta, T., Uchiyama, I., Baba, T., Yuzawa, H., Kobayashi, I.,
 Cui, L., Oguchi, A., Aoki, K., Nagai, Y., Lian, J., Ito, T., Kanamori, H.,
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 Sekimizu, K., Hirakawa, H., Kohara, S., Goto, S., Yabuzaki, J.,
 Kanehisa, M., Yamashita, A., Oshima, K., Furuya, K., Yoshino, C.,
 Shiba, T., Hattori, M., Ogasawara, N., Hayashi, H. and Hiramatsu, K.
 Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus
 Lancet 357 (9264), 1225-1240 (2001)
 JOURNAL
 MEDLINE
 21311952
 PUBMED
 11418146
 REFERENCE
 2 (bases 1 to 348527)
 AUTHORS
 Ohta, T.
 TITLE
 Direct Submission
 Submitted (28-FEB-2001) Toshiko Ohta, University of Tsukuba College
 of Medical Technology and Nursing, Department of Medical
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 (E-mail: tohite@tsukuba.ac.jp, Tel: 81-298-53-3454,
 Fax: 81-298-53-3454)
 On May 29, 2001 this sequence version replaced gi:13874937.
 COMMENT
 FEATURES
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Matches 231; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DEFINITION Bacteriophage phi PVL proviral DNA, complete sequence.
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JOURNAL
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COMMENT
FEATURES
source

3 (bases 1 to 41401)
Kaneko,J., Kimura,T., Narita,S., Tomita,T. and Kamio,Y.
Direct Submission
Submitted (17-DEC-1997) Jun Kaneko, Tohoku University, Dept. Appl.
Biol. Chem., Faculty of Agriculture, 1-1 Tsutsumi-dori
Aramiyamachi, Aoba-ku, Sendai, Miyagi 981, Japan
(E-mail: jkaneko@biochem.tohoku.ac.jp, Tel: 81-22-717-8781,
Fax: 81-22-717-8780)
On May 24, 2000 this sequence version replaced gi:3341907.
Sequence updated (06-Feb-1998)
Sequence updated (22-May-2000).
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Query Match 57.9%; Score 172; DB 7; Length 41401;
Best Local Similarity 99.3%; Pred. No. 3.5e-83;
Matches 272; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 24 GGAGGAAGTCAAGATGTATTACGAATAAGCGAAATCATACGCAAAAATATTCATGTTAA 83
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DB 30540 GGAGGAAGTCAAGATGTATTACGAATAAGCGAAATCATACGCAAAAATATTCATGTTAA 30599
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QY 84 CGGATTCGATTTTAAGCTATTCATTTTAAAGGTCATATGGCATTATCATACAACTTAA 143
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DB 30600 CGGATTCGATTTTAAGCTATTCATTTTAAAGGTCATATGGCATTATCATACAACTTAA 30659

QY 144 AGATATGAACAAGTACCAATTTAAACATGCTTATGTGTAGATGAGATGACTAGATAT 203
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DB 30660 AGATATGAACAAGTACCAATTTAAACATGCTTATGTGTAGATGAGATGACTAGATAT 30719
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QY 204 GGATTCACACTATTATTAACCAAGCATATGATGAATGGATTGAAGAGAACACAGCAACA 263
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DB 30720 GGATTCACACTATTATTAACCAAGCATATGATGAATGGATTGAAGAGAACACAGCAACA 30779
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QY 264 GGACAGACTAATTAAGTACATGAAATGGTAG 297
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DB 30780 GGACAGACTAATTAAGTACATGAAATGGTAG 30813

RESULT 8
AB045978 42942 bp DNA linear PHG 26-MAY-2001
LOCUS
DEFINITION Staphylococcus aureus temperate phage phiSLT genomic DNA, complete
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
JOURNAL
FEATURES
source
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CDS
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Staphylococcus aureus temperate phage phiSLT
Staphylococcus aureus temperate phage phiSLT
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
1 (sites)
Narita,S., Kaneko,J., Chiba,J., Piemont,Y., Jarraud,S., Etienne,J.
and Kamio,Y.
Phage conversion of Pantone-Valentine leukocidin in Staphylococcus
aureus: molecular analysis of a PVL-converting phage, phiSLT
Gene 268 (1-2), 193-206 (2001)
21261956
11368915
2 (bases 1 to 42942)
Kaneko,J., Narita,S. and Kamio,Y.
Direct Submission
Submitted (12-JUL-2000) Jun Kaneko, Tohoku University, Graduate
school of Agricultural Sciences; 1-1 Tautsumidori Amamiyamachi,
Sendai, Miyagi 981-8555, Japan
(E-mail:jkaneko@biochem.tohoku.ac.jp, Tel:81-22-717-8781,
Fax:81-22-747-8780)

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8730..9173
CDS
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Best Local Similarity 100.0%; Pred. No. 3.9e-77;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 7294 ATCTACGCAAAATATTCATGTTAAGCATTCATTTTAAGCATTCATTTAAAGGT 733
|||||
QY 118 CATATGGCATTCATATACAGTTAAAGATATGAACAGCATTAACATGCTAT 177
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DB 7354 CATATGGCATTCATATACAGTTAAAGATATGAACAGCATTAACATGCTAT 7413
QY 178 GTGTATGATGAGTACTAGATATGCGATGACTTAT 218
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DB 7414 GTGTATGATGAGTACTAGATATGCGATGACTTAT 7454
RESULT 9
AP001553 43081 bp DNA circular PHG 14-MAR-2001
LOCUS
DEFINITION Bacteriophage phi ETA DNA, complete genome.
ACCESSION AP001553
VERSION AP001553.1 GI:8918415
KEYWORDS
SOURCE Bacteriophage phi ETA
ORGANISM Bacteriophage phi ETA
Virus; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
1 (ates)
REFERENCE
AUTHORS Yamaguchi,T., Hayashi,T., Takami,H., Nakasone,K., Ohnishi,M.,
Nakayama,K., Yamada,S., Komatsuzaawa,H. and Sugai,M.
TITLE Phage conversion of exfoliative toxin A production in
Staphylococcus aureus
JOURNAL Mol. Microbiol. 38 (4), 694-705 (2000)
MEDLINE 20566787
PUBMED 1115106
REFERENCE 2 (bases 1 to 43081)
AUTHORS Sugai,M., Yamaguchi,T., Hayashi,T., Nakasone,K. and Takami,H.
TITLE Direct Submission
JOURNAL Submitted (28-MAR-2000) Motoyuki Sugai, Hiroshima University
Faculty of Dentistry, Microbiology; Kasumi 1-2-3, Hiroshima,
Hiroshima 734-8553, Japan (E-mail:sugai@hiroshima-u.ac.jp,
Tel:81-82-257-5637, Fax:81-82-257-5639)
FEATURES
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CDS

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CDS

CDS

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QY	161 CAATTAACATGCTTATGTCGTAGATGAGATGACTAGATGCGCATGACTATATTTA	220
Db	7060 CAATTAACATGCTTATGTCGTAGATGAGATGACTAGATGCGCATGACTATATTTA	7119
QY	221 ACCAGCAATGATGATGATGATGAGAGACAGACGACAGACGACGACTAATTAAC	280
Db	7120 ACCAGCAATGATGATGATGATGAGAGACAGACGACAGACGACGACTAATTAAC	7179
QY	281 TAGT 284	
Db	7180	TAGT 7183
RESULT 10		
AP003135/c		
LOCUS		
DEFINITION		
ACCESSION		
VERSION		
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS		
1		
Kuroda,M., Ohta,T., Uchiyama,I., Baba,T., Yuzawa,H., Kobayashi,I.,		
Cull,L., Oguchi,A., Aoki,K., Nagai,Y., Ito,T., Ito,T., Kanemori,M.,		
Matsumaru,H., Maruyama,A., Murekami,H., Hosoyama,A.,		
Mizutani-Uti,Y., Takahashi,N.K., Sawano,T., Inoue,R., Kaito,C.,		
Sekimizu,K., Hirakawa,H., Kubera,S., Goto,S., Yabuzaki,J.,		
Kenishia,M., Yamashita,A., Oshima,K., Furuya,K., Yoshino,C.,		
Shiba,T., Hattori,M., Ogasawara,N., Hayashi,H. and Hiramatsu,K.		
Whole genome sequencing of methicillin-resistant <i>Staphylococcus</i>		
<i>aureus</i>		
Lancet 357 (9264), 1225-1240 (2001)		
JOURNAL		
MEDLINE		
PUBMED		
REFERENCE		
2		
(bases 1 to 291150)		
Director-General, Biotechnology Center, Aoki,K., Oguchi,A.,		
Hosoyama,A., Nagai,Y., Kuroda,M., Hiramatsu,K. and Kikuchi,H.		
Submitted (30-JAN-2001) Director-General, Biotechnology Center,		
National Institute of Technology and Evaluation, Biotechnology		
Center; 2Chome 48-10 Nishihara, Shiba-ku, Tokyo 151-0066, Japan		
(E-mail:bio@nite.go.jp, URL:htp://www.bio.nite.go.jp/,		
Tel:81-3-3481-1933, Fax:81-3-3481-8424)		
On Jun 12, 2001 this sequence version replaced gi:13701545.		
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DB 240001 GAAACGAGACGACTAATTAATTAATGCTATGCTAG 239963

RESULT 11
AX618246 267 bp DNA linear PAT 20-FEB-2003
LOCUS Sequence 1209 from Patent WO02094686.
DEFINITION AX618246
ACCESSION AX618246
VERSION AX618246.1 GI:26446442
KEYWORDS
SOURCE
ORGANISM
Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE
1 Maignani,V.C., Mora,M.C. and Scazzell,M.C.
AUTHORS

TITLE
JOURNAL
Staphylococcus aureus proteins and nucleic acids
Patent: WO 02094686-A 1209 28-NOV-2002;
Chiron Spa (IT)

FEATURES
source
Location/Qualifiers
1..267
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Oy 233 ATGAATGATTGAAGAACACACAGACGAA 261
DB 206 ATGAATGATTGAAGAACACACAGACGAA 234

RESULT 12
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LOCUS AF424783
DEFINITION Staphylococcus aureus phage phi 13, complete genome.
ACCESSION AF424783
VERSION AF424783.1 GI:18920591
KEYWORDS
SOURCE
Staphylococcus aureus phage phi 13
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
ORGANISM
REFERENCE
1 (bases 1 to 42722)
Iandolo,J.J., Worrell,V., Roe,B., Qian,Y., Tian,R.,
Kenton,S., Dorman,A., Ji,H., Lin,S., Loh,P., Qi,S., Zhu,H. and
Roe,B.A.
TITLE
JOURNAL
Comparative analysis of the genomes of the temperate bacteriophages
phi11, phi12 and phi13 of Staphylococcus aureus 8325
MEDLINE
Gene 289 (1-2), 109-116 (2002)
PUBMED
12036589
REFERENCE
2 (bases 1 to 42722)
Iandolo,J.J., Worrell,V., Roe,B., Qian,Y., Dorman,A., Tian,R.,
Lin,S. and Ji,H.
TITLE
JOURNAL
Direct Submission
Submitted (26-SEP-2001) Microbiology and Immunology, Univ. of
Oklahoma Health Sciences Center, 940 S.L. Young Blvd, Oklahoma City,
OK 73190, USA
FEATURES
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Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 7035 ATGAATGATGGAAGACACAGACGAA 7063
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LOCUS
DEFINITION
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strain:MW2, section 7/10.
AP004828 BA000033
AP004828.1 GI:21204850
ACCESSION
VERSION
KEYWORDS
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ORGANISM
REFERENCE
AUTHORS
1
Baba,T., Takeuchi,F., Kuroda,M., Yuzawa,H., Aoki,K., Oguchi,A.,
Nagai,Y., Iwama,N., Asano,K., Naimi,T., Kuroda,H., Ohi,L.,
Yamamoto,K. and Hiramatsu,K.
Genome and virulence determinants of high virulence
community-acquired MRSA
Lancet 359 (9320), 1815-1827 (2002)
22040717
PUBMED
12044378
2 (bases 1 to 272850)
REFERENCE
AUTHORS
Director-General, Biotechnology Center, Aoki,K., Oguchi,A.,
Nagai,Y., Asano,K., Iwama,N., Baba,T., Kuroda,M., Hiramatsu,K. and
Kikuchi,H.
Submitted (06-MAR-2002) Director-General, Biotechnology
National Institute of Technology and Evaluation, Biotechnology
Center, 2Chome 49-10 Nishihara, Shibuya-Ku, Tokyo 151-0066, Japan
(E-mail:bioelite.go.jp, URL:http://www.bio.mite.go.jp/
Tel:81-3-3481-1933, Fax:81-3-3481-8424)
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DEFINITION Sequence 1203 from patent US 6593114.
ACCESSION AR355085
VERSION AR355085.1 GI:33761169
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 580)
AUTHORS Kunach, C.A., Chol, G.H., Barash, S., Dillon, P.J., Fannon, M.R. and
Rosen, C.A.

TITLE Staphylococcus aureus polynucleotides and sequences
JOURNAL Patent: US 6593114-A 1203 15-JUL-2003;
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DEFINITION Development of novel antibiotics based on bacteriophage genomics.
ACCESSION BD245634
VERSION BD245634.1 GI:33055404
KEYWORDS JP 2002531107-A/369.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 43594)
AUTHORS Pelletier, J., Gros, P., and Dubow, M.
TITLE Development of novel antibiotics based on bacteriophage genomics
JOURNAL Patent: JP 2002531107-A 369 24-SEP-2002;
COMMENT PHARGETECH INC
OS Staphylococcus aureus bacteriophage 96
PN JP 2002531107-A/369
PD 24-SEP-2002
PE 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992, 03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804, 30-SEP-1999 US 60/157218 PR
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PELLETIER, PHILIPPE GROS, MICHAEL DUBOW
PC C12N15/09, A01N63/00, A61K38/00, A61K45/00, A61P31/04, C07K14/005,
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Run on: October 14, 2004, 18:55:29 ; Search time 198.132 Seconds
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Minimum DB seq length: 0
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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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6	28	9.4	380	2	AAV75314 Staphyloc
7	28	9.4	43576	3	AAA68609 Bacterioph

8	25	8.4	258	7	ACF73076	ACF73076	Staphyloc
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c 153	16	5	4	602	6	ABQ28649	Abq28649 Oligonuc1	c 210	16	5	4	1532	6	ABL40773	AbL40773 Human pro
c 154	16	5	4	602	6	ABQ28648	Abq28648 Oligonuc1	c 211	16	5	4	1532	6	ABK63579	Abk63579 Human nov
c 155	16	5	4	607	6	ABQ13791	Abq13791 Oligonuc1	c 212	16	5	4	1592	9	ADK31956	Adk31956 Rat seq
c 156	16	5	4	607	6	ABQ13790	Abq13790 Oligonuc1	c 213	16	5	4	1592	9	ADK63579	Adk63579 Rat seq
c 157	16	5	4	610	6	ABQ17906	Abq17906 Oligonuc1	c 214	16	5	4	1592	9	ADK63579	Adk63579 Rat seq
c 158	16	5	4	617	5	ABV58971	Abv58971 Human pro	c 215	16	5	4	1716	4	AAH14069	Aah14069 Human c1N
c 159	16	5	4	621	7	ABK42307	Abk42307 Streptoco	c 216	16	5	4	1735	4	AAK51789	Aak51789 Staphyloc
c 160	16	5	4	648	6	ABQ48108	Abq48108 Oligonuc1	c 217	16	5	4	1735	7	ABT14961	Abt14961 Pathogen
c 161	16	5	4	648	6	ABQ48109	Abq48109 Oligonuc1	c 218	16	5	4	1755	7	ACF75079	Acf75079 Staphyloc
c 162	16	5	4	665	4	AAK78214	AAk78214 Human imm	c 219	16	5	4	1758	4	AAK54885	Aak54885 Staphyloc
c 163	16	5	4	665	4	AAK78215	AAk78215 Human imm	c 220	16	5	4	1758	7	ACK20340	Ack20340 Prokaryot
c 164	16	5	4	675	6	ABQ25447	Abq25447 Oligonuc1	c 221	16	5	4	1778	6	ABQ45202	Abq45202 Oligonuc1
c 165	16	5	4	675	6	ABQ25446	Abq25446 Oligonuc1	c 222	16	5	4	1778	6	ABQ45203	Abq45203 Oligonuc1
c 166	16	5	4	700	4	AAH93105	Aah93105 Human inf	c 223	16	5	4	1779	2	AAV65219	Aav65219 DNA encod
c 167	16	5	4	700	4	AAH93104	Aah93104 Human inf	c 224	16	5	4	1785	2	AAZ96412	Aaz96412 s. pneumo
c 168	16	5	4	716	4	AAI94861	Aai94861 Human neu	c 225	16	5	4	1803	7	ADK68440	Adk68440 Arabidops
c 170	16	5	4	726	6	ABQ47367	Abq47367 Oligonuc1	c 226	16	5	4	1803	7	ADK30294	Adk30294 Prokaryot
c 171	16	5	4	726	6	ABQ47366	Abq47366 Oligonuc1	c 227	16	5	4	1964	4	AAH15484	Aah15484 Human c1N
c 172	16	5	4	727	6	ABQ22702	Abq22702 Oligonuc1	c 228	16	5	4	1964	4	AAH15484	Aah15484 Human c1N
c 173	16	5	4	727	6	ABQ22703	Abq22703 Oligonuc1	c 229	16	5	4	2000	6	ABT17385	Abt17385 Arabidops
c 174	16	5	4	739	6	ABL40776	AbL40776 Human pro	c 230	16	5	4	2025	7	AAZ76335	Aaz76335 L. cuprin
c 175	16	5	4	775	6	ABL40777	AbL40777 Human pro	c 231	16	5	4	2157	5	AAK583775	Aak583775 DNA encod
c 176	16	5	4	792	6	ABQ13798	Abq13798 Oligonuc1	c 232	16	5	4	2181	7	ADK53781	Adk53781 Human cod
c 177	16	5	4	815	6	ABQ13799	Abq13799 Oligonuc1	c 233	16	5	4	2257	5	AAK83773	Aak83773 DNA encod
c 178	16	5	4	815	6	ABQ29894	Abq29894 Oligonuc1	c 234	16	5	4	2307	5	AAK79636	Aak79636 Eucel1yptu
	16	5	4	815	6	ABQ29895	Abq29895 Oligonuc1	c 235	16	5	4	2315	2	AAV52327	Aav52327 Streptoco

c 236	16	5.4	2545	4	AAH14381	Abh14381 Human cDN	c 293	16	5.4	7312	6	AA561350	AA561350 Human gen
c 237	16	5.4	2665	4	AA660317	AA660317 Human ISO	c 294	16	5.4	7517	4	AAK89061	AAK89061 Human dtg
c 238	16	5.4	2918	2	AA400074	AA400074 Colon can	c 295	16	5.4	7643	9	ADC30027	ADC30027 Human nov
c 239	16	5.4	3047	4	AAH17851	AAH17851 Human cDN	c 296	16	5.4	8265	4	ADJ08192	ADJ08192 Drosophill
c 240	16	5.4	3112	7	ABX71034	ABX71034 Novel hum	c 297	16	5.4	8298	6	AEN80191	AEN80191 Human che
c 241	16	5.4	3141	7	ADA53313	ADA53313 Human cod	c 298	16	5.4	8748	5	ABAL15607	ABAL15607 Human nov
c 242	16	5.4	3201	7	ABZ80500	ABZ80500 Human sph	c 299	16	5.4	10002	7	ABZ76333	ABZ76333 Human che
c 243	16	5.4	3212	4	ABH12047	ABH12047 Drosophill	c 300	16	5.4	10341	7	ABZ76340	ABZ76340 L. cuprin
c 244	16	5.4	3226	4	AA513803	AA513803 Human cDN	c 301	16	5.4	10433	6	AAV74337	AAV74337 Human imm
c 245	16	5.4	3370	9	ADB62184	ADB62184 Human cDN	c 302	16	5.4	11394	2	AAV74331	AAV74331 Staphyloc
c 246	16	5.4	3483	4	ABL25574	ABL25574 Drosophill	c 303	16	5.4	11812	4	AA545501	AA545501 Chemical
c 247	16	5.4	3534	4	ABL25564	ABL25564 Drosophill	c 304	16	5.4	11812	4	AA545671	AA545671 Tumour su
c 248	16	5.4	3604	4	AA162638	AA162638 Human bre	c 305	16	5.4	11812	4	AB134118	AB134118 Human imm
c 249	16	5.4	3604	4	AA106732	AA106732 Human rep	c 306	16	5.4	11812	6	ABK28431	ABK28431 DNA trans
c 250	16	5.4	3637	6	AA035236	AA035236 Human pro	c 307	16	5.4	11812	6	ABK28431	ABK28431 DNA trans
c 251	16	5.4	3637	6	AA058500	AA058500 Human RSK	c 308	16	5.4	12711	6	AB134524	AB134524 Human met
c 252	16	5.4	3819	7	ACA37440	ACA37440 Prokaryot	c 309	16	5.4	12711	6	AB170249	AB170249 Chemical
c 253	16	5.4	3879	4	ABH13243	ABH13243 Drosophill	c 310	16	5.4	13133	6	ABK31231	ABK31231 Signal tr
c 254	16	5.4	3907	6	ABK34640	ABK34640 Human cDN	c 311	16	5.4	13440	2	AAV52261	AAV52261 Streptoco
c 255	16	5.4	4042	5	AA583774	AA583774 DNA encod	c 312	16	5.4	13714	6	AB133173	AB133173 Human imm
c 256	16	5.4	4226	5	ABX21324	ABX21324 Human ner	c 313	16	5.4	15714	6	ABQ67058	ABQ67058 Human ang
c 257	16	5.4	4307	4	AA037332	AA037332 Human rep	c 314	16	5.4	17141	6	ADA26486	ADA26486 Bovine ga
c 258	16	5.4	4307	4	ABA07915	ABA07915 Human ova	c 315	16	5.4	17417	8	ADA12195	ADA12195 Actinocoba
c 259	16	5.4	4651	5	AA569311	AA569311 DNA encod	c 316	16	5.4	17417	8	AAV59831	AAV59831 Actinocoba
c 260	16	5.4	4672	5	ABY25301	ABY25301 Human pro	c 317	16	5.4	17646	7	ABT17023	ABT17023 Human sec
c 261	16	5.4	5060	10	ADE77064	ADE77064 Human cDN	c 318	16	5.4	17646	7	AB268163	AB268163 Human sec
c 262	16	5.4	5275	6	AB132285	AB132285 Human imm	c 319	16	5.4	17646	7	AB274645	AB274645 Secreted
c 263	16	5.4	5337	6	AB132438	AB132438 Human imm	c 320	16	5.4	17646	7	ADA98997	ADA98997 Human sec
c 264	16	5.4	5377	6	ABK28380	ABK28380 DNA trans	c 321	16	5.4	17946	4	AA136812	AA136812 Human car
c 265	16	5.4	5448	4	ABH14644	ABH14644 Drosophill	c 322	16	5.4	17946	5	AA151608	AA151608 Human ner
c 266	16	5.4	5464	6	AA563343	AA563343 Chemical	c 323	16	5.4	17946	9	ADE47506	ADE47506 Human car
c 267	16	5.4	5572	4	AB102846	AB102846 Drosophill	c 324	16	5.4	17946	9	AAE47506	AAE47506 Human car
c 268	16	5.4	5841	6	ABY92872	ABY92872 Soybean d	c 325	16	5.4	18679	6	AEN80300	AEN80300 Human che
c 269	16	5.4	5882	4	ABD12046	ABD12046 Drosophill	c 326	16	5.4	19718	2	AAV52232	AAV52232 Streptoco
c 270	16	5.4	6034	9	ADD14806	ADD14806 Human src	c 327	16	5.4	21521	4	AAK76175	AAK76175 Human imm
c 271	16	5.4	6061	6	AB132140	AB132140 Human imm	c 328	16	5.4	21521	5	ABA21357	ABA21357 Human imm
c 272	16	5.4	6092	6	AB133020	AB133020 Human imm	c 329	16	5.4	22507	6	AB578886	AB578886 E. coli C
c 273	16	5.4	6124	6	AB132965	AB132965 Human imm	c 330	16	5.4	25656	4	AB113242	AB113242 Drosophill
c 274	16	5.4	6124	6	AB134517	AB134517 Human met	c 331	16	5.4	28136	4	AAK69755	AAK69755 Human imm
c 275	16	5.4	6124	6	AB170242	AB170242 Chemical	c 332	16	5.4	31749	4	AAK72959	AAK72959 Human imm
c 276	16	5.4	6160	6	AB133533	AB133533 Human imm	c 333	16	5.4	32236	4	AAK91250	AAK91250 Human dtg
c 277	16	5.4	6161	6	ABK31299	ABK31299 Signal tr	c 334	16	5.4	35425	9	ADC87616	ADC87616 Human GPC
c 278	16	5.4	6161	6	AB170278	AB170278 Chemical	c 335	16	5.4	36651	6	AAAD28072	AAAD28072 Human kln
c 279	16	5.4	6161	6	AA561201	AA561201 Human gen	c 336	16	5.4	36998	6	AAAD3981	AAAD3981 Human tra
c 280	16	5.4	6176	6	AAAD21847	AAAD21847 Zea mays	c 337	16	5.4	62909	4	AAE28545	AAE28545 Genomic f
c 281	16	5.4	6233	7	ABK63371	ABK63371 Human cDN	c 338	16	5.4	69327	6	ABS55821	ABS55821 Human tra
c 282	16	5.4	6283	6	ABK31434	ABK31434 Signal tr	c 339	16	5.4	72332	8	ADA02552	ADA02552 Human WNT
c 283	16	5.4	6283	6	AB170403	AB170403 Chemical	c 340	16	5.4	72332	9	ADB72290	ADB72290 Human WNT
c 284	16	5.4	6283	6	AA561351	AA561351 Human gen	c 341	16	5.4	78925	3	AAK89888	AAK89888 Human FN
c 285	16	5.4	6345	6	AB133771	AB133771 Human imm	c 342	16	5.4	96389	8	ADA02675	ADA02675 Mouse Top
c 286	16	5.4	6345	6	AB170392	AB170392 Chemical	c 343	16	5.4	96389	9	AAK95240	AAK95240 Mouse Top
c 287	16	5.4	6426	5	ABA20367	ABA20367 Human ner	c 344	16	5.4	110000	4	AAK96733	AAK96733 Continuation (12 o
c 288	16	5.4	6459	6	AB555225	AB555225 Human myo	c 345	16	5.4	110000	4	AAK96733	AAK96733 Continuation (12 o
c 289	16	5.4	6459	7	ABX11412	ABX11412 DNA encod	c 346	16	5.4	110000	6	ABT00010	ABT00010 Continuation (12 o
c 290	16	5.4	7201	6	AB132337	AB132337 Human imm	c 347	16	5.4	110000	6	ABK08336	ABK08336 Human pho
c 291	16	5.4	7312	6	AB133815	AB133815 Human imm	c 348	16	5.4	110000	6	ABA92787	ABA92787 Buchnera
c 292	16	5.4	7312	6	AB170402	AB170402 Chemical	c 349	16	5.4	110000	6	ABT01503	ABT01503 Continuation (12 o

c 350	16	5.4	110000	6	ABA03041_08	Continuation (9 of	c 407	15	5.1	231	4	AA548447	AA548447 Enterococ
c 351	16	5.4	110000	7	AB556454_06	Continuation (7 of	c 408	15	5.1	231	7	ACA13136	ACA13136 Prokaryot
c 352	16	5.4	110000	7	AB556454_13	Continuation (14 o	c 409	15	5.1	234	3	AA020084	AA020084 Human sec
c 353	16	5.4	110000	7	AB556454_16	Continuation (17 o	c 410	15	5.1	234	3	AA020084	AA020084 Human sec
c 354	16	5.4	110000	7	AB556454_20	Continuation (21 o	c 411	15	5.1	235	4	AAK77774	AAK77774 Human tmm
c 355	16	5.4	110000	8	ACR03408_0	Continuation (21 o	c 412	15	5.1	235	4	AAK77774	AAK77774 Human tmm
c 356	16	5.4	111282	6	AA144261	Human pho	c 413	15	5.1	244	6	AB163616	AB163616 Breast ca
c 357	16	5.4	111282	6	AB555190	Genomic D	c 414	15	5.1	244	6	AA101119	AA101119 Rat liver
c 358	16	5.4	139032	6	AB079105	Genomic D	c 415	15	5.1	244	6	AA101119	AA101119 Rat liver
c 359	16	5.4	139257	9	ADCB89520	Human COR	c 416	15	5.1	244	6	AA101119	AA101119 Rat liver
c 360	16	5.4	139904	6	ABK83362	ADCB89520 Human COR	c 417	15	5.1	247	4	AA151531	AA151531 Rat liver
c 361	16	5.4	265118	5	AAH41227	AAH41227 Pyrococcus	c 418	15	5.1	247	4	AA151531	AA151531 Rat liver
c 362	16	5.4	349901	9	ADCB89440	ADCB89440 Human GPC	c 419	15	5.1	247	4	AA151531	AA151531 Rat liver
c 363	16	5.4	349901	9	ADCB89440	ADCB89440 Human GPC	c 420	15	5.1	247	4	AA151531	AA151531 Rat liver
c 364	16	5.4	349938	9	ADCB89440	ADCB89440 Human GPC	c 421	15	5.1	247	4	AA151531	AA151531 Rat liver
c 365	15	5.1	25	7	ACF03399	M. gallii	c 422	15	5.1	247	4	AA151531	AA151531 Rat liver
c 366	15	5.1	33	2	AA212528	AA212528 PCR prime	c 423	15	5.1	268	6	AAK38292	AAK38292
c 367	15	5.1	33	6	AB225162	Ab225162 Cu/Zn SOD	c 424	15	5.1	268	6	AAK38292	AAK38292
c 368	15	5.1	47	3	AA267197	Human map	c 425	15	5.1	268	7	AAK38292	AAK38292
c 369	15	5.1	56	2	AA76389	AA76389 Staphyloc	c 426	15	5.1	268	7	AAK38292	AAK38292
c 370	15	5.1	91	4	AA547846	AA547846 Enterococ	c 427	15	5.1	268	10	AAE72335	AAE72335
c 371	15	5.1	91	7	ACA12573	ACA12573 Prokaryot	c 428	15	5.1	286	7	AAK12295	AAK12295
c 372	15	5.1	117	7	ACA19997	ACA19997 Prokaryot	c 429	15	5.1	287	7	AAK87507	AAK87507
c 373	15	5.1	150	2	AAH86832	AAH86832 Human sin	c 430	15	5.1	294	5	AAV58694	AAV58694
c 374	15	5.1	152	3	AA022270	AA022270 Human sec	c 431	15	5.1	297	6	AB517999	AB517999
c 375	15	5.1	165	4	AB74657	AB74657 Human foe	c 432	15	5.1	324	6	ABQ68225	ABQ68225
c 376	15	5.1	165	4	AA155150	AA155150 Probe #23	c 433	15	5.1	325	6	AA158836	AA158836
c 377	15	5.1	165	4	AA49303	AA49303 Human bon	c 434	15	5.1	332	6	AAH18909	AAH18909
c 378	15	5.1	165	4	AAK23130	AAK23130 Human bra	c 435	15	5.1	334	4	AA547653	AA547653
c 379	15	5.1	165	4	AB548942	AB548942 Human liv	c 436	15	5.1	334	7	ACA12352	ACA12352
c 380	15	5.1	165	6	AB522824	AB522824 Human gen	c 437	15	5.1	337	4	AA188499	AA188499
c 381	15	5.1	167	6	AB178996	AB178996 Human ova	c 438	15	5.1	337	4	AA188499	AA188499
c 382	15	5.1	176	4	AA547723	AA547723 Enterococ	c 439	15	5.1	339	6	AB778392	AB778392
c 383	15	5.1	176	7	ACA12419	ACA12419 Prokaryot	c 440	15	5.1	350	7	AB256662	AB256662
c 384	15	5.1	178	6	AB208290	AB208290 Human leu	c 441	15	5.1	351	2	AAQ60794	AAQ60794
c 385	15	5.1	191	4	AA547538	AA547538 Enterococ	c 442	15	5.1	353	2	AAQ60794	AAQ60794
c 386	15	5.1	191	4	AA547582	AA547582 Enterococ	c 443	15	5.1	357	3	AA028211	AA028211
c 387	15	5.1	191	4	AA547542	AA547542 Enterococ	c 444	15	5.1	370	5	AAV17434	AAV17434
c 388	15	5.1	191	4	AA547557	AA547557 Enterococ	c 445	15	5.1	370	7	ABK45244	ABK45244
c 389	15	5.1	191	7	ACA12277	ACA12277 Prokaryot	c 446	15	5.1	375	4	AA114275	AA114275
c 390	15	5.1	191	7	ACA12236	ACA12236 Prokaryot	c 447	15	5.1	384	4	AA113791	AA113791
c 391	15	5.1	191	7	ACA12237	ACA12237 Prokaryot	c 448	15	5.1	384	4	AA155501	AA155501
c 392	15	5.1	191	7	ACA12249	ACA12249 Prokaryot	c 449	15	5.1	384	4	AA135151	AA135151
c 393	15	5.1	195	3	AA014255	AA014255 Human sec	c 450	15	5.1	384	4	ABK45029	ABK45029
c 394	15	5.1	198	6	AB184328	AB184328 Human ova	c 451	15	5.1	384	4	ABK45029	ABK45029
c 395	15	5.1	230	4	AA548353	AA548353 Enterococ	c 452	15	5.1	384	4	AAK25217	AAK25217
c 396	15	5.1	230	4	AA548429	AA548429 Enterococ	c 453	15	5.1	384	4	AAK03735	AAK03735
c 397	15	5.1	230	4	AA548284	AA548284 Enterococ	c 454	15	5.1	384	4	AB528816	AB528816
c 398	15	5.1	230	4	AA548388	AA548388 Enterococ	c 455	15	5.1	384	5	AA103667	AA103667
c 399	15	5.1	230	4	AA548332	AA548332 Enterococ	c 456	15	5.1	386	2	AAV159751	AAV159751
c 400	15	5.1	230	4	AA548462	AA548462 Enterococ	c 457	15	5.1	386	2	AAV15998	AAV15998
c 401	15	5.1	230	7	ACA13142	ACA13142 Prokaryot	c 458	15	5.1	393	4	AAH00774	AAH00774
c 402	15	5.1	230	7	ACA13033	ACA13033 Prokaryot	c 459	15	5.1	398	4	AA192814	AA192814
c 403	15	5.1	230	7	ACA13046	ACA13046 Prokaryot	c 460	15	5.1	403	2	AA062791	AA062791
c 404	15	5.1	230	7	ACA13056	ACA13056 Prokaryot	c 461	15	5.1	407	7	ABK36649	ABK36649
c 405	15	5.1	230	7	ACA13145	ACA13145 Prokaryot	c 462	15	5.1	407	7	ABK62547	ABK62547
c 406	15	5.1	230	7	ACA13008	ACA13008 Prokaryot	c 463	15	5.1	414	8	ADK31018	ADK31018 DNA encod

c 464	15	5.1	423	6	ABN19543	Abn19543 Human ORF	c 521	15	5.1	529	4	AA547497	AA547497 Enterococ
c 465	15	5.1	426	5	ABV47228	Abv47228 Human pro	c 522	15	5.1	529	4	AA547502	AA547502 Enterococ
c 466	15	5.1	426	3	ABx44832	Abx44832 Bovine ES	c 523	15	5.1	529	5	ABV47427	ABV47427 Human pro
c 467	15	5.1	428	7	AAc57698	AAc57698 Acrethidn	c 524	15	5.1	529	7	ACM12204	ACM12204 Prokaryot
c 468	15	5.1	430	5	ABV00400	Abv00400 Human pro	c 525	15	5.1	531	6	ABQ45170	ABQ45170 Oligonuc1
c 469	15	5.1	432	6	ABK76313	Abk76313 Bacillus	c 526	15	5.1	531	6	ABQ45170	ABQ45170 Oligonuc1
c 470	15	5.1	433	5	ABV48231	Abv48231 Human pro	c 527	15	5.1	532	6	ABQ47632	ABQ47632 Oligonuc1
c 471	15	5.1	435	5	ABV52504	Abv52504 Human pro	c 528	15	5.1	532	6	ABQ47633	ABQ47633 Oligonuc1
c 472	15	5.1	437	5	ABAI6674	Abai6674 Human ner	c 529	15	5.1	532	7	ACM12192	ACM12192 Prokaryot
c 473	15	5.1	438	4	AA549430	AA549430 Stephyloc	c 530	15	5.1	541	6	ABQ39476	ABQ39476 Oligonuc1
c 474	15	5.1	438	7	ACAI6657	ACai6657 Prokaryot	c 531	15	5.1	541	6	ABQ39477	ABQ39477 Oligonuc1
c 475	15	5.1	447	8	ADA48769	Ada48769 Banana ge	c 532	15	5.1	541	9	ADD33178	ADD33178 Human mlt
c 476	15	5.1	456	6	ABV95163	Abv95163 Human pan	c 533	15	5.1	543	6	ABQ37914	ABQ37914 Oligonuc1
c 477	15	5.1	457	8	ACH26876	Ach26876 Human adu	c 534	15	5.1	543	6	ABQ37915	ABQ37915 Oligonuc1
c 478	15	5.1	458	5	ABV09569	Abv09569 Human pro	c 535	15	5.1	550	6	ABQ22438	ABQ22438 Oligonuc1
c 479	15	5.1	459	5	ABV39713	Abv39713 Human pro	c 536	15	5.1	550	6	ABQ22439	ABQ22439 Oligonuc1
c 480	15	5.1	459	5	ABV30745	Abv30745 Human pro	c 537	15	5.1	551	7	ABX57175	ABx57175 Acrebidops
c 481	15	5.1	460	8	ACH25839	Ach25839 Human adu	c 538	15	5.1	554	6	ABQ32977	ABq32977 Oligonuc1
c 482	15	5.1	468	4	ABA58555	Abas58555 Human foe	c 539	15	5.1	554	6	ABQ32976	ABq32976 Oligonuc1
c 483	15	5.1	468	4	AA138216	AA138216 Probe #69	c 540	15	5.1	558	6	ABQ18099	ABq18099 Oligonuc1
c 484	15	5.1	468	4	AAK32370	AAk32370 Human bon	c 541	15	5.1	558	6	ABQ18098	ABq18098 Oligonuc1
c 485	15	5.1	468	4	AAK06674	AAk06674 Human bra	c 542	15	5.1	559	6	ABQ53806	ABq53806 Oligonuc1
c 486	15	5.1	468	4	ABS32078	Abs32078 Human liv	c 543	15	5.1	559	6	ABQ53807	ABq53807 Oligonuc1
c 487	15	5.1	468	6	ABS07153	Abs07153 Human gen	c 544	15	5.1	566	6	ABQ22523	ABq22523 Oligonuc1
c 488	15	5.1	478	6	ABS05296	Abso5296 Human gen	c 545	15	5.1	566	6	ABQ22522	ABq22522 Oligonuc1
c 489	15	5.1	480	4	AAK79680	AAk79680 Human imm	c 546	15	5.1	567	2	AAK27703	AAk27703 T7 RNA po
c 490	15	5.1	483	5	AAK78335	AAk78335 DNA encod	c 547	15	5.1	567	2	AAK27703	AAk27703 T7 RNA po
c 491	15	5.1	485	8	ACH14945	ACH14945 Human adu	c 548	15	5.1	567	8	AAK92622	AAk92622 Human cDN
c 492	15	5.1	488	5	ABAI6716	Abai6716 Human ner	c 549	15	5.1	569	2	AAK27765	AAk27765 Sequence
c 493	15	5.1	488	5	ABAI6715	Abai6715 Human ner	c 550	15	5.1	570	4	ABL13333	ABl13333 Prokaryot
c 494	15	5.1	488	5	ABAI6713	Abai6713 Human ner	c 551	15	5.1	570	4	ABX59707	ABx59707 Human foe
c 495	15	5.1	491	6	ABV99050	Abv99050 Human pan	c 552	15	5.1	570	4	AAK39572	AAk39572 Human liv
c 496	15	5.1	492	5	ABV59181	Abv59181 Human col	c 553	15	5.1	570	4	AAK39572	AAk39572 Human liv
c 497	15	5.1	492	6	ABJ36418	Abj36418 Human col	c 554	15	5.1	572	2	AAQ44852	AAq44852 Bacillus
c 498	15	5.1	493	7	ACC60444	Acc60444 Rice leaf	c 555	15	5.1	576	6	ABQ45688	ABq45688 Oligonuc1
c 499	15	5.1	498	3	AAc94504	AAc94504 Cat flea	c 556	15	5.1	576	6	ABQ45689	ABq45689 Oligonuc1
c 500	15	5.1	498	4	AAK77857	AAk77857 Human imm	c 557	15	5.1	579	6	ABQ25430	ABq25430 Oligonuc1
c 501	15	5.1	499	6	ABQ57276	Abq57276 Human col	c 558	15	5.1	579	6	ABQ25431	ABq25431 Oligonuc1
c 502	15	5.1	500	6	ABK53395	Abk53395 Human eos	c 559	15	5.1	581	6	ABQ38266	ABq38266 Oligonuc1
c 503	15	5.1	502	6	ABQ28401	Abq28401 Oligonuc1	c 560	15	5.1	581	6	ABQ38267	ABq38267 Oligonuc1
c 504	15	5.1	502	6	ABQ28400	Abq28400 Oligonuc1	c 561	15	5.1	581	7	ACM10275	ACM10275 Rice leaf
c 505	15	5.1	506	6	ABJ99505	Abj99505 Target ca	c 562	15	5.1	582	7	ACF73303	ACf73303 Stephyloc
c 506	15	5.1	508	6	ABQ49691	Abq49691 Oligonuc1	c 563	15	5.1	586	6	ABQ33378	ABq33378 Oligonuc1
c 507	15	5.1	508	6	ABQ49680	Abq49680 Oligonuc1	c 564	15	5.1	586	6	ABQ33379	ABq33379 Oligonuc1
c 508	15	5.1	510	6	ABQ22280	Abq22280 Oligonuc1	c 565	15	5.1	587	5	ABAI15400	ABai15400 Human ner
c 509	15	5.1	510	6	ABQ22281	Abq22281 Oligonuc1	c 566	15	5.1	590	6	ABQ25857	ABq25857 Oligonuc1
c 510	15	5.1	511	4	AA192763	AA192763 Human pol	c 567	15	5.1	590	6	ABQ25856	ABq25856 Oligonuc1
c 511	15	5.1	514	9	ADD17902	ADD17902 DNA (Seq)	c 568	15	5.1	592	4	AAK62163	AAk62163 Human foe
c 512	15	5.1	515	6	ABQ33939	Abq33939 Oligonuc1	c 569	15	5.1	592	4	AAK42117	AAk42117 Probe #10
c 513	15	5.1	515	6	ABQ33938	Abq33938 Oligonuc1	c 570	15	5.1	592	4	AAK36383	AAk36383 Human bon
c 514	15	5.1	520	3	AAK39612	AAk39612 Acrebidops	c 571	15	5.1	592	4	AAK10484	AAk10484 Human bra
c 515	15	5.1	522	4	AAK62328	AAk62328 Human liv	c 572	15	5.1	592	4	ABX36058	ABx36058 Human liv
c 516	15	5.1	523	6	ABQ50101	Abq50101 Oligonuc1	c 573	15	5.1	592	6	ABQ10424	ABq10424 Human gen
c 517	15	5.1	523	6	ABQ50100	Abq50100 Oligonuc1	c 574	15	5.1	594	6	ABQ24018	ABq24018 Oligonuc1
c 518	15	5.1	525	7	ACA35322	ACA35322 Prokaryot	c 575	15	5.1	594	6	ABQ24019	ABq24019 Oligonuc1
c 519	15	5.1	527	6	ABQ13981	Abq13981 Oligonuc1	c 576	15	5.1	609	6	ABQ43749	ABq43749 Oligonuc1
c 520	15	5.1	527	6	ABQ13980	Abq13980 Oligonuc1	c 577	15	5.1	609	6	ABQ43748	ABq43748 Oligonuc1

578	15	5.1	610	6	ABQ25735	Abq25735 Oligonuc1	c 635	15	5.1	754	4	AAK51627	Aak51627 Human pol
c 579	15	5.1	610	6	ABQ25734	Abq25734 Oligonuc1	c 636	15	5.1	753	3	AAK42653	Aac42653 Arabidops
580	15	5.1	613	6	ABQ66774	Abq666774 Arabidops	c 637	15	5.1	756	2	AAQ43704	Aaq43704 Sequence
581	15	5.1	614	2	AAZ96182	Aaz96182 S. pneumo	c 638	15	5.1	756	6	ABK84157	Abk84157 Human cIN
c 582	15	5.1	615	6	ABQ27520	Abq27520 Oligonuc1	c 639	15	5.1	760	6	ABE17054	Abz17054 Arabidops
583	15	5.1	615	6	ABQ27521	Abq27521 Oligonuc1	c 640	15	5.1	760	7	ADN69199	Ada69199 Arabidops
584	15	5.1	616	5	ABY51537	Abv51537 Human pro	c 641	15	5.1	772	3	AAZ97291	Aaz97291 Human pro
585	15	5.1	620	2	AA198607	DNA encod	c 642	15	5.1	774	6	ABQ32213	Abq32213 Oligonuc1
586	15	5.1	620	7	ADA68382	Ada68382 Arabidops	c 643	15	5.1	774	6	ABQ32212	Abq32212 Oligonuc1
587	15	5.1	621	1	ABE14361	Abz14361 Arabidops	c 644	15	5.1	775	4	AA123383	AA123383 Human bre
588	15	5.1	621	7	ABZ42092	Abz42092 Arabidops	c 645	15	5.1	786	4	AA123137	AA123137 Human bre
589	15	5.1	624	6	ABK77940	Abk77940 Bacillus	c 646	15	5.1	786	6	ABN69343	Abn69343 Streptoco
590	15	5.1	626	6	ABO53873	Abq53873 Oligonuc1	c 647	15	5.1	788	6	ABQ47918	Abq47918 Oligonuc1
c 591	15	5.1	626	6	ABO53872	Abq53872 Oligonuc1	c 648	15	5.1	788	6	ABQ47919	Abq47919 Oligonuc1
c 592	15	5.1	628	6	ABQ25852	Abq25852 Oligonuc1	c 649	15	5.1	793	6	ABQ22881	Abq22881 Oligonuc1
593	15	5.1	628	6	ABQ25853	Abq25853 Oligonuc1	c 650	15	5.1	793	6	ABQ22880	Abq22880 Oligonuc1
c 594	15	5.1	632	3	AAE10192	AAe10192 Fusarium	c 651	15	5.1	794	5	ABV24895	Abv24895 Human pro
595	15	5.1	632	3	ABK80225	Abk80225 Bacillus	c 652	15	5.1	813	4	AA194687	AA194687 Human neu
c 596	15	5.1	637	7	ABX12499	Abx12499 cDNA encod	c 653	15	5.1	826	6	ABQ37703	Abq37703 Oligonuc1
597	15	5.1	642	6	ABK77941	Abk77941 Bacillus	c 654	15	5.1	826	6	ABQ37702	Abq37702 Oligonuc1
c 598	15	5.1	646	6	ABQ20336	Abq20336 Oligonuc1	c 655	15	5.1	828	2	AAE67865	AAe67865 H. pylori
599	15	5.1	646	6	ABQ20337	Abq20337 Oligonuc1	c 656	15	5.1	828	2	AAE67865	AAe67865 H. pylori
600	15	5.1	649	4	AA184272	AA184272 Human pol	c 657	15	5.1	835	4	AA195446	AA195446 Human neu
601	15	5.1	657	6	ABQ33195	Abq33195 Oligonuc1	c 658	15	5.1	837	2	AAE67694	AAe67694 H. pylori
c 602	15	5.1	657	6	ABQ33194	Abq33194 Oligonuc1	c 659	15	5.1	860	6	ABQ52665	Abq52665 Oligonuc1
c 603	15	5.1	658	4	AAE22946	AAe22946 Human pro	c 660	15	5.1	860	6	ABQ52664	Abq52664 Oligonuc1
c 604	15	5.1	664	6	ABQ53676	Abq53676 Oligonuc1	c 661	15	5.1	861	6	ABE25158	ABz25158 H. SOD
605	15	5.1	664	6	ABQ53677	Abq53677 Oligonuc1	c 662	15	5.1	876	7	ACA30332	ACA30332 Protekayot
606	15	5.1	674	3	AAQ59543	Aaq59543 Human sec	c 663	15	5.1	876	7	ACA49440	ACA49440 Protekayot
c 607	15	5.1	674	6	ABQ48436	Abq48436 Oligonuc1	c 664	15	5.1	879	4	AA556047	AA556047 Salmonell
608	15	5.1	674	6	ABQ48437	Abq48437 Oligonuc1	c 665	15	5.1	879	7	ACA52000	Aac52000 Protekayot
c 609	15	5.1	682	6	ABN65486	Abn65486 Human can	c 666	15	5.1	899	6	ABQ36688	Abq36688 Oligonuc1
c 610	15	5.1	683	3	AAE11854	AAe11854 Aspergill	c 667	15	5.1	899	6	ABQ36687	Abq36687 Oligonuc1
c 611	15	5.1	687	7	ACF73899	Acf73899 Stephyloc	c 668	15	5.1	899	6	ABQ36465	Abq36465 Oligonuc1
c 612	15	5.1	690	7	ACA20358	Aca20358 Protekayot	c 669	15	5.1	899	6	ABQ36464	Abq36464 Oligonuc1
613	15	5.1	693	4	AAK65577	Aak65577 Human imm	c 670	15	5.1	909	6	ABQ28075	Abq28075 Oligonuc1
c 614	15	5.1	694	6	ABQ41430	Abq41430 Oligonuc1	c 671	15	5.1	909	6	ABQ28074	Abq28074 Oligonuc1
615	15	5.1	694	6	ABQ41431	Abq41431 Oligonuc1	c 672	15	5.1	930	6	ABQ35481	Abq35481 Oligonuc1
c 616	15	5.1	697	6	ABQ41812	Abq41812 Oligonuc1	c 673	15	5.1	930	6	ABQ35480	Abq35480 Oligonuc1
617	15	5.1	697	6	ABQ41813	Abq41813 Oligonuc1	c 674	15	5.1	943	6	ABQ17439	Abq17439 Oligonuc1
618	15	5.1	699	7	ACA33230	Aca33230 Protekayot	c 675	15	5.1	943	6	ABQ17438	Abq17438 Oligonuc1
619	15	5.1	702	4	AA552808	AA552808 Enterococ	c 676	15	5.1	945	4	AAH32127	AAh32127 Human o1f
c 620	15	5.1	706	6	ABQ31819	Abq31819 Oligonuc1	c 677	15	5.1	945	7	ABZ77950	ABz77950 Human G P
c 621	15	5.1	706	6	ABQ31818	Abq31818 Oligonuc1	c 678	15	5.1	947	8	AA161111	AA161111 Human T81
c 622	15	5.1	707	6	ABQ48894	Abq48894 Oligonuc1	c 679	15	5.1	949	4	AAH32324	AAh32324 Human o1f
623	15	5.1	707	6	ABQ48895	Abq48895 Stephyloc	c 680	15	5.1	954	7	ACF73679	Acf73679 Stephyloc
624	15	5.1	708	6	ABN91859	Abn91859 Stephyloc	c 681	15	5.1	956	9	ADZ53698	Adz53698 Human pro
c 625	15	5.1	709	6	ABQ31714	Abq31714 Oligonuc1	c 682	15	5.1	971	6	ABQ16238	Abq16238 Oligonuc1
626	15	5.1	709	6	ABQ31715	Abq31715 Oligonuc1	c 683	15	5.1	971	6	ABQ16239	Abq16239 Oligonuc1
c 627	15	5.1	711	4	AB128355	Ab128355 Drosophil	c 684	15	5.1	985	4	AA197659	AA197659 Human neu
628	15	5.1	714	4	AAE22944	AAe22944 Human pro	c 685	15	5.1	993	3	AAZ45340	Aaz45340 DNA encod
629	15	5.1	717	4	AA195196	AA195196 Human neu	c 686	15	5.1	996	4	AAAD12949	AAad12949 Human G-P
c 630	15	5.1	738	6	ABQ16644	Abq16644 Oligonuc1	c 687	15	5.1	996	5	AA542281	AA542281 Human cIN
c 631	15	5.1	738	6	ABQ17370	Abq17370 Oligonuc1	c 688	15	5.1	996	6	ABQ41998	Abq41998 Oligonuc1
632	15	5.1	738	6	ABQ17371	Abq17371 Oligonuc1	c 689	15	5.1	996	6	ABZ42987	ABz42987 Human GPC
633	15	5.1	738	6	ABQ16845	Abq16845 Oligonuc1	c 690	15	5.1	996	6	ABZ42987	ABz42987 Human GPC
c 634	15	5.1	747	2	AAV74964	AAv74964 Stephyloc	c 691	15	5.1	996	6	ABK68496	ABk68496 Human DNA

c 692	15	5.1	996	6	ABK37567	Abk37567 DNA encod	748	15	5.1	1380	4	AAH23395	Aah23395 S. aureus
c 693	15	5.1	996	6	ADN1816	Adn1816 Human G-P	749	15	5.1	1380	7	ACA46380	Aca46380 Prokaryot
c 694	15	5.1	999	9	ACA21167	Ac21167 Prokaryot	750	15	5.1	1389	6	AB213533	Ab213533 Arabidops
c 695	15	5.1	1000	8	ADB23173	Ad23173 Envlfrome	751	15	5.1	1388	7	ACF74361	Acf74361 Stephyloc
c 696	15	5.1	1003	4	AAI17913	Aai17913 G-protein	752	15	5.1	1401	9	ADC40611	Adc40611 Putative
c 697	15	5.1	1004	4	AAI17914	Aai17914 G-protein	753	15	5.1	1401	9	ADC40609	Adc40609 Putative
c 698	15	5.1	1005	4	AAI17915	Aai17915 G-protein	754	15	5.1	1404	3	AAI17347	Aai17347 Arabidops
c 699	15	5.1	1008	3	AAI17917	Aai17917 Human sec	755	15	5.1	1407	4	AAI17347	Aai17347 Arabidops
c 700	15	5.1	1008	3	AAI17917	Aai17917 Human sec	756	15	5.1	1407	4	AAI17347	Aai17347 Arabidops
c 701	15	5.1	1008	3	AAI17917	Aai17917 Human sec	757	15	5.1	1408	3	AAI17347	Aai17347 Arabidops
c 702	15	5.1	1008	3	AAI17917	Aai17917 Human sec	758	15	5.1	1420	4	AAI17629	Aai17629 Stephyloc
c 703	15	5.1	1019	4	AAI17917	Aai17917 Human sec	759	15	5.1	1428	4	AAI17629	Aai17629 Stephyloc
c 704	15	5.1	1019	4	AAI17917	Aai17917 Human sec	760	15	5.1	1431	4	AAI18357	Aai18357 Enterococ
c 705	15	5.1	1031	4	AAI17917	Aai17917 Human sec	761	15	5.1	1431	4	AAI18357	Aai18357 Enterococ
c 706	15	5.1	1034	2	AAI17917	Aai17917 Human sec	762	15	5.1	1443	3	AAI18357	Aai18357 Enterococ
c 707	15	5.1	1047	2	AAI17917	Aai17917 Human sec	763	15	5.1	1443	3	AAI18357	Aai18357 Enterococ
c 708	15	5.1	1047	2	AAI17917	Aai17917 Human sec	764	15	5.1	1449	7	AAI18357	Aai18357 Enterococ
c 709	15	5.1	1052	4	AAI17917	Aai17917 Human sec	765	15	5.1	1455	7	AAI18357	Aai18357 Enterococ
c 710	15	5.1	1074	7	AAI17917	Aai17917 Human sec	766	15	5.1	1458	2	AAI18357	Aai18357 Enterococ
c 711	15	5.1	1081	7	AAI17917	Aai17917 Human sec	767	15	5.1	1458	3	AAI18357	Aai18357 Enterococ
c 712	15	5.1	1082	7	AAI17917	Aai17917 Human sec	768	15	5.1	1460	3	AAI18357	Aai18357 Enterococ
c 713	15	5.1	1082	7	AAI17917	Aai17917 Human sec	769	15	5.1	1465	3	AAI18357	Aai18357 Enterococ
c 714	15	5.1	1088	6	AAI17917	Aai17917 Human sec	770	15	5.1	1477	2	AAI18357	Aai18357 Enterococ
c 715	15	5.1	1096	2	AAI17917	Aai17917 Human sec	771	15	5.1	1491	6	AAI18357	Aai18357 Enterococ
c 716	15	5.1	1099	6	AAI17917	Aai17917 Human sec	772	15	5.1	1491	7	AAI18357	Aai18357 Enterococ
c 717	15	5.1	1099	6	AAI17917	Aai17917 Human sec	773	15	5.1	1494	4	AAI18357	Aai18357 Enterococ
c 718	15	5.1	1107	7	AAI17917	Aai17917 Human sec	774	15	5.1	1501	2	AAI18357	Aai18357 Enterococ
c 719	15	5.1	1115	6	AAI17917	Aai17917 Human sec	775	15	5.1	1501	2	AAI18357	Aai18357 Enterococ
c 720	15	5.1	1115	6	AAI17917	Aai17917 Human sec	776	15	5.1	1501	2	AAI18357	Aai18357 Enterococ
c 721	15	5.1	1128	9	AAI17917	Aai17917 Human sec	777	15	5.1	1560	6	AAI18357	Aai18357 Enterococ
c 722	15	5.1	1152	6	AAI17917	Aai17917 Human sec	778	15	5.1	1571	3	AAI18357	Aai18357 Enterococ
c 723	15	5.1	1152	6	AAI17917	Aai17917 Human sec	779	15	5.1	1573	3	AAI18357	Aai18357 Enterococ
c 724	15	5.1	1188	5	AAI17917	Aai17917 Human sec	780	15	5.1	1581	3	AAI18357	Aai18357 Enterococ
c 725	15	5.1	1188	5	AAI17917	Aai17917 Human sec	781	15	5.1	1590	6	AAI18357	Aai18357 Enterococ
c 726	15	5.1	1200	7	AAI17917	Aai17917 Human sec	782	15	5.1	1593	6	AAI18357	Aai18357 Enterococ
c 727	15	5.1	1227	6	AAI17917	Aai17917 Human sec	783	15	5.1	1594	6	AAI18357	Aai18357 Enterococ
c 728	15	5.1	1232	4	AAI17917	Aai17917 Human sec	784	15	5.1	1594	6	AAI18357	Aai18357 Enterococ
c 729	15	5.1	1245	9	AAI17917	Aai17917 Human sec	785	15	5.1	1671	3	AAI18357	Aai18357 Enterococ
c 730	15	5.1	1282	2	AAI17917	Aai17917 Human sec	786	15	5.1	1674	6	AAI18357	Aai18357 Enterococ
c 731	15	5.1	1289	4	AAI17917	Aai17917 Human sec	787	15	5.1	1674	6	AAI18357	Aai18357 Enterococ
c 732	15	5.1	1306	6	AAI17917	Aai17917 Human sec	788	15	5.1	1695	4	AAI18357	Aai18357 Enterococ
c 733	15	5.1	1306	6	AAI17917	Aai17917 Human sec	789	15	5.1	1695	4	AAI18357	Aai18357 Enterococ
c 734	15	5.1	1332	6	AAI17917	Aai17917 Human sec	790	15	5.1	1695	4	AAI18357	Aai18357 Enterococ
c 735	15	5.1	1332	6	AAI17917	Aai17917 Human sec	791	15	5.1	1695	4	AAI18357	Aai18357 Enterococ
c 736	15	5.1	1332	6	AAI17917	Aai17917 Human sec	792	15	5.1	1695	4	AAI18357	Aai18357 Enterococ
c 737	15	5.1	1332	6	AAI17917	Aai17917 Human sec	793	15	5.1	1695	4	AAI18357	Aai18357 Enterococ
c 738	15	5.1	1332	6	AAI17917	Aai17917 Human sec	794	15	5.1	1695	4	AAI18357	Aai18357 Enterococ
c 739	15	5.1	1332	6	AAI17917	Aai17917 Human sec	795	15	5.1	1695	4	AAI18357	Aai18357 Enterococ
c 740	15	5.1	1332	6	AAI17917	Aai17917 Human sec	796	15	5.1	1695	4	AAI18357	Aai18357 Enterococ
c 741	15	5.1	1362	8	AAI17917	Aai17917 Human sec	797	15	5.1	1695	4	AAI18357	Aai18357 Enterococ
c 742	15	5.1	1367	3	AAI17917	Aai17917 Human sec	798	15	5.1	1695	4	AAI18357	Aai18357 Enterococ
c 743	15	5.1	1367	3	AAI17917	Aai17917 Human sec	799	15	5.1	1695	4	AAI18357	Aai18357 Enterococ
c 744	15	5.1	1367	3	AAI17917	Aai17917 Human sec	800	15	5.1	1695	4	AAI18357	Aai18357 Enterococ
c 745	15	5.1	1373	3	AAI17917	Aai17917 Human sec	801	15	5.1	1695	4	AAI18357	Aai18357 Enterococ
c 746	15	5.1	1374	3	AAI17917	Aai17917 Human sec	802	15	5.1	1695	4	AAI18357	Aai18357 Enterococ
c 747	15	5.1	1379	3	AAI17917	Aai17917 Human sec	803	15	5.1	1695	4	AAI18357	Aai18357 Enterococ
c 748	15	5.1	1380	4	AAI17917	Aai17917 Human sec	804	15	5.1	1695	4	AAI18357	Aai18357 Enterococ

805	15	5.1	1968	AAH66042	Aah66042	C. glutami	862	15	5.1	2776	5	AB200040	Aba20040	Human ner
C 806	15	5.1	1974	AAH87504	DNA encod	Aa87504	863	15	5.1	2840	5	AAH14222	Aah14222	Human cDN
C 807	15	5.1	1997	ABX09818	Promoter	Ab09818	864	15	5.1	2840	6	ABL35318	Ab13518	Human rec
C 808	15	5.1	2000	AB215616	Ab215616	Ab15616	865	15	5.1	2840	6	ABA95211	AbA95211	Human mei
C 809	15	5.1	2000	AB217290	Ab217290	Ab17290	866	15	5.1	2840	9	ABF79542	AbF79542	Human tra
C 810	15	5.1	2000	AB217513	Ab217513	Ab17513	867	15	5.1	2841	2	AAV74488	AaV74488	Strepbyloc
C 811	15	5.1	2000	AB215450	Ab215450	Ab15450	868	15	5.1	2844	4	ABL22730	AbL22730	Human cDN
C 812	15	5.1	2000	AB217249	Ab217249	Ab17249	869	15	5.1	2853	7	ACA17230	Aca17230	Prokaryot
C 813	15	5.1	2000	AB215172	Ab215172	Ab15172	870	15	5.1	2860	4	AAH42602	AaH42602	Human cDN
C 814	15	5.1	2000	AB217176	Ab217176	Ab17176	871	15	5.1	2872	2	AAQ21001	AaQ21001	Murine re
C 815	15	5.1	2000	AB216922	Ab216922	Ab16922	872	15	5.1	2872	2	AAI36881	AaI36881	Murine re
C 816	15	5.1	2000	ACC61839	Gene sequ	Acc61839	873	15	5.1	2881	4	AAI29853	AaI29853	Murine re
C 817	15	5.1	2000	ACC60610	Gene sequ	Acc60610	874	15	5.1	2881	4	AAI29853	AaI29853	Murine re
C 818	15	5.1	2000	ADA72965	Rice gene	Ada72965	875	15	5.1	2881	4	AAI29853	AaI29853	Murine re
C 819	15	5.1	2000	ADA69209	Arabidops	Ada69209	876	15	5.1	2942	7	ADA3471	Ada3471	Human cDN
C 820	15	5.1	2000	ADA72289	Rice gene	Ada72289	877	15	5.1	2988	4	ABL03856	AbL03856	Human cDN
C 821	15	5.1	2000	ADA71503	Rice gene	Ada71503	878	15	5.1	3021	4	AAH52380	AaH52380	S. epidid
C 822	15	5.1	2000	ADA72698	Rice gene	Ada72698	879	15	5.1	3034	6	ABQ14765	AbQ14765	Oligonuc
C 823	15	5.1	2000	ADA69039	Arabidops	Ada69039	880	15	5.1	3046	6	ABQ14765	AbQ14765	Oligonuc
C 824	15	5.1	2003	ABL19153	Ab119153	Ab119153	881	15	5.1	3081	2	AAI67542	AaI67542	H. pylori
C 825	15	5.1	2009	ABX09827	Arabidops	Abx09827	882	15	5.1	3081	2	AAI67542	AaI67542	H. pylori
C 826	15	5.1	2018	AB211954	Ab211954	Ab11954	883	15	5.1	3081	2	AAI67542	AaI67542	H. pylori
C 827	15	5.1	2036	ADDE9644	Human pol	Adde9644	884	15	5.1	3125	9	ABE18630	AbE18630	Human gen
C 828	15	5.1	2089	ABL29641	Human RbM	AbL29641	885	15	5.1	3125	9	ADDE8074	AdE8074	Human gen
C 829	15	5.1	2136	ABX08460	DNA encod	Abx08460	886	15	5.1	3129	7	ADDE8070	AdE8070	Human gen
C 830	15	5.1	2179	AAI58600	Human REC	AaI58600	887	15	5.1	3148	4	AAH54695	AaH54695	S. epidid
C 831	15	5.1	2183	ABL25012	Ab25012	Ab125012	888	15	5.1	3148	6	ABO70799	AbO70799	Listeria
C 832	15	5.1	2271	3	AAI39453	Abc39453	889	15	5.1	3162	4	AAH51358	AaH51358	Enterococ
C 833	15	5.1	2276	4	ABL23704	Ab123704	890	15	5.1	3173	5	AAH54390	AaH54390	S. epidid
C 834	15	5.1	2286	6	AAI38066	Ab138066	891	15	5.1	3199	5	AAH57311	AaH57311	DNA encod
C 835	15	5.1	2346	2	AAI49160	Ab49160	892	15	5.1	3213	5	AAH55545	AaH55545	DNA encod
C 836	15	5.1	2400	6	AB232122	Ab232122	893	15	5.1	3251	4	ABL03846	AbL03846	Human tra
C 837	15	5.1	2457	4	AAH15791	Ab15791	894	15	5.1	3270	4	ABL27756	AbL27756	Prokaryot
C 838	15	5.1	2457	6	ABA95212	Ab153519	895	15	5.1	3278	7	ACCO0397	Aco00397	Human cel
C 839	15	5.1	2457	6	ABA95212	Ab153519	895	15	5.1	3278	7	ACCO0397	Aco00397	Human cel
C 840	15	5.1	2457	9	ACF79543	Human tra	896	15	5.1	3295	4	AAK71764	AaK71764	Human car
C 841	15	5.1	2457	9	ACF79543	Human tra	897	15	5.1	3295	4	AAK71764	AaK71764	Human car
C 842	15	5.1	2463	6	ABK75400	Becl11us	898	15	5.1	3295	4	AAK71764	AaK71764	Human car
C 843	15	5.1	2474	4	ABL25010	Ab25010	899	15	5.1	3308	3	AAI26917	AaI26917	Essential
C 844	15	5.1	2481	4	AAI25945	Human cDN	900	15	5.1	3308	4	AAI26917	AaI26917	Essential
C 845	15	5.1	2481	7	ABK73286	Human nov	901	15	5.1	3308	4	AAI26917	AaI26917	Essential
C 846	15	5.1	2497	7	ACA29300	Prokaryot	902	15	5.1	3308	9	ADBF3670	AaDf3670	Mutant ba
C 847	15	5.1	2497	7	ACA29300	Prokaryot	903	15	5.1	3308	9	ADBF3670	AaDf3670	Mutant ba
C 848	15	5.1	2541	4	ABL27442	Drosophi	904	15	5.1	3344	4	AAH54378	AaH54378	S. epidid
C 849	15	5.1	2570	4	ABL27442	Drosophi	905	15	5.1	3368	5	AAH53563	AaH53563	DNA encod
C 850	15	5.1	2598	4	ABL164986	Neitella	906	15	5.1	3410	7	ABL18618	AbL18618	Human NOV
C 851	15	5.1	2604	4	AAH15797	Human cDN	907	15	5.1	3440	7	AB224210	Ab224210	Human SIC
C 852	15	5.1	2631	3	AAI92471	Shewanell	908	15	5.1	3481	7	AB224210	Ab224210	Human SIC
C 853	15	5.1	2652	3	AAI23702	Drosophi	909	15	5.1	3482	4	AAI04161	AaI04161	Human rep
C 854	15	5.1	2672	4	AAI23702	Drosophi	910	15	5.1	3482	4	AAI04161	AaI04161	Human rep
C 855	15	5.1	2680	9	ADB62602	Human cDN	911	15	5.1	3526	6	AAH061182	AaH061182	Human cDN
C 856	15	5.1	2680	9	ADB62602	Human cDN	911	15	5.1	3526	6	AAH061182	AaH061182	Human cDN
C 857	15	5.1	2711	3	AAA48642	Human cDN	912	15	5.1	3545	7	ABK73306	AbK73306	Human nov
C 858	15	5.1	2711	3	AAA48642	Human cDN	912	15	5.1	3545	7	ABK73306	AbK73306	Human nov
C 859	15	5.1	2725	6	ABK35276	Human cDN	916	15	5.1	3639	4	AAH51721	AaH51721	Prokaryot
C 860	15	5.1	2742	9	ADCF9086	E. faeciu	917	15	5.1	3651	7	ACAI8331	AcaI8331	Prokaryot
C 861	15	5.1	2769	6	AB211334	Human pol	918	15	5.1	3651	7	ACF74791	Acf74791	Strepbyloc

QY 1 ATGTCATATATTAACGAAAAACGAGAAAGTCAAGATGATATTACAAATAGCGAAATC 60
 DB 29268 ATGTCATATATTAACGAAAAACGAGAAAGTCAAGATGATATTACAAATAGCGAAATC 29327
 QY 61 ATACGCAAAAATATTCATGTTACGAGATCGATTTTAAGCTATTCATTTTAAAGGTCAT 120
 DB 29328 ATACGCAAAAATATTCATGTTACGAGATCGATTTTAAGCTATTCATTTTAAAGGTCAT 29387
 QY 121 ATGGGATATCAATACAGTTAAAGATATGACAAAGTACCAATTAAACATGCTTATGTC 180
 DB 29388 ATGGGATATCAATACAGTTAAAGATATGACAAAGTACCAATTAAACATGCTTATGTC 29447
 QY 181 GTAGATGAGATGACTTATGATGATGCTCAAGCTATTATTACCAAGCAATAGATGATGG 240
 DB 29448 GTAGATGAGATGACTTATGATGATGCTCAAGCTATTATTACCAAGCAATAGATGATGG 29507
 QY 241 ATTGAAGAGACACAGACAGACAGACGACTAATTAACTTATGTCGAATGGTATG 297
 DB 29508 ATTGAAGAGACACAGACAGACAGACGACTAATTAACTTATGTCGAATGGTATG 29564

RESULT 3
 AAC86106
 ID AAC86106 standard; cDNA; 41708 BP.
 XX
 AC AAC86106;
 XX
 DT 06-AUG-2003 (revised)
 DT 29-AUG-2001 (first entry)
 XX
 DE Complete genome of bacteriophage 77.
 XX
 KW DnaI; S. aureus; inhibitor; bacteriophage 77; ORF 104; phage 77ORF104;
 KW screening assay; ss.
 XX
 OS Bacteriophage.
 XX
 PN W0200146383-A2.
 XX
 PD 28-JUN-2001.
 XX
 PF 21-DEC-2000; 2000WO-US035180.
 XX
 PR 22-DEC-1999; 98US-00470512.
 PR 12-OCT-2000; 2000US-00689952.
 XX
 PA (PHAG-) PHAGE TECH INC.
 PA (WILL-) WILLIAMS K M.
 XX
 PI Pollettier J, Gros P, Dubow M;
 XX
 DR WPI, 2001-418052/44.
 XX
 PT Novel DnaI polypeptides useful for treating and diagnosing microbial,
 PT preferably bacterial, diseases such as those caused by *Staphylococcus*
 PT *aureus*.

XX
 PS Disclosure; Fig 2; 107pp; English.
 XX
 CC This sequence represents the genome of Bacteriophage 77. The growth
 CC inhibitory gene product of ORF 104 interacts with DnaI derived from S.
 CC aureus, to form the basis of a screening assay. DnaI polypeptides and
 CC polynucleotides are useful for treating microbial, preferably bacterial,
 CC especially *Staphylococcus*, infections. DnaI polypeptides and
 CC polynucleotides are useful for biological, diagnostic, prophylactic,
 CC clinical and therapeutic use, and as components in databases useful for
 CC search analyses as well as in sequence analysis algorithms. (Updated on
 CC 06-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 41708 BP; 15607 A; 5698 C; 8088 G; 12115 T; 0 U; 0 Other;
 Query Match 100.0%; Score 297; DB 4; Length 41708;
 Best Local Similarity 100.0%; Pred. No. 7.6e-138;
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCATATATTAACGAAAAACGAGAAAGTCAAGATGATATTACAAATAGCGAAATC 60
 DB 29268 ATGTCATATATTAACGAAAAACGAGAAAGTCAAGATGATATTACAAATAGCGAAATC 29327
 QY 61 ATACGCAAAAATATTCATGTTACGAGATCGATTTTAAGCTATTCATTTTAAAGGTCAT 120
 DB 29328 ATACGCAAAAATATTCATGTTACGAGATCGATTTTAAGCTATTCATTTTAAAGGTCAT 29387
 QY 121 ATGGGATATCAATACAGTTAAAGATATGACAAAGTACCAATTAAACATGCTTATGTC 180
 DB 29388 ATGGGATATCAATACAGTTAAAGATATGACAAAGTACCAATTAAACATGCTTATGTC 29447
 QY 181 GTAGATGAGATGACTTATGATGATGCTCAAGCTATTATTACCAAGCAATAGATGATGG 240
 DB 29448 GTAGATGAGATGACTTATGATGATGCTCAAGCTATTATTACCAAGCAATAGATGATGG 29507
 QY 241 ATTGAAGAGACACAGACAGACAGACGACTAATTAACTTATGTCGAATGGTATG 297
 DB 29508 ATTGAAGAGACACAGACAGACAGACGACTAATTAACTTATGTCGAATGGTATG 29564

RESULT 4
 AAA68250
 ID AAA68250 standard; DNA; 261 BP.
 XX
 AC AAA68250;
 XX
 DT 15-SEP-2003 (revised)
 DT 06-AUG-2003 (revised)
 DT 27-OCT-2000 (first entry)
 XX
 DE Bacteriophage 77 77ORF043 nucleotide sequence.
 XX
 KW Bacteriophage; antimicrobial; genome; identification; antibacterial;
 KW bacterial growth inhibition; bacterial infection; ds.
 XX
 OS *Staphylococcus aureus*; bacteriophage 77.
 XX

PN WO200032825-A2.
XX
XX 08-JUN-2000.
XX
XX 03-DEC-1999; 99WO-1B002040.
XX
XX 03-DEC-1998; 98US-0110992P.
PR 03-JUN-1999; 99US-00326144.
PR 28-SEP-1999; 99US-00407804.
PR 30-SEP-1999; 99US-0157218P.
PR 01-DEC-1999; 99US-0168777P.
PR 02-DEC-1999; 99US-00454252.
XX
XX (PHAG-) PHAGE TECH INC.
XX
XX Polletier J, Gros P, Dubow M;
XX WPI; 2000-412361/35.
XX P-PSDB; AAB16525.
XX
XX Identifying a bacteriophage coding region for treating bacterial
PT infections comprises identifying a nucleic acid encoding a product that
PT inhibits bacteria when a bacteriophage infects a bacterium.
XX
XX
XX Disclosure; Page 157; 456pp; English.
XX
XX
XX The present invention describes a method for identifying a bacteriophage
CC coding region encoding a product active on an essential bacterial target.
CC The method comprises identifying a nucleic acid sequence encoding a gene
CC product that provides a bacteria-inhibiting function when an
CC uncharacterized bacteriophage infects a pathogenic bacterium. The
CC compound active on a target of a bacteriophage inhibitor protein in a
CC bacteria is used to treat or prevent a bacterial infection in an animal.
CC AAB6243 to AAB69442 and AAB16523 to AAB16954 represent bacteriophage
CC nucleotide and protein sequences which are used in the exemplification of
CC the present invention. (Updated on 06-AUG-2003 to correct OS field.)
CC (Updated on 15-SEP-2003 to standardise OS field)
XX
XX Sequence 261 BP; 105 A; 36 C; 49 G; 71 T; 0 U; 0 Other;
XX
XX Query Match 87.9%; Score 261; DB 3; Length 261;
XX Best Local Similarity 100.0%; Pred. No. 7.7e-120;
XX Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 37 ATGTATTACGAATAGCGCAATCATACGCAAAATATTATCATGTAAAGCATTCATTT 96
XX |
XX |
XX |
XX 1 ATGTATTACGAATAGCGCAATCATACGCAAAATATTATCATGTAAAGCATTCATTT 60
XX |
XX |
XX |
XX 97 AAGCTATTCATTTAAAGGTCAATGCGCATATCATATACAGTTAAAGATAGAACAC 156
XX |
XX |
XX |
XX 61 AAGCTATTCATTTAAAGGTCAATGCGCATATCATATACAGTTAAAGATAGAACAC 120
XX |
XX |
XX |
XX 157 GTACCAATTAAACATGCTTATGTCTAGATGAGAAATGAGTAAATGGCATGAGCTTA 216
XX |
XX |
XX |
XX 121 GTACCAATTAAACATGCTTATGTCTAGATGAGAAATGAGTAAATGGCATGAGCTTA 180
XX |
XX |
XX |
XX 217 TTAAACCAAGCATATGATGATGATTGAAGAAACAGACAGACAGACTAAT 276

DB 181 TTTAACCAAGCATATGATGATGATTGAAGAAACAGACAGACAGACTAAT 240
XX
XX
XX 277 AACTAGTCATGAATGGTAG 297
XX |
XX |
XX |
XX 241 AACTAGTCATGAATGGTAG 261
XX
XX
XX RESULT 5
XX ACF72925
XX ID ACF72925 standard; DNA; 267 BP.
XX
XX ACF72925;
XX
XX 20-NOV-2003 (first entry)
XX
XX Staphylococcus aureus DNA #605.
XX
XX
XX Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
XX enzymatic assay; antibiotic target; gene; ds.
XX
XX Staphylococcus aureus.
XX
XX WO200294868-A2.
XX
XX 28-NOV-2002.
XX
XX 27-MAR-2002; 2002WO-1B002637.
XX
XX 27-MAR-2001; 2001GB-00007661.
XX
XX (CHIR-) CHIRON SPA.
XX
XX Masignani V, More M, Scarselli M;
XX WPI; 2003-120786/11.
XX P-PSDB; AABM1365.
XX
XX New Staphylococcus aureus protein, useful as a vaccine for treating or
PT preventing Staphylococcal infection, specifically an infection caused by
PT S. aureus, e.g. sepsis.
XX
XX Claim 6; SEQ ID NO 1209; 49pp; English.
XX
XX The invention relates to novel genes and encoded proteins from
CC Staphylococcus aureus. A composition comprising the S. aureus protein, a
CC nucleic acid encoding the protein, or an antibody to the protein, is
CC useful as a pharmaceutical, particularly as a vaccine for treating or
CC preventing infection due to Staphylococcus bacteria, specifically an
CC infection caused by S. aureus. The composition is particularly useful for
CC treating or preventing sepsis in a patient. The composition can also be
CC used for diagnostics. The protein is also used in an assay for enzymatic
CC studies and as a target for antibiotics. This sequence represents one of
CC the novel S. aureus genes of the invention
XX
XX Sequence 267 BP; 108 A; 31 C; 52 G; 76 T; 0 U; 0 Other;

Query Match 9.8%; Score 29; DB 7; Length 267;
 Best Local Similarity 100.0%; Pred. No. 0.0002;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 233 ATGATGATTGAGAGAACAGACGAA 261
 |||||
 DB 206 ATGATGATTGAGAGAACAGACGAA 234

RESULT 6
 AAV75514
 ID AAV75514 standard; DNA; 580 BP.
 XX
 AC AAV75514;
 XX
 DT 16-MAR-1999 (first entry)
 XX
 DE Staphylococcus aureus contig SEQ ID #1203.
 XX
 KW Computer readable medium; vaccine; S.aureus infection; immunodetection;
 KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KW skin infection; surgical wound infection; scalded skin syndrome;
 KW toxic shock syndrome; ds.
 XX
 OS Staphylococcus aureus.
 XX
 PN EF786519-A2.
 XX
 PD 30-JUL-1997.
 XX
 PF 07-JAN-1997; 97EP-00100117.
 XX
 PR 05-JAN-1996; 96US-0009861P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Kunach CA; Choi GH; Barash SC; Dillon PJ; Fannon MR; Rosen CA;
 XX
 DR WPI; 1997-374922/35.
 XX
 PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -
 PT stored on computer readable medium and used in the production of anti-
 XX S.aureus vaccines.
 XX
 PS Claim 1; Page 1876; 3271pp; English.
 XX
 CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences
 CC of the invention. The DNA sequences are recorded on a computer readable
 CC medium, preferably selected from a floppy or hard disk, random access
 CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
 CC the S.aureus DNA sequences allows putative functions to be assigned so
 CC that protein-encoding or regulatory regions of commercial, therapeutic or
 CC industrial importance can be obtained. Specifically, sequences which are
 CC likely to encode antigens have been identified and these polypeptides can
 CC be used in a vaccine composition against S.aureus infection. The
 CC polypeptides can also be used in a kit for the immunodetection of
 CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,

CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
 CC skin and surgical wound infections, scalded skin syndrome, toxic shock
 CC syndrome, etc. Organisms transformed with the DNA sequences can be used
 CC for recombinant production of the polypeptides. The new DNA sequences
 CC (and their fragments) are useful as primers or probes for isolating
 CC homologues of any of the S.aureus DNA sequences contained on the computer
 CC readable medium

XX
 SQ Sequence 580 BP; 255 A; 62 C; 123 G; 135 T; 0 U; 5 Other;

Query Match 9.4%; Score 28; DB 2; Length 580;
 Best Local Similarity 100.0%; Pred. No. 0.00061;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 270 ACTAATTAAGTATGATGAAATGTTAG 297
 |||||
 DB 437 ACTAATTAAGTATGATGAAATGTTAG 464

RESULT 7
 AAA68609
 ID AAA68609 standard; DNA; 43576 BP.
 XX
 AC AAA68609;
 XX
 DT 15-SEP-2003 (revised)
 DT 06-AUG-2003 (revised)
 DT 27-OCT-2000 (first entry)
 XX
 DE Bacteriophage 96 complete genome sequence.
 XX
 KW Bacteriophage; antimicrobial; genome; identification; antibacterial;
 KW bacterial growth inhibition; bacterial infection; ds.
 XX
 OS Staphylococcus aureus; bacteriophage 96.
 XX
 PN WO200032825-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 03-DEC-1999; 99WO-1B002040.
 XX
 PR 03-DEC-1998; 98US-0110992P.
 PR 03-JUN-1999; 99US-00326144.
 PR 28-SEP-1999; 99US-00407804.
 PR 30-SEP-1999; 99US-0157218P.
 PR 01-DEC-1999; 99US-0168777P.
 PR 02-DEC-1999; 99US-00454252.
 XX
 PA (PHAG-) PHAGETECH INC.
 XX
 PI Pelletier J; Gros P; Dubow M;
 XX
 DR WPI; 2000-412361/35.
 XX
 PT Identifying a bacteriophage coding region for treating bacterial
 PT infections comprises identifying a nucleic acid encoding a product that

OK nucleic - nucleic search, using sw model

Run on: October 14, 2004, 22:42:59 ; Search time 1388.12 Seconds

(without alignments)
6389.277 Million cell updates/sec

SUMMARIES

28: gb_gsa1: +
29: gb_gsa2: +
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Title:		US-09-407-804A-9	
Perfect score:		297	
Sequence:		1 atgttcacatataaacgaaa.....actagtcacgaatggtg 297	
Scoring table:		OLIGO_NUC	
		Gapop 60.0 , Gapext 60.0	
Searched:		27513289 seqs, 14931090276 residues	
Word size :		0	
Total number of hits satisfying chosen parameters:		55026578	
Minimum DB seq length: 0			
Maximum DB seq length: 2000000000			
Post-processing: Listing first 1000 summaries			
Database :		EST: +	
		1: em_gsa1: +	
		2: em_gsa2: +	
		3: em_gsa3: +	
		4: em_gsa4: +	
		5: em_gsa5: +	
		6: em_gsa6: +	
		7: em_gsa7: +	
		8: em_gsa8: +	
		9: gb_gsa1: +	
		10: gb_gsa2: +	
		11: gb_gsa3: +	
		12: gb_gsa4: +	
		13: gb_gsa5: +	
		14: gb_gsa6: +	
		15: em_gsa7: +	
		16: em_gsa8: +	
		17: em_gsa9: +	
		18: em_gsa10: +	
		19: em_gsa11: +	
		20: em_gsa12: +	
		21: em_gsa13: +	
		22: em_gsa14: +	
		23: em_gsa15: +	
		24: em_gsa16: +	
		25: em_gsa17: +	
		26: em_gsa18: +	
		27: em_gsa19: +	

Result		Query		Description	
No.		Score	Match Length DB ID		
1	23	7.7	1015 29	CHS07IMP	AL440663 T3 end of
2	20	6.7	571 12	B0618748	B0618748 B0618748
3	20	6.7	736 28	BH514116	BH514116 B06W26TF
4	20	6.7	737 29	CE760387	CE760387 t1gr-gsa-
5	19	6.4	121 9	A1951540	A1951540 wv36d07.k
6	19	6.4	188 14	CF856022	CF856022 pMLO064H
7	19	6.4	423 28	B2920613	B2920613 CH240_70C
8	19	6.4	522 29	CG428882	CG428882 ZMWBB024
9	19	6.4	540 29	BX183031	BX183031 Danilo_rar
10	19	6.4	614 28	A2938334	A2938334 2M0196H21
11	19	6.4	656 14	CB330526	CB330526 SPES7506b
12	19	6.4	663 29	CE786696	CE786696 t1gr-gsa-
13	19	6.4	668 28	A2466117	A2466117 1M0278N03
14	19	6.4	672 28	A2647829	A2647829 1M0514J06
15	19	6.4	686 28	A0484294	A0484294 RPCI-11-2
16	19	6.4	692 13	BX777633	BX777633 BX777633
17	19	6.4	692 14	CA346528	CA346528 677448 NC
18	19	6.4	738 13	BU482454	BU482454 604128833
19	19	6.4	782 14	CK138726	CK138726 AGNOCOURT
20	19	6.4	828 28	B2422617	B2422617 1d56b06.b
21	19	6.4	923 28	A2539374	A2539374 ENTGH84TF
22	19	6.4	935 28	A2549644	A2549644 ENTGL62TF
23	19	6.4	937 28	BH165826	BH165826 ENTQV67TF
24	19	6.4	968 29	CC976887	CC976887 ZUMH432TH
25	19	6.4	1349 10	BF973749	BF973749 602241818
26	18	6.1	303 28	AF179090	AF179090 AF179090
27	18	6.1	320 9	AA872489	AA872489 g110c03.s
28	18	6.1	347 29	CC859605	CC859605 NDL.101N1
29	18	6.1	349 28	BH825920	BH825920 BACPR2-J
30	18	6.1	354 9	AA282587	AA282587 z59c002.r
31	18	6.1	360 28	A0265943	A0265943 CTRBT-EL-
32	18	6.1	390 28	B37409	B37409 HS-1043-B1-
33	18	6.1	403 29	CE641065	CE641065 t1gr-gsa-
34	18	6.1	408 9	AA088591	AA088591 2k64d07.r
35	18	6.1	409 9	AA630685	AA630685 a665h06.s
36	18	6.1	412 9	AA255702	AA255702 z521c04.r
37	18	6.1	414 10	AA9917645	AA9917645 EST348949
38	18	6.1	414 13	BY484641	BY484641 BY484641
39	18	6.1	416 28	A2598867	A2598867 1M0413H22
40	18	6.1	420 10	AA9917612	AA9917612 EST348947
41	18	6.1	444 28	BH212049	BH212049 SALX_0070
42	18	6.1	457 29	CE704213	CE704213 t1gr-gsa-
43	18	6.1	458 9	AA047153	AA047153 2K74f07.r
44	18	6.1	461 12	B046548	B046548 B046548

c 46	18	6.1	462	13	BV573081	BV573081	BV573081	103	18	6.1	699	14	CB466979	CB466979	732693	MA
c 47	18	6.1	463	29	CG989891	CG989891	CH240.156	c 104	18	6.1	705	14	CF795789	CF795789	891982	MA
c 48	18	6.1	468	14	189328	189328	ye13609.s1	105	18	6.1	706	13	BK488598	BK488598	DKE2686L	EX
c 49	18	6.1	486	29	BX124558	BX124558	Danlo fer	106	18	6.1	708	12	BG809404	BG809404	mphe0032x	BX
c 50	18	6.1	494	12	BJ046014	BJ046014	BJ046014	c 107	18	6.1	710	13	Bu677557	Bu677557	UI-CF-EEO	BX
c 51	18	6.1	495	13	BX872646	BX872646	BX872646	108	18	6.1	713	29	BK172652	BK172652	Danlo fer	CE217017
c 52	18	6.1	508	28	AO375859	AO375859	RPCI11-14	109	18	6.1	715	29	CG275417	CG275417	OCGCL06TH	CG275417
c 53	18	6.1	509	9	AM021842	AM021842	d129a06.y	c 110	18	6.1	717	29	CG275417	CG275417	OCGCL06TH	CG275417
c 54	18	6.1	510	12	BI963093	BI963093	1e62g06.y	111	18	6.1	720	29	CG275417	CG275417	OCGCL06TH	CG275417
c 55	18	6.1	511	9	AA801416	AA801416	EST190913	112	18	6.1	723	28	BZ458710	BZ458710	BONP637F	AI290974
c 56	18	6.1	511	9	AA146950	AA146950	z043d12.f	113	18	6.1	725	9	AI290974	AI290974	gm15c08.x	BI087876
c 57	18	6.1	515	10	BE031338	BE031338	133469.MA	114	18	6.1	748	12	BI087876	BI087876	602852679	AI181447
c 58	18	6.1	518	9	AI958218	AI958218	fc92d12.y	c 115	18	6.1	749	29	CNS0242Y	CNS0242Y	tetracdon	CA1312676
c 59	18	6.1	524	12	Bu642732	Bu642732	AMQNNC.N	c 116	18	6.1	760	14	BE539851	BE539851	601061965	BZ085908
c 60	18	6.1	532	14	CB718807	CB718807	tlgrf-gss-	117	18	6.1	779	10	BE539851	BE539851	11h3Bb01.	BZ085908
c 61	18	6.1	532	29	CE201002	CE201002	RPCI-23-1	c 118	18	6.1	780	28	BZ085908	BZ085908	603593512	BZ085908
c 62	18	6.1	533	28	AZ553820	AZ553820	RPCI-23-1	119	18	6.1	785	13	Bu246775	Bu246775	603593512	BZ085908
c 63	18	6.1	533	28	BZ518982	BZ518982	BOMP216TR	120	18	6.1	789	28	BH527597	BH527597	BOCZ730TR	BH527597
c 64	18	6.1	546	13	BU295921	BU295921	603802505	121	18	6.1	799	28	BK200998	BK200998	Danlo fer	BX200998
c 65	18	6.1	547	10	BF54762	BF54762	UI-R-A0-A	c 122	18	6.1	804	13	BE614108	BE614108	601503850	BE614108
c 66	18	6.1	560	12	BU070385	BU070385	AV590721	123	18	6.1	811	10	BE614108	BE614108	601503850	BE614108
c 67	18	6.1	563	9	AV590721	AV590721	AV590721	124	18	6.1	824	9	AU118315	AU118315	601503850	AU118315
c 68	18	6.1	563	12	BM190058	BM190058	POSM01000	125	18	6.1	830	12	BG784002	BG784002	SEAMC003	BG784002
c 69	18	6.1	564	28	BH008399	BH008399	eF15c01.x	c 126	18	6.1	833	28	AZ702636	AZ702636	RPCI-23-2	AZ702636
c 70	18	6.1	573	12	BI444760	BI444760	daa93a07.	127	18	6.1	838	28	BH660714	BH660714	BONP612TR	BH660714
c 71	18	6.1	575	29	CE495919	CE495919	tlgrf-gss-	c 128	18	6.1	841	13	BU116745	BU116745	603139747	CG825123
c 72	18	6.1	578	14	CA386811	CA386811	668508.NC	c 129	18	6.1	843	29	CG825123	CG825123	SOAC94TV	CG825123
c 73	18	6.1	584	14	CD678706	CD678706	hp12b06.y	c 130	18	6.1	846	14	CA987036	CA987036	AGNOCOURT	BF694081
c 74	18	6.1	588	14	CA650925	CA650925	wreln.pk1	131	18	6.1	847	10	BF694081	BF694081	602862686	BK467886
c 75	18	6.1	590	9	AL704631	AL704631	DKE26860	132	18	6.1	855	13	BK467886	BK467886	602862686	BK467886
c 76	18	6.1	592	9	AA818734	AA818734	UI-R-A0-A	133	18	6.1	872	12	EG399577	EG399577	602441871	BF618320
c 77	18	6.1	598	12	BM970383	BM970383	UI-CF-ECL	134	18	6.1	891	10	BF618320	BF618320	CHVME000	CC509879
c 78	18	6.1	602	13	BU070239	BU070239	Im11b01.x	c 135	18	6.1	900	29	CC509879	CC509879	CH240.353	BU201993
c 79	18	6.1	606	9	AA149491	AA149491	z12Bb05.f	136	18	6.1	910	13	BU201993	BU201993	603951810	CF108627
c 80	18	6.1	606	14	CA375660	CA375660	653788.NC	137	18	6.1	920	14	CF108627	CF108627	Shu1tzm1	BU481226
c 81	18	6.1	609	14	CD931537	CD931537	GR45.114M	138	18	6.1	937	13	BU481226	BU481226	603469859	BF209546
c 82	18	6.1	628	12	BM509287	BM509287	1h19h05.x	139	18	6.1	964	10	BF209546	BF209546	601872730	BF209546
c 83	18	6.1	632	12	BI492771	BI492771	dE29a06.w	140	18	6.1	998	28	BZ466016	BZ466016	BONKw64TF	BZ466016
c 84	18	6.1	645	29	CE511088	CE511088	tlgrf-gss-	c 141	18	6.1	1149	28	CC274388	CC274388	CH261-112	BE875565
c 85	18	6.1	648	12	BU091083	BU091083	BJ091083	142	18	6.1	1183	10	BE875565	BE875565	601487003	AK081376
c 86	18	6.1	650	14	CA780127	CA780127	MP1384.4	143	18	6.1	4693	11	AK081376	AK081376	Mus muscu	CB870415
c 87	18	6.1	653	28	AZ638156	AZ638156	1M0497120	144	17	5.7	178	14	CB870415	CB870415	HCI4E06w	CB870415
c 88	18	6.1	656	29	CG069104	CG069104	PURK44TD	c 145	17	5.7	190	14	CB485548	CB485548	602862686	CB485548
c 89	18	6.1	657	13	BU433855	BU433855	603258238	146	17	5.7	212	10	BF228723	BF228723	SMOVL3CAN	BE228723
c 90	18	6.1	658	10	BF637378	BF637378	NF028A03P	c 147	17	5.7	213	10	BE009943	BE009943	PM3-RN017	BE009943
c 91	18	6.1	667	10	BE539553	BE539553	601060265	148	17	5.7	214	9	AV020077	AV020077	PFEST0ab2	BO597041
c 92	18	6.1	672	14	CA310990	CA310990	UI-CF-FNO	149	17	5.7	227	13	BQ597041	BQ597041	60200068	BM027341
c 93	18	6.1	677	13	BQ477501	BQ477501	1k87g12.x	c 150	17	5.7	229	12	BM027341	BM027341	G1T000068	AZ782938
c 94	18	6.1	681	12	BM491033	BM491033	PMP2n.pk0	151	17	5.7	233	28	AZ782938	AZ782938	2M0024P12	AU059887
c 95	18	6.1	682	14	CF2723187	CF2723187	EST2749.Z	152	17	5.7	243	9	AU059887	AU059887	2M0024P12	AA121205
c 96	18	6.1	682	28	BH428060	BH428060	BONHUS1TR	153	17	5.7	245	9	AA121205	AA121205	zn30b10.f	BO757813
c 97	18	6.1	682	29	CE721090	CE721090	tlgrf-gss-	154	17	5.7	247	9	BQ757813	BQ757813	602862686	CD141160
c 98	18	6.1	684	14	CF273024	CF273024	EST2586.Z	c 155	17	5.7	260	13	CD141160	CD141160	MEI-0069T	BF803200
c 99	18	6.1	685	14	CD931536	CD931536	GR45.114M	c 156	17	5.7	263	14	CD141160	CD141160	602862686	BI703410
c 100	18	6.1	688	14	CA367832	CA367832	643832.NC	157	17	5.7	282	10	BF803200	BF803200	602862686	AV339529
c 101	18	6.1	688	14	CA367832	CA367832	643832.NC	c 158	17	5.7	287	12	BI703410	BI703410	602862686	AV339529
c 102	18	6.1	698	28	AZ702634	AZ702634	RPCI-23-2	159	17	5.7	298	9	AV339529	AV339529	602862686	AV339529

c 160	17	5.7	299	14	CD063005	CD063005	MA1-00290	c 217	17	5.7	446	14	CD159741	CD159741	ML1-0064G
c 161	17	5.7	301	9	AV428985	AV428985	AV428985	c 218	17	5.7	447	13	BX356924	BX356924	BX356924
c 162	17	5.7	305	12	BI703411	BI703411	fs90c04.y	c 219	17	5.7	449	9	A1384718	A1384718	B006D09.x
c 163	17	5.7	314	14	CF002778	CF002778	QEH15606.y	c 220	17	5.7	453	13	BY472564	BY472564	BY472564
c 164	17	5.7	321	14	CD159773	CD159773	ML1-0064G	c 221	17	5.7	455	14	H43732	H43732	Y221b05.r1
c 165	17	5.7	325	12	BG354250	BG354250	947033D10	c 222	17	5.7	458	9	AJ283752	AJ283752	A43B-NAF-
c 166	17	5.7	338	12	BI350479	BI350479	fr34c01.x	c 223	17	5.7	459	9	AA794496	AA794496	vt46g01.s
c 167	17	5.7	340	9	AL501134	AL501134	AL501134	c 224	17	5.7	460	14	CB377792	CB377792	ML1-0064G
c 168	17	5.7	345	10	AA481192	AA481192	34786 MAR	c 225	17	5.7	460	14	CD159785	CD159785	ML1-0064G
c 169	17	5.7	347	13	CA000609	CA000609	HS07M19u	c 226	17	5.7	462	12	BI880146	BI880146	fm32d03.x
c 170	17	5.7	348	9	AA487238	AA487238	ab21e11.s	c 227	17	5.7	462	29	CE697617	CE697617	tlgr-g9s-
c 171	17	5.7	351	28	AZ411905	AZ411905	1M0193H15	c 228	17	5.7	463	14	CF165371	CF165371	SP_0082.B
c 172	17	5.7	352	13	BO518498	BO518498	EST625913	c 229	17	5.7	463	28	AZ485372	AZ485372	BM755606-
c 173	17	5.7	359	29	CE018865	CE018865	tlgr-g9s-	c 230	17	5.7	463	28	AZ647024	AZ647024	1M0513N16
c 174	17	5.7	360	13	CA7083	CA7083	Yuj1	c 231	17	5.7	476	14	CD151335	CD151335	ML1-0032T
c 175	17	5.7	360	14	D76260	D76260	CELK116B4F	c 232	17	5.7	479	28	AZ165551	AZ165551	SP_0082.B
c 176	17	5.7	360	28	CC428366	CC428366	PUEID2TD	c 233	17	5.7	485	13	BY243809	BY243809	BY243809
c 177	17	5.7	361	10	AM164055	AM164055	Lj1lrppest	c 234	17	5.7	485	29	CE629783	CE629783	tlgr-g9s-
c 178	17	5.7	361	12	BI703322	BI703322	fr84d10.y	c 235	17	5.7	486	28	BH437009	BH437009	BO80Z4TF
c 179	17	5.7	364	28	AZ702724	AZ702724	RPCI-23-2	c 236	17	5.7	490	14	CD923032	CD923032	G750.106B
c 180	17	5.7	365	12	BG380121	BG380121	UI-R-CS0-	c 237	17	5.7	490	28	AQ213527	AQ213527	HS_3021.B
c 181	17	5.7	378	14	CD171473	CD171473	MS1-0010T	c 238	17	5.7	495	9	AA534580	AA534580	nf81a01.s
c 182	17	5.7	382	12	BI863990	BI863990	ft16d01.x	c 239	17	5.7	495	12	BM737776	BM737776	K-EST0000
c 183	17	5.7	386	13	BU882152	BU882152	UM73TC09	c 240	17	5.7	496	12	BJ461905	BJ461905	BI461905
c 184	17	5.7	388	12	BI992287	BI992287	102005980	c 241	17	5.7	496	12	BM959014	BM959014	PLATE_10-
c 185	17	5.7	394	13	BX492477	BX492477	DKXP781E	c 242	17	5.7	498	12	EM025230	EM025230	Fu53g08.y
c 186	17	5.7	395	13	BI613376	BI613376	BY613376	c 243	17	5.7	500	9	AU086596	AU086596	AU086596
c 187	17	5.7	399	9	AV653367	AV653367	AV653367	c 244	17	5.7	501	12	BJ462291	BJ462291	BJ462291
c 188	17	5.7	399	9	AV653455	AV653455	AV653455	c 245	17	5.7	503	29	CG161066	CG161066	PUM6547B
c 189	17	5.7	403	13	BY510745	BY510745	BY510745	c 246	17	5.7	504	10	BF439218	BF439218	pump61b09.
c 190	17	5.7	403	14	CB766715	CB766715	AMGNNC:S	c 247	17	5.7	509	28	AQ321707	AQ321707	RPCI11-98
c 191	17	5.7	405	14	CD063383	CD063383	MA1-0049T	c 248	17	5.7	510	28	AQ440696	AQ440696	HS_5114.B
c 192	17	5.7	407	9	AA332691	AA332691	EST36794	c 249	17	5.7	513	29	CG865235	CG865235	ZMWBB033
c 193	17	5.7	408	10	BE237268	BE237268	146582 NA	c 250	17	5.7	516	10	BB134753	BB134753	BB134753
c 194	17	5.7	410	28	AQ363028	AQ363028	nbab00538	c 251	17	5.7	516	10	BB640566	BB640566	BB640566
c 195	17	5.7	411	13	BY623508	BY623508	AV610147	c 252	17	5.7	516	28	BH820400	BH820400	BACPR14-D
c 196	17	5.7	414	13	BY623508	BY623508	MS1-0025T	c 253	17	5.7	518	9	A1732799	A1732799	ab21e11.x
c 197	17	5.7	417	14	CD180546	CD180546	MS1-0025T	c 254	17	5.7	518	10	AM505521	AM505521	UI-HR-BM0
c 198	17	5.7	417	28	AQ186008	AQ186008	HS_3070.A	c 255	17	5.7	518	12	BM959057	BM959057	PLATE_15
c 199	17	5.7	419	9	AA487179	AA487179	ab21c11.s	c 256	17	5.7	518	14	CA360520	CA360520	633907 NC
c 200	17	5.7	420	9	AI686161	AI686161	tt92g12.x	c 257	17	5.7	519	13	CA000637	CA000637	HS07E03u
c 201	17	5.7	421	13	BQ662116	BQ662116	HRO1K02u	c 258	17	5.7	520	12	BI864898	BI864898	ft19f09.x
c 202	17	5.7	423	29	CC945736	CC945736	BOICG66TF	c 259	17	5.7	521	14	CD489268	CD489268	T21_A03 T
c 203	17	5.7	424	14	CD179786	CD179786	MS1-0019T	c 260	17	5.7	524	14	CD535231	CD535231	lm01T09.y
c 204	17	5.7	426	13	BK106841	BK106841	BX106841	c 261	17	5.7	524	28	AZ433259	AZ433259	1M0219102
c 205	17	5.7	427	12	BM178861	BM178861	900216 AV	c 262	17	5.7	526	12	BI350855	BI350855	fr40b02.y
c 206	17	5.7	428	29	CE292254	CE292254	tlgr-g9s-	c 263	17	5.7	528	14	CB485130	CB485130	otrchm10
c 207	17	5.7	434	9	AV792912	AV792912	AV792912	c 264	17	5.7	529	14	N65371	N65371	20411 lamed
c 208	17	5.7	436	14	CB792209	CB792209	AMGNNC:S	c 265	17	5.7	532	13	CA000132	CA000132	HS05H20u
c 209	17	5.7	439	14	CD071932	CD071932	MA2-0036G	c 266	17	5.7	533	28	BH774356	BH774356	uzmbd003f0
c 210	17	5.7	442	14	CD163698	CD163698	ML1-0083U	c 267	17	5.7	533	28	AZ058293	AZ058293	RPCI-23-4
c 211	17	5.7	442	29	DR24E16T	DR24E16T	Danlo rer	c 268	17	5.7	535	28	AQ5682734	AQ5682734	RPCI-11-4
c 212	17	5.7	443	10	BB736326	BB736326	BB736326	c 269	17	5.7	536	14	CB223434	CB223434	1J3J23D9
c 213	17	5.7	443	10	BB840465	BB840465	BB840465	c 270	17	5.7	536	28	BZ130904	BZ130904	CH230-452
c 214	17	5.7	443	28	AQ333975	AQ333975	HS_5003.A	c 271	17	5.7	537	28	AZ043135	AZ043135	RPCI-23-3
c 215	17	5.7	444	28	AZ664379	AZ664379	1M0544F03	c 272	17	5.7	538	13	BY474785	BY474785	BY474785
c 216	17	5.7	445	14	N65216	N65216	20256 lamed	c 273	17	5.7	539	9	AL911728	AL911728	AL911728

274	17	5.7	539	9	AL923185	AL923185	331	17	5.7	592	12	BI429029	BI429029	f-r71e03.y
275	17	5.7	539	12	BU019717	BU019717	332	17	5.7	597	28	CC393970	CC393970	PUEFL437D
276	17	5.7	541	12	BG082063	H3072A10	333	17	5.7	598	12	BI497547	BI497547	
277	17	5.7	541	12	BM160508	EST563031	334	17	5.7	598	13	BQ723941	BQ723941	AGNOCOURT
278	17	5.7	541	14	CF893896	A0128H12-	335	17	5.7	599	10	AM967995	AM967995	EST379980
279	17	5.7	543	28	AZ521059	RPCI-11-2	336	17	5.7	600	12	BG802981	BG802981	0193-45 M
280	17	5.7	544	28	AZ043949	RPCI-23-2	337	17	5.7	600	13	BI9319815	BI9319815	
281	17	5.7	546	10	AM333199	S18F4 AGS	338	17	5.7	602	9	AL699109	AL699109	DKF2p686B
282	17	5.7	548	14	CA194954	SCMG8108	339	17	5.7	602	9	AL719598	AL719598	AL719598
283	17	5.7	548	14	CF532854	UI-M-GHO-	340	17	5.7	602	12	BI103294	BI103294	
284	17	5.7	550	10	AM773600	EST332586	341	17	5.7	602	13	BK082315	BK082315	BX082315
285	17	5.7	551	12	BI429315	fFe8a03.y	342	17	5.7	603	13	CM025081	CM025081	H251C14F
286	17	5.7	552	12	BI428471	HS-5111.A	343	17	5.7	602	29	CE203989	CE203989	t1g-r-gss-
287	17	5.7	553	28	AQ410320	NS410320	344	17	5.7	603	10	AM970362	AM970362	EST362443
288	17	5.7	556	29	CE514470	t1g-r-gss-	345	17	5.7	604	13	BQ075080	BQ075080	fFe27408.x
289	17	5.7	556	14	CD185112	MS1-0051T	346	17	5.7	604	14	CF622008	CF622008	1aE11gY08.
290	17	5.7	558	12	BI936043	BS196043	347	17	5.7	605	14	BQ913336	BQ913336	QHA7B02.y
291	17	5.7	559	14	CB536735	771778 MA	348	17	5.7	605	28	AZ459386	AZ459386	1M0264111
292	17	5.7	562	10	AM353125	S43E1 AGS	349	17	5.7	605	28	BZ709988	BZ709988	OGSM037C
293	17	5.7	563	9	AU024507	AU024507	350	17	5.7	607	12	BI267928	BI267928	NFL14H121
294	17	5.7	563	10	BE123231	AO923373	351	17	5.7	607	14	CE244577	CE244577	UI-M-PYO-
295	17	5.7	563	28	AQ923373	RPCI-23-2	352	17	5.7	607	29	CE723430	CE723430	t1g-r-gss-
296	17	5.7	564	28	BZ759503	621_4L.G1	353	17	5.7	611	12	BM072582	BM072582	fV08N05.y
297	17	5.7	564	12	BZ595304	fA64b05.y	354	17	5.7	611	28	AZ418860	AZ418860	1M0194014
298	17	5.7	565	28	AQ720634	HS_5546.B	355	17	5.7	612	13	BK621393	BK621393	BX621393
299	17	5.7	566	29	CE095411	t1g-r-gss-	356	17	5.7	615	28	BZ432878	BZ432878	1d544d05.y
300	17	5.7	567	13	BO971251	QHB6F15.y	357	17	5.7	617	13	BO911962	BO911962	QHL9R923.y
301	17	5.7	569	12	BM275708	BM275708	358	17	5.7	618	28	AZ247021	AZ247021	RPCI-23-9
302	17	5.7	569	13	BK737918	BK737918	359	17	5.7	619	12	BI126743	BI126743	
303	17	5.7	569	28	BZ679198	PUBB8497D	360	17						

388	17	5.7	641	28	B267272	1h51d09.1b	c 445	17	5.7	709	14	CA762859	CA762859	BR060008A
389	17	5.7	642	12	B687872	MEST43-F0	c 446	17	5.7	709	14	CF534097	CF534097	UI-M-GHO-
390	17	5.7	643	14	CF532744	UI-M-GHO-	c 447	17	5.7	710	13	BQ180624	BQ180624	UI-M-GHO-
c 391	17	5.7	644	13	BK510120	DKFEP686D	c 448	17	5.7	711	12	BJ021333	BJ021333	UI-M-GHO-
392	17	5.7	644	14	CF745029	UI-M-GVO-	c 449	17	5.7	711	13	BK077221	BK077221	UI-M-GHO-
393	17	5.7	646	14	CF723748	UI-M-FYO-	c 450	17	5.7	712	10	BG069039	BG069039	UI-M-GHO-
394	17	5.7	647	9	AU253519	AU253519	c 451	17	5.7	712	10	CC790062	CC790062	UI-M-GHO-
395	17	5.7	649	28	AC912617	RPCT-24-1	c 452	17	5.7	712	29	CG693958	CG693958	UI-M-GHO-
c 396	17	5.7	652	13	CA160894	SCMCR306	c 453	17	5.7	713	12	BJ540962	BJ540962	UI-M-GHO-
397	17	5.7	653	10	BF298122	060PbE01	c 454	17	5.7	713	14	CA325245	CA325245	UI-M-GHO-
398	17	5.7	655	29	AG148030	Pan treg1	c 455	17	5.7	713	14	CF182447	CF182447	UI-M-GHO-
399	17	5.7	656	28	AZ369500	1M0120D10	c 456	17	5.7	713	29	CE338908	CE338908	UI-M-GHO-
c 400	17	5.7	657	12	BJ509403	BJ509403	c 457	17	5.7	714	13	CF534147	CF534147	UI-M-GHO-
401	17	5.7	657	13	BQ480954	Ea67206.	c 458	17	5.7	714	13	BQ546146	BQ546146	UI-M-GHO-
c 402	17	5.7	663	13	BU715011	SCMBS001	c 459	17	5.7	717	14	CB249979	CB249979	UI-M-GHO-
403	17	5.7	663	14	CB519872	UI-M-GHO-	c 460	17	5.7	717	14	CB526633	CB526633	UI-M-GHO-
c 404	17	5.7	665	13	BY741953	BY741953	c 461	17	5.7	717	28	AZ381379	AZ381379	UI-M-GHO-
405	17	5.7	666	14	CF540041	UI-M-GVO-	c 462	17	5.7	720	12	BJ539515	BJ539515	UI-M-GHO-
c 406	17	5.7	667	10	BB521610	BB521610	c 463	17	5.7	722	12	CA384982	CA384982	UI-M-GHO-
407	17	5.7	667	28	AZ245826	RPCT-23-4	c 464	17	5.7	723	14	CB248828	CB248828	UI-M-GHO-
408	17	5.7	669	12	BI261287	602969018	c 465	17	5.7	723	14	CB289966	CB289966	UI-M-GHO-
c 409	17	5.7	669	28	BH955056	cd108604.	c 466	17	5.7	723	14	CB658962	CB658962	UI-M-GHO-
410	17	5.7	670	14	CD349458	UI-M-FYO-	c 467	17	5.7	723	29	CE761977	CE761977	UI-M-GHO-
411	17	5.7	670	28	AZ093842	RPCT-23-4	c 468	17	5.7	724	14	CB429306	CB429306	UI-M-GHO-
412	17	5.7	671	14	CF744025	UI-M-GVO-	c 469	17	5.7	726	14	CA919348	CA919348	UI-M-GHO-
c 413	17	5.7	672	29	CS820908	SCMCR306	c 470	17	5.7	726	14	CF536851	CF536851	UI-M-GHO-
414	17	5.7	673	13	BK305022	UI-M-GHO-	c 471	17	5.7	726	14	BH007589	BH007589	UI-M-GHO-
415	17	5.7	675	28	AZ468744	1M0281J17	c 472	17	5.7	727	12	BG618564	BG618564	UI-M-GHO-
416	17	5.7	676	9	AV653243	AV653243	c 473	17	5.7	728	11	CA348418	CA348418	UI-M-GHO-
c 417	17	5.7	676	29	CG052463	PUMP42TD	c 474	17	5.7	729	14	CNS0803G	CNS0803G	UI-M-GHO-
418	17	5.7	678	14	CB214436	OML04716	c 475	17	5.7	730	13	BU347809	BU347809	UI-M-GHO-
419	17	5.7	682	28	CC324799	TAN32-10C	c 476	17	5.7	730	28	AQ291302	AQ291302	UI-M-GHO-
c 420	17	5.7	683	28	BH824342	BACP20-N	c 477	17	5.7	730	28	B2368356	B2368356	UI-M-GHO-
421	17	5.7	689	14	CB519117	UI-M-GHO-	c 478	17	5.7	731	29	CC504377	CC504377	UI-M-GHO-
422	17	5.7	690	14	CB248922	UI-M-GHO-	c 479	17	5.7	732	12	BW943819	BW943819	UI-M-GHO-
423	17	5.7	690	14	CB248922	UI-M-GHO-	c 480	17	5.7	733	12	CD350082	CD350082	UI-M-GHO-
424	17	5.7	690	14	CB447711	701732 MA	c 481	17	5.7	734	14	BI738982	BI738982	UI-M-GHO-
425	17	5.7	694	14	CB525130	UI-M-FYO-	c 482	17	5.7	735	14	CB249760	CB249760	UI-M-GHO-
426	17	5.7	695	14	CB249774	UI-M-GHO-	c 483	17	5.7	736	29	AG081460	AG081460	UI-M-GHO-
c 427	17	5.7	695	29	CC711044	OGED34TV	c 484	17	5.7	738	14	CB520841	CB520841	UI-M-GHO-
c 428	17	5.7	696	28	BZ423864	1d54c02.9	c 485	17	5.7	738	29	AG049971	AG049971	UI-M-GHO-
429	17	5.7	698	14	CK239312	AGENCOURT	c 486	17	5.7	740	28	BH427301	BH427301	UI-M-GHO-
c 430	17	5.7	699	13	BU722530	BU722530	c 487	17	5.7	741	13	BQ180496	BQ180496	UI-M-GHO-
c 431	17	5.7	700	12	BP115175	BP115175	c 488	17	5.7	741	13	CA139810	CA139810	UI-M-GHO-
432	17	5.7	700	14	CB578408	UI-M-FYO-	c 489	17	5.7	742	14	CB519090	CB519090	UI-M-GHO-
433	17	5.7	701	13	BK673897	BK673897	c 490	17	5.7	743	13	CA752208	CA752208	UI-M-GHO-
434	17	5.7	701	28	BH054777	RPCT-24-2	c 491	17	5.7	743	13	CA752208	CA752208	UI-M-GHO-
435	17	5.7	702	14	CA384914	665680 NC	c 492	17	5.7	744	13	BK083166	BK083166	UI-M-GHO-
c 436	17	5.7	702	28	CC072258	CSU-K33r.	c 493	17	5.7	744	13	CF182763	CF182763	UI-M-GHO-
437	17	5.7	703	28	BZ012105	06134d06.	c 494	17	5.7	746	28	CC128622	CC128622	UI-M-GHO-
c 438	17	5.7	704	29	CG924814	MDEK85TF	c 495	17	5.7	749	28	CC247469	CC247469	UI-M-GHO-
c 439	17	5.7	707	14	BG965957	601659850	c 496	17	5.7	752	14	CB521168	CB521168	UI-M-GHO-
440	17	5.7	707	14	CB528208	UI-M-FYO-	c 497	17	5.7	753	14	CA138569	CA138569	UI-M-GHO-
c 441	17	5.7	708	10	BF362333	PMO-NN004	c 498	17	5.7	754	12	BM167220	BM167220	UI-M-GHO-
c 442	17	5.7	708	12	BJ508392	BJ508392	c 499	17	5.7	754	14	CB519577	CB519577	UI-M-GHO-
443	17	5.7	708	13	BQ442269	UI-M-GHO-	c 500	17	5.7	754	14	CF532371	CF532371	UI-M-GHO-
444	17	5.7	708	14	CF728091	CF728091	c 501	17	5.7	754	28	CC087704	CC087704	UI-M-GHO-

502	17	5.7	755	13	BK082316	BK082316	c 559	17	5.7	904	28	B2176853
503	17	5.7	758	13	BK081852	BK081852	c 560	17	5.7	908	29	CG951474
504	17	5.7	759	28	BH606187	BH606187	c 561	17	5.7	915	10	BE739615
505	17	5.7	760	28	BE709997	BE709997	c 562	17	5.7	921	10	BE7689582
506	17	5.7	761	13	BK082712	BK082712	c 563	17	5.7	924	29	CGNS04DEL
507	17	5.7	762	12	BM963405	BM963405	c 564	17	5.7	926	29	AG131045
508	17	5.7	763	12	BK082712	BK082712	c 565	17	5.7	932	10	BE794648
509	17	5.7	763	14	CH027696	CH027696	c 566	17	5.7	938	10	BE986784
510	17	5.7	763	28	BZ442109	BZ442109	c 567	17	5.7	944	10	BE104206
511	17	5.7	764	29	CG761621	CG761621	c 568	17	5.7	945	28	AZ166857
512	17	5.7	764	29	CG888560	CG888560	c 569	17	5.7	949	28	CG187881
513	17	5.7	765	13	BK082712	BK082712	c 570	17	5.7	953	28	CG187881
514	17	5.7	766	29	CG952252	CG952252	c 571	17	5.7	953	28	AZ546793
515	17	5.7	766	29	CG952252	CG952252	c 572	17	5.7	962	29	CG864763
516	17	5.7	772	14	CH431066	CH431066	c 573	17	5.7	970	13	BQ945887
517	17	5.7	774	14	CH535686	CH535686	c 574	17	5.7	979	12	BM415718
518	17	5.7	774	28	BZ502796	BZ502796	c 575	17	5.7	979	12	CG937630
519	17	5.7	775	28	CG904137	CG904137	c 576	17	5.7	985	29	CG215171
520	17	5.7	776	28	BZ063714	BZ063714	c 577	17	5.7	1001	14	CA471037
521	17	5.7	777	14	CF182590	CF182590	c 578	17	5.7	1002	13	BK408717
522	17	5.7	782	29	CHS01KVM	CHS01KVM	c 579	17	5.7	1008	12	BG482252
523	17	5.7	784	13	BK083167	BK083167	c 580	17	5.7	1015	13	BQ934321
524	17	5.7	785	12	B1851873	B1851873	c 581	17	5.7	1019	28	CC282360
525	17	5.7	793	12	BK073840	BK073840	c 582	17	5.7	1024	28	CC304758
526	17	5.7	793	12	BK073840	BK073840	c 583	17	5.7	1028	28	CC304758
527	17	5.7	795	13	BK073840	BK073840	c 584	17	5.7	1033	29	CG907498
528	17	5.7	796	14	CF550433	CF550433	c 585	17	5.7	1033	29	CG907498
529	17	5.7	801	28	BH069243	BH069243	c 586	17	5.7	1041	28	CG907498
530	17	5.7	807	13	BK077222	BK077222	c 587	17	5.7	1041	28	CG907498
531	17	5.7	808	14	CA969404	CA969404	c 588	17	5.7	1045	12	BG295596
532	17	5.7	809	29	CG539302	CG539302	c 589	17	5.7	1092	12	BF342427
533	17	5.7	816	28	CC173934	CC173934	c 590	17	5.7	1094	28	CC2734352
534	17	5.7	818	14	CH027506	CH027506	c 591	17	5.7	1156	12	BG539949
535	17	5.7	823	12	B1852870	B1852870	c 592	17	5.7	1167	12	BG539949
536	17	5.7	828	28	CC086956	CC086956	c 593	17	5.7	1197	28	CC261180
537	17	5.7	831	28	BZ463862	BZ463862	c 594	17	5.7	1201	14	CG028287
538	17	5.7	831	28	BZ604705	BZ604705	c 595	17	5.7	1204	29	CG750473
539	17	5.7	832	13	BK082517	BK082517	c 596	17	5.7	1212	12	BM549314
540	17	5.7	832	14	CH027506	CH027506	c 597	17	5.7	1230	28	CC189151
541	17	5.7	836	29	BK169244	BK169244	c 598	17	5.7	1234	12	BE1686981
542	17	5.7	837	13	BK078183	BK078183	c 599	17	5.7	1253	12	CG748711
543	17	5.7	843	29	CG922445	CG922445	c 600	17	5.7	1254	12	BM467495
544	17	5.7	847	13	CH082517	CH082517	c 601	17	5.7	1266	29	CG743976
545	17	5.7	847	29	CG539494	CG539494	c 602	17	5.7	1277	29	CG746704
546	17	5.7	861	13	BK082517	BK082517	c 603	17	5.7	1299	29	CG750474
547	17	5.7	861	28	AG197691	AG197691	c 604	17	5.7	1315	29	CG749195
548	17	5.7	867	29	CHS04E1H	CHS04E1H	c 605	17	5.7	1320	29	CG755797
549	17	5.7	868	14	CG514443	CG514443	c 606	17	5.7	1326	11	AY109265
550	17	5.7	873	13	BK082506	BK082506	c 607	17	5.7	1360	29	CG757149
551	17	5.7	873	13	BK082506	BK082506	c 608	17	5.7	1370	29	CG757666
552	17	5.7	877	13	BK0716790	BK0716790	c 609	17	5.7	1385	29	CG757667
553	17	5.7	883	28	BZ411388	BZ411388	c 610	17	5.7	1464	12	B1758637
554	17	5.7	889	14	CG517722	CG517722	c 611	17	5.7	1812	28	BZ572834
555	17	5.7	893	13	BK082517	BK082517	c 612	17	5.7	2914	11	AK044809
556	17	5.7	896	13	BK082517	BK082517	c 613	17	5.7	3404	11	AK046376
557	17	5.7	903	29	CG955735	CG955735	c 614	17	5.7	4793	11	AK049003
558	17	5.7	904	28	AZ539065	AZ539065	c 615	17	5.7	7886	11	BC034956
								16	5.4	113	10	AW453141

616	16	5	4	128	28	A2121241	A2121241	RPCI-23-1	673	16	5	4	243	9	AU229087	AU229087	AU229087
c 617	16	5	4	131	12	B6125723	B6125723	EST471369	c 674	16	5	4	243	9	AA282595	AA282595	ct13f03.s
618	16	5	4	139	9	AV331698	AV331698	AV331698	c 675	16	5	4	243	10	BB000141	BB000141	BB000141
619	16	5	4	144	9	BB373750	BB373750	BB373750	c 676	16	5	4	246	28	B58499	B58499	CIT-HSP-201
c 620	16	5	4	146	12	BM388843	BM388843	UI-R-DM1-	c 677	16	5	4	247	9	AV244224	AV244224	AV244224
c 621	16	5	4	148	12	BM196797	BM196797	C0337E11-	c 678	16	5	4	247	10	BB077321	BB077321	BB077321
c 622	16	5	4	157	28	CC152863	CC152863	CSU-K34.1	c 679	16	5	4	247	10	BB438388	BB438388	BB438388
c 623	16	5	4	158	10	BB278128	BB278128	BB278128	c 680	16	5	4	248	10	BF554421	BF554421	BF554421
c 624	16	5	4	165	13	BY373743	BY373743	BY373743	c 681	16	5	4	249	9	AV244424	AV244424	AV244424
c 625	16	5	4	166	13	BY461142	BY461142	BY461142	c 682	16	5	4	251	9	AA002435	AA002435	AA002435
c 626	16	5	4	167	10	BB606644	BB606644	BB606644	c 683	16	5	4	253	9	AV221200	AV221200	AV221200
c 627	16	5	4	170	10	BB349050	BB349050	BB349050	c 684	16	5	4	254	9	AV983111	AV983111	AV983111
c 628	16	5	4	172	28	BE475541	BE475541	BONDV91TR	c 685	16	5	4	254	10	BB428157	BB428157	BB428157
c 629	16	5	4	174	12	BM979993	BM979993	UI-CF-ECL	c 686	16	5	4	254	14	CD062627	CD062627	MA1-0026P
c 630	16	5	4	177	9	AT795260	AT795260	RAMACA61	c 687	16	5	4	255	28	A2263446	A2263446	RPCI-23-6
c 631	16	5	4	188	13	BQ311725	BQ311725	MRO-BN007	c 688	16	5	4	255	28	BH859539	BH859539	BH859539
c 632	16	5	4	190	10	BB569076	BB569076	BB569076	c 689	16	5	4	255	28	BH859542	BH859542	B5 0846.5
c 633	16	5	4	191	9	AT566420	AT566420	tr95c09.x	c 690	16	5	4	256	13	BX633276	BX633276	BX633276
c 634	16	5	4	194	14	H31987	H31987	EST106594.R	c 691	16	5	4	260	10	BB384549	BB384549	BB384549
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 Job time : 1393.12 secs

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Perfect score: 297
Sequence: 1 atgttcacatataaacgaae.....actcagtcacgaatgtag 297

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl: +
1: gb_ba: +
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12: gb_sy: +
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	297	100.0	41708	6	BD245281 Developme
3	297	100.0	41708	6	AR368770 Sequence
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5	284.8	95.9	43081	7	AP001553 Bacteriop
6	273	91.9	45366	7	AB044554 Staphyloc
7	261	87.9	261	6	BD245277 Developme
8	256.2	86.3	42942	7	AB045978 Staphyloc
9	256.2	86.3	348527	1	AP003360 Staphyloc
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11	132.8	44.7	580	6	AP003364 Staphyloc
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14	130.8	44.0	42722	7	AF424783 Staphyloc
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16	128.4	43.2	258	6	AX618548 Sequence
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18	101	34.0	291150	1	AP001335 Staphyloc
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20	47.6	16.0	175406	5	BK000522 Zebrafish
21	47.4	16.0	192780	9	AL162723 Human DNA
22	47	15.8	1496	3	CEY53C12D Plasmodi
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25	45.8	15.4	209287	9	AC012077 Homo sapi
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37 44.4 14.9 195046 2 BX294187 BX294187 Dantio rer
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39 44.4 14.9 256945 2 AC097423 AC097423 Rattus no
40 44.4 14.9 292343 2 AC106536 AC106536 Rattus no
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ALIGNMENTS

RESULT 1
BD245280 297 bp DNA linear PAT 17-JUL-2003
LOCUS BD245280
DEFINITION Development of novel antibiotics based on bacteriophage genomics.
ACCESSION BD245280.1 GI:33055050
VERSION JP 2002531107-A/15.
KEYWORDS
SOURCE unidentified
ORGANISM unidentified

REFERENCE
1 (bases 1 to 297)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Development of novel antibiotics based on bacteriophage genomics
JOURNAL Patent: JP 2002531107-A 15 24-SEP-2002;
PUBTECH INC

COMMENT
OS Staphylococcus aureus bacteriophage 77
PN JP 2002531107-A/15
PD 24-SEP-2002
PF 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR
01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454252 PI JERRY
PELLETIER,PHILIPPE GROS,MICHAEL DUBOW
PC C12N15/09,A01N63/00,A61K38/00,A61K45/00,A61P31/04,C07K14/005,
PC C12N15/00,
PC C12N1/21,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/566, PC
C12N15/00,

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Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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BD245281 41708 bp DNA linear PAT 17-JUL-2003
LOCUS BD245281
DEFINITION Development of novel antibiotics based on bacteriophage genomics.
ACCESSION BD245281.1 GI:33055051
VERSION JP 2002531107-A/16.
KEYWORDS
SOURCE unidentified
ORGANISM unidentified

REFERENCE
1 (bases 1 to 41708)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Development of novel antibiotics based on bacteriophage genomics
JOURNAL Patent: JP 2002531107-A 16 24-SEP-2002;
PUBTECH INC

COMMENT
OS Staphylococcus aureus bacteriophage 77
PN JP 2002531107-A/16
PD 24-SEP-2002
PF 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR
01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454252 PI JERRY
PELLETIER,PHILIPPE GROS,MICHAEL DUBOW
PC C12N15/09,A01N63/00,A61K38/00,A61K45/00,A61P31/04,C07K14/005,
PC C12N1/00,
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ACCESSION AR368770
VERSION AR368770.1 GI:34603077
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 41708)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Compositions and methods involving an essential Staphylococcus
aureus gene and its encoded protein
JOURNAL Patent: US 6376652-A 3 23-APR-2002;
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DEFINITION AB009866.2 GI:8051688
ACCESSION AB009866
VERSION
KEYWORDS dUTPase; dsDNA binding protein; anti repressor; repressor;
integrase; luke-PV; luke-PV; holin; amidase (peptidoglycan
hydrolase); capsid protein; portal protein.
SOURCE Staphylococcus aureus bacteriophage PVL
ORGANISM Staphylococcus aureus bacteriophage PVL
REFERENCE Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
1 (sites)
AUTHORS Kaneo,J., Kimura,T., Kawakami,Y., Tomita,T. and Kamio,Y.
TITLE Pantone-valentine leukocidin genes in a phage-like particle isolated
JOURNAL from mitomycin C-treated Staphylococcus aureus V8 (ATCC 49775)
MEDLINE Biosci. Biotechnol. Biochem. 61 (11), 1960-1962 (1997)
PUBMED 9404084
REFERENCE 2 (sites)
AUTHORS Kaneo,J., Kimura,T., Narita,S., Tomita,T. and Kamio,Y.
TITLE Complete nucleotide sequence and molecular characterization of the
JOURNAL temperate staphylococcal bacteriophage phiPVL carrying
MEDLINE Pantone-Valentine leukocidin genes
PUBMED Gene 215 (1), 57-67 (1998)
98332719
REFERENCE 3 (bases 1 to 41401)
PUBMED 9666077
AUTHORS Kaneo,J., Kimura,T., Narita,S., Tomita,T. and Kamio,Y.
TITLE Direct Submission
JOURNAL Submitted (17-DEC-1997) Jun Kaneo, Tohoku University, Dept. Appl.
Biol. Chem., Faculty of Agriculture; 1-1 Tsutsumi-dori
Amamiyamachi, Aoba-ku, Sendai, Miyagi 981, Japan

(E-mail: jkaneko@biochem.tohoku.ac.jp, Tel: 81-22-717-8761,
Fax: 81-22-717-8780)
On May 24, 2000 this sequence version replaced gi:3341907.
Sequence updated (06-Feb-1998)
Sequence updated (22-May-2000).
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CDS

CDS

CDS

CDS

CDS
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CDS complement(5731..6396)
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95.9%; Score 284.8; DB 7; Length 43081;

Best Local Similarity 97.6%; Pred. No. 3,4e-49;
Matches 289; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2 TGTTCAATATATAAGAAAAAGGAGAGTCAAGATGATTACGAATAGCGGAATCA 61
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DB 7021 TGGCATATCATACAGGTTAAAGATATGACACGTCACATTTAAACGTCATTGTCG 7080
QY 182 TAGATGAGATGACTAGATAGTGGCAGTCACTATTAAACCAATAGATGATGA 241
DB 7081 TAGATGAGATGACTAGATAGTGGCAGTCACTATTAAACCAATAGATGATGA 7140
QY 242 TTGAAGAGACACAGACGACGACGACGACGACGACGACGACGACGACGACGACG 297
DB 7141 TTGAAGAGACACAGACGACGACGACGACGACGACGACGACGACGACGACG 7196
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AB044534 45636 bp DNA linear PHG 04-JUL-2000
LOCUS
DEFINITION
Staphylococcus aureus prophage phiPV83 proviral DNA, complete
sequence.
AB044554
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
Location/Qualifiers
1 (sites)
Kaneko,J., Kimura,T., Kawakami,Y., Tomita,T. and Kamio,Y.
Panton-valentine leukocidin genes in a phage-like particle isolated
from mitomycin C-treated Staphylococcus aureus V8 (ATCC 49775)
Biosci. Biotechnol. Biochem. 61 (11), 1960-1962 (1997)
98067870
9404084
2 (sites)
Zou,D., Kaneko,J., Narita,S. and Kamio,Y.
Complete nucleotide sequence and molecular characterization of
prophage PV83pro carrying lukM-lukF-PV(p83) gene cluster in
Staphylococcus aureus strain p83
Unpublished
3 (bases 1 to 45636)
Kaneko,J., Zou,D. and Kamio,Y.
Direct Submission
Submitted (09-JUN-2000) Jun Kaneko, Tohoku University, Graduate
school of Agricultural sciences, 1-1 Tsurumai-dori Aomiyamachi,
Aoba-ku, Sendai, Miyagi 981-8555, Japan
(E-mail:j.kaneko@biocnem.tohoku.ac.jp, Tel:81-22-717-8781,
Fax:81-22-717-8780)
Location/Qualifiers

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/organism="Staphylococcus aureus prophage phiPV83"
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CDS complement(423..1139)
/note="C-terminal portion truncated
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VAQPTTINSTRVNGMTVCYILDODDVIDIFDRDIITVFPENGTETDEYCE
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FADSVAGSDNSILVGEILAKILQNGVDIQQNRLFMLRNNGYLIRKSGESYNLPYQKS
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Best Local Similarity 94.9%; Pred. No. 9e-47;
Matches 282; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 ATGTCAATATATTAACGAAAGGAAAGTCAAGATGATATTAAGAAATAGCGAAATC 60
DB 6999 AAGTTAATTAATCAAAATATACGAGAGTCAAGATGATATTAAGAAATAGCGAAATC 6998
QY 61 ATACGCAAAATATTCATGTTAAGCATTTTAAAGCATTTTAAAGCAT 120
DB 6999 ATACGCAAAATATTCATGTTAAGCATTTTAAAGCATTTTAAAGCAT 7058
QY 121 ATGGCAATATCAATCAAGTAAAGTAAAGCAAGTCAATTAACATGCTATATC 180
DB 7059 ATGGCAATATCAATCAAGTAAAGTAAAGTAAAGCAAGTCAATTAACATGCTATATC 7118
QY 181 GTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
DB 7119 GTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 7178
QY 241 ATGAAAGAAACAGACGAAACGACGACGATTAATTAAGTATGATGATGATGATGATGATG 297
DB 7179 ATGAAAGAAACAGACGAAACGACGACGATTAATTAAGTATGATGATGATGATGATGATG 7235
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BD245277
LOCUS BD245277 261 bp DNA linear PAT 17-JUL-2003
DEFINITION Development of novel antibiotics based on bacteriophage genomes.
ACCESSION BD245277
VERSION BD245277.1 GI:33055047
KEYWORDS JP 2002531107-A/12.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 261)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Development of novel antibiotics based on bacteriophage genomes
JOURNAL Patent: JP 2002531107-A/12 24-SEP-2002;
COMMENT PHAGETECH INC
OS Staphylococcus aureus bacteriophage 77
PN JP 2002531107-A/12
PD 24-SEP-2002
PR 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR
PR 28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR
PR 01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454252 PI JERRY
PELLETIER,PHILIPPE GROS,MICHAEL DUBOW
PC C12N15/09,A01N63/00,A61K38/00,A61K45/00,A61P31/04,C07K14/005,
PC C12N1/21,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/566,PC
C12N15/00,
PC A61K37/02
CC Coding Sequence
FH Key Location/Qualifiers
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aureus bacteriophage

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/db_xref="taxon:32644"

Sendai, Miyagi 981-8555, Japan
(E-mail: jkaneko@biochem.tohoku.ac.jp, tel: 81-22-717-8781,
Fax: 81-22-747-8780)
Location/Qualifiers
source 1..42942
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Best Local Similarity 100.0%; Pred. No. 4, 6e-44;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGATTACGAATAGCGGAATCATACGCAAAATATCATGTTACGATTCGATTT 60
QY 97 AACGATTCATTTAAAGGTCATATGGGCATATCAATACAGTTAAAGATGAAC 156
DB 61 AACGATTCATTTAAAGGTCATATGGGCATATCAATACAGTTAAAGATGAAC 120
QY 157 GTACCAATTAAACATGCTTATGTGTAGATGAAGTGAATGATGATGATGAT 216
DB 121 GTACCAATTAAACATGCTTATGTGTAGATGAAGTGAATGATGATGATGAT 180
QY 217 TTACCAAGCAATAGATGATGATGATGATGATGATGATGATGATGATGAT 276
DB 181 TTACCAAGCAATAGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 277 AACTAGTCATGAATGATGATGATGATGATGATGATGATGATGATGAT 297
DB 241 AACTAGTCATGAATGATGATGATGATGATGATGATGATGATGATGAT 261

CDS

RESULT 8
AB045978 42942 bp DNA linear PHG 26-MAY-2001
LOCUS Staphylococcus aureus temperate phage phiSLT genomic DNA, complete
DEFINITION
AB045978
VERSION
AB045978.1 GI:12697822
KEYWORDS
Staphylococcus aureus temperate phage phiSLT
ORGANISM
Staphylococcus aureus temperate phage phiSLT
REFERENCE
1 (dites)
Narita, S., Kaneko, J., Chiba, J., Piemont, Y., Jarraud, S., Etienne, J.,
and Kamio, Y.
TITLE
Phage conversion of Pantone-Valentine leukocidin in Staphylococcus
aureus: molecular analysis of a PVL-converting phage, phiSLT
JOURNAL
Gene 266 (1-2), 195-206 (2001)
MEDLINE
21261956
PUBMED
11368915
REFERENCE
2 (bases 1 to 42942)
Narita, S., Kaneko, J., and Kamio, Y.
TITLE
Direct Submission
AUTHORS
Submitted (12-JUL-2000) Jun Kaneko, Tohoku University, Graduate
JOURNAL
School of Agricultural Science, 1-1 Tsutsunodori Aomori Yamachi,

CDS

CDS

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CDS

Query Match 86.3%; Score 256.2; DB 7; Length 42942;
Best Local Similarity 98.9%; Pred. No. 2,6e-43;
Matches 258; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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97 AAGCTATGCTTTTAAAGGTCATAGGCGATTCATACATCAAGTTAAAGATGAAAC 156
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DB 7333 AAGCTATGCTTTTAAAGGTCATAGGCGATTCATACATCAAGTTAAAGATGAAAC 7392
157 GTACCAATTAACATGCTTATGTGCTAGATGAGATGACTTAAAGTCAAGCTTA 216
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DB 7393 GTACCAATTAACATGCTTATGTGCTAGATGAGATGACTTAAAGTCAAGCTTA 7452
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DB 7453 TTACCAAGCAATGATGATGATGAGATGAGACAGACAGACAGACAGACTAANT 7512
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DB

RESULT 9
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LOCUS
DEFINITION
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sequence, section 3/9.
ACCESSION
AP003360.2 GI:14246388
VERSION
AP003360.2 GI:14246388
KEYWORDS
Staphylococcus aureus subsp. aureus Mu50
Staphylococcus aureus subsp.
ORGANISM
Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE
1 Kuroda,M., Ohta,T., Uehiyama,I., Baba,T., Yuzawa,H., Kobayashi,I.,
Cui,L., Oguchi,A., Aoki,K., Nagai,Y., Itoh,J., Ito,T., Kanamori,M.,
Matsumaru,H., Maruyama,A., Murakami,H., Hosoyama,A.,
Matsuda-Uji,Y., Takahashi,N.K., Sawano,T., Inoue,R., Kaito,C.,
Sekimizu,K., Hiraoka,H., Kuhnara,S., Goto,S., Yabuzaki,J.,
Kanehisa,M., Yamashita,A., Oshima,K., Furuya,K., Yoshino,C.,
Shiba,T., Hattori,M., Ogasawara,N., Hayashi,H. and Hiramatsu,K.
Whole genome sequencing of methicillin-resistant Staphylococcus
aureus

TITLE
JOURNAL
MEDLINE
PUBMED
Lancet 357 (9264), 1225-1240 (2001)
2131952
11418146

REFERENCE 2 (bases 1 to 348527)
AUTHORS
Ohta,T.
TITLE
Direct Submission
JOURNAL
Submitted (28-FEB-2001) Toshiko Ohta, University of Tsukuba College
of Medical Technology and Nursing, Department of Medical
Technology; 1-1-1 Ten-noda1, Tsukuba, Ibaraki 305-8577, Japan
(E-mail:tohta@tsukuba.ac.jp, Tel:81-298-53-3454,
Fax:81-298-53-3454)
COMMENT
On May 29, 2001 this sequence version replaced gi:13874937.
FEATURES
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location/Qualifiers
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Query Match 86.3%; Score 256.2; DB 1; Length 348527;
Best Local Similarity 98.9%; Pred. No. 2.1e-43;
Matches 258; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 37 ATGATTTACGAAATAGCGAAATCATACGCAAAATATTCATGTTACGATTCGATTT 96
DB 230674 ATGATTTACGAAATAGCGATCATACGCAAAATATTCATGTTACGATTCGATTT 230733

QY 97 AAGCTATTCATTTTAAAGGTGATATGGGATATCATATACAGTTAAAGATATGACAC 156
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QY 157 GTACCAATTAAACATGCTATATGCTAGATGAGATGACTTATGATGCGATCACTTA 216
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DB 230854 TTTAACCAAGCATATGATGATGATTGAAAGAAACAGACAGACAGACAGATTAAT 230913

QY 277 AACTTAGTCATGAAATGCTAG 297
DB 230914 AACTTAGTCATGATGCTAG 230934

Search completed: October 14, 2004, 16:00:39
Job time : 1528.57 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using SW model

Run on: October 14, 2004, 07:30:59 ; Search time 198 Seconds
(without alignments)
6372.297 Million cell updates/sec

Title: US-09-407-804A-9
Perfect score: 297
Sequence: 1 atgtcataataaagcaaa.....acttagcatgaatgtag 297

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04: +
1: geneseqn1980s: +
2: geneseqn1990s: +
3: geneseqn2000s: +
4: geneseqn2001s: +
5: geneseqn2001bs: +
6: geneseqn2002s: +
7: geneseqn2003as: +
8: geneseqn2003bs: +
9: geneseqn2003cs: +
10: geneseqn2004s: +

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	297	100.0	41708	4	AAA68247 Bacterioph
3	297	100.0	41708	4	AAC86106 Complete
4	261	87.9	261	3	AAA68250 Bacterioph
5	132.8	44.7	380	2	AAV75314 Staphyloc
6	132.8	44.7	43576	3	AAA68609 Bacterioph
7	128.4	43.2	258	7	ACF73076 Staphyloc

8	118.6	40.0	267	7	ACE72925	Ace72925	Staphylococcus aureus
9	41.6	14.0	4147	2	AAx13202	Aax13202	Enterococcus faecalis
10	41.6	14.0	4147	6	ABs98997	ABs98997	Enterococcus faecalis
11	41.4	13.9	50000	6	ABLS5643	ABLS5643	Ampey gene
12	40.8	13.7	17137	6	ABL32190	ABL32190	Human
13	40.6	13.7	14649	4	ABAS45415	ABAS45415	Human
14	40.6	13.7	14649	6	ABK8268	ABK8268	DNA trans
15	40.2	13.5	2685	7	ACE28606	ACE28606	Prokaryotic
16	40	13.5	6089	6	ABN00254	ABN00254	Human
17	39.6	13.3	5413	6	ABL22554	ABL22554	Human
18	39.4	13.3	746	6	ABO31421	ABO31421	Human
19	39.4	13.3	746	6	ABO31420	ABO31420	Oligonucleotide
20	39	13.1	2653	9	ADB85527	ADB85527	Human
21	38.8	13.1	8524	4	AAAS46588	AAAS46588	Human
22	38.8	13.1	8524	6	ABL33841	ABL33841	Human
23	38.6	13.0	3365	4	ABLO6224	ABLO6224	Human
24	38.6	13.0	6048	4	AAAS46613	AAAS46613	Tumour su
25	38.4	12.9	2178	7	ACA28148	ACA28148	Prokaryotic
26	38.4	12.9	7158	4	ABLO6884	ABLO6884	Drosophila
27	38.4	12.9	110000	6	ABA050521_07	ABA050521_07	Continuation (9 of
28	38.4	12.9	110000	6	ABA050521_08	ABA050521_08	Continuation (9 of
29	38.2	12.9	32392	6	ABL70603	ABL70603	Ampey gene
30	38.2	12.9	34548	6	ABL70603	ABL70603	Photorehab
31	37.8	12.7	1348	7	ACE68040	ACE68040	Human
32	37.8	12.7	7341	6	AAAS61395	AAAS61395	Human
33	37.8	12.7	110000	7	ACE67367_07	ACE67367_07	Continuation (8 of
34	37.8	12.7	110000	7	ACE65384_1	ACE65384_1	Continuation (2 of
35	37.6	12.7	2000	7	ADA71938	ADA71938	Rice gene
36	37.6	12.7	6487	6	ABK13353	ABK13353	Signal tr
37	37.6	12.7	6487	6	ABL70320	ABL70320	Chemical
38	37.6	12.7	6487	6	AAAS61267	AAAS61267	Human
39	37.4	12.6	1419	7	ACA52799	ACA52799	Prokaryotic
40	37.4	12.6	5035	2	AAT91010	AAT91010	Leptospira
41	37.4	12.6	5035	7	ABX14745	ABX14745	cDNA encod
42	37.4	12.6	17738	6	ABL33558	ABL33558	Human
43	37.4	12.6	110000	5	AAI61373_2	AAI61373_2	Continuation (3 of
44	37.2	12.5	2688	6	ABN79832	ABN79832	Fungal
45	37.2	12.5	5998	6	ABL13665	ABL13665	Human

ALIGNMENTS

RESULT 1
AAA68253

ID AAA68253 standard; DNA; 297 BP.

AC AAA68253;

XX
15-CPD-2003 (rev. 2004)

DT	06-AUG-2003	(revised)
D1	13-SEP-2003	(revised)

DT 27-OCT-2000 (first entry)

DE Bacteriophage 77 77ORF182 nucleotide sequence.

KW Bacteriophage; antimicrobial; genome; identification; antibacterial.
KW bacterial growth inhibition; bacterial infection; ds.

Db 121 ATGGGCATATCAATACAGTTAAAGATATGACACGATACCATTTAAACGCTTATGTC 180
 QY 181 GTAGATGAGATGACTAGATATGGCATCAGACTTATTTAACGACCAATAGATG 240
 Db 181 GTAGATGAGATGACTAGATATGGCATCAGACTTATTTAACGACCAATAGATG 240
 QY 241 ATTGAAGAACACAGACGACGACGACTAATTAAGTATGCTGTAATGGTATG 297
 Db 241 ATTGAAGAACACAGACGACGACGACTAATTAAGTATGCTGTAATGGTATG 297
 RESULT 2
 AAA68247
 ID AAA68247 standard; DNA; 41708 BP.
 AC AAA68247;
 XX
 DT 15-SEP-2003 (revised)
 DT 06-AUG-2003 (revised)
 DT 27-OCT-2000 (first entry)
 XX
 DE Bacteriophage 77 complete genome sequence.
 XX
 KW Bacteriophage; antimicrobial; genome; identification; antibacterial;
 KW bacterial growth inhibition; bacterial infection; ds.
 OS
 XX Staphylococcus aureus; bacteriophage 77.
 PN W0200032825-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 03-DEC-1999; 99WO-18002040.
 XX
 PR 03-DEC-1998; 98US-0110992P.
 PR 03-JUN-1999; 99US-00326144.
 PR 28-SEP-1999; 99US-00407804.
 PR 30-SEP-1999; 99US-0157218P.
 PR 01-DEC-1999; 99US-0168777P.
 PR 02-DEC-1999; 99US-00454252.
 XX
 PA (PHAG-) PHAGETECH INC.
 XX
 PI Polietlor J, Gros P, Dubow M;
 XX
 DR WPI; 2000-412361/35.
 XX
 PT Identifying a bacteriophage coding region for treating bacterial
 PT infections comprises identifying a nucleic acid encoding a product that
 PT inhibits bacteria when a bacteriophage infects a bacterium.
 XX
 PS Example 3; Page 141-151; 456pp; English.
 XX
 CC The present invention describes a method for identifying a bacteriophage
 CC coding region encoding a product active on an essential bacterial target.
 CC The method comprises identifying a nucleic acid sequence encoding a gene
 CC product that provides a bacteria-inhibiting function when an

CC uncharacterised bacteriophage infects a pathogenic bacterium. The
 CC compound active on a target of a bacteriophage inhibitor protein in a
 CC bacteria is used to treat or prevent a bacterial infection in an animal.
 CC AAA68243 to AAA69442 and AAB16523 to AAB16954 represent bacteriophage
 CC nucleotide and protein sequences which are used in the exemplification of
 CC the present invention. (updated on 06-AUG-2003 to correct OS field.)
 CC (updated on 15-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 U; 0 other;
 Query Match 100.0%; Score 297; DB 3; Length 41708;
 Best Local Similarity 100.0%; Pred. No. 3,1e-64;
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGTCATATATTAACGAAAAACGAGAGAACTCAAGATGATTAAGAAATAGCGAAATC 60
 Db 29268 ATGTCATATATTAACGAAAAACGAGAGAACTCAAGATGATTAAGAAATAGCGAAATC 29327
 QY 61 ATACGCAAAAATATTCATGTTAACGATTCGATTTTAAGTATTCATTTAAAAAGTCAAT 120
 Db 29328 ATACGCAAAAATATTCATGTTAACGATTCGATTTTAAGTATTCATTTAAAAAGTCAAT 29387
 QY 121 ATGGGCATATCAATACAGTTAAAGATATGACACGATACCATTTAAACGCTTATGTC 180
 Db 29388 ATGGGCATATCAATACAGTTAAAGATATGACACGATACCATTTAAACGCTTATGTC 29447
 QY 181 GTAGATGAGATGACTAGATATGGCATCAGACTTATTTAACGACCAATAGATG 240
 Db 29448 GTAGATGAGATGACTAGATATGGCATCAGACTTATTTAACGACCAATAGATG 29507
 QY 241 ATTGAAGAACACAGACGACGACGACTAATTAAGTATGCTGTAATGGTATG 297
 Db 29508 ATTGAAGAACACAGACGACGACGACTAATTAAGTATGCTGTAATGGTATG 29564
 RESULT 3
 AAC86106
 ID AAC86106 standard; cDNA; 41708 BP.
 AC AAC86106;
 XX
 DT 06-AUG-2003 (revised)
 DT 29-AUG-2001 (first entry)
 XX
 DE Complete genome of bacteriophage 77.
 XX
 KW DnaI; S. aureus; inhibitor; bacteriophage 77; ORF 104; phage 77ORF104;
 KW screening assay; ss.
 OS Bacteriophage.
 XX
 PN W0200146383-A2.
 XX
 PD 28-JUN-2001.
 XX
 PF 21-DEC-2000; 2000WO-US035180.
 XX

PR 22-DEC-1999; 99US-00470512.
PR 12-OCT-2000; 2000US-00689352.
XX
PA (PHAG-) PHAGETECH INC.
PA (WILL/) WILLIAMS K M.
XX
PI Pollettier J, Groe P, Dubow M;
XX
DR WPI; 2001-418052/44.
XX
XX Novel DnaI polypeptides useful for treating and diagnosing microbial,
PT preferably bacterial, diseases such as those caused by Staphylococcus
PT aureus.
XX
XX Disclosure; Fig 2, 107pp; English.
PS
PS This sequence represents the genome of Bacteriophage 77. The growth
CC inhibitory gene product of ORF 104 interacts with DnaI derived from S.
CC aureus, to form the basis of a screening assay. DnaI polypeptides and
CC polynucleotides are useful for treating microbial, preferably bacterial,
CC especially Staphylococcus, infections. DnaI polypeptides and
CC polynucleotides are useful for biological, diagnostic, prophylactic,
CC clinical and therapeutic use, and as components in databases useful for
CC search analyses as well as in sequence analysis algorithms. (Updated on
CC 06-AUG-2003 to correct 05 field.)
XX
XX Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 297; DB 4; Length 41708;
Best Local Similarity 100.0%; Prod. No. 3.1e-64;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTCATATTAACGAAAAAGGAGGATGATGATTAACGAAATAGCGCAATC 60
DB 29268 ATGTCATATTAACGAAAAAGGAGGATGATGATTAACGAAATAGCGCAATC 29327
QY 61 ATACGCAAAATATTCATGTTAAGCATGATTTTAAAGGTCAT 120
DB 29328 ATACGCAAAATATTCATGTTAAGCATGATTTTAAAGGTCAT 29387
QY 121 ATGGCATATCAATACGATTAAGATATGACAGTATTAACATGCTTATGTC 180
DB 29388 ATGGCATATCAATACGATTAAGATATGACAGTATTAACATGCTTATGTC 29447
QY 181 GTAGATGAGATGACTATGATGTCATGACTTATTAAACAGCAATAGATGAG 240
DB 29448 GTAGATGAGATGACTATGATGTCATGACTTATTAAACAGCAATAGATGAG 29507
QY 241 ATTGAAGAGACACAGACGAGGAGCACTAATTAACTACTGAAATGGTGG 297
DB 29508 ATTGAAGAGACACAGACGAGGAGCACTAATTAACTACTGAAATGGTGG 29564

RESULT 4
AAA68250
ID AAA68250 standard; DNA; 261 BP.
XX

AC AAA68250;
XX
XX 15-SEP-2003 (revised)
DT 06-AUG-2003 (revised)
DT 27-OCT-2000 (first entry)
XX
XX Bacteriophage 77 77ORF043 nucleotide sequence.
XX
XX Bacteriophage; antimicrobial; genome; identification; antibacterial;
KW bacterial growth inhibition; bacterial infection; ds.
XX
OS Staphylococcus aureus; bacteriophage 77.
XX
XX W0200032825-A2.
XX
XX 08-JUN-2000.
XX
XX 03-DEC-1999; 99WO-1B002040.
XX
XX 03-DEC-1999; 98US-0110992P.
PR 03-JUN-1999; 99US-00326144.
PR 28-SEP-1999; 99US-00407804.
PR 30-SEP-1999; 99US-0157218P.
PR 01-DEC-1999; 99US-0168777P.
PR 02-DEC-1999; 99US-00454252.
XX
XX (PHAG-) PHAGETECH INC.
XX
XX Pollettier J, Groe P, Dubow M;
PI WPI; 2000-412361/35.
XX
XX P-PSDB; AAB16525.
DR
XX
XX Identifying a bacteriophage coding region for treating bacterial
PT infections comprises identifying a nucleic acid encoding a product that
PT inhibits bacteria when a bacteriophage infects a bacterium.
XX
XX Disclosure; Page 157; 456pp; English.
XX
XX The present invention describes a method for identifying a bacteriophage
CC coding region encoding a product active on an essential bacterial target.
CC The method comprises identifying a nucleic acid sequence encoding a gene
CC product that provides a bacteria-inhibiting function when an
CC uncharacterised bacteriophage infects a pathogenic bacterium. The
CC compound active on a target of a bacteriophage inhibitor protein in a
CC bacteria is used to treat or prevent a bacterial infection in an animal.
CC AAA68243 to AAB16942 and AAB16954 represent bacteriophage
CC nucleotide and protein sequences which are used in the exemplification of
CC the present invention. (Updated on 06-AUG-2003 to correct 05 field.)
CC (Updated on 15-SEP-2003 to standardise 05 field)
SQ Sequence 261 BP; 105 A; 36 C; 49 G; 71 T; 0 U; 0 Other;
Query Match 87.9%; Score 261; DB 3; Length 261;
Best Local Similarity 100.0%; Prod. No. 1.1e-55;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 ATGATTACGAATAGCGAAATCATACGAAAAATTCATGTTACGATTCATTT 96
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 ATGATTACGAATAGCGAAATCATACGAAAAATTCATGTTACGATTCATTT 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 97 AAGCTATTCATTTAAAGGTCATATGGGCATTCATACAGTTAAAGATGAAAC 156
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 AAGCTATTCATTTAAAGGTCATATGGGCATTCATACAGTTAAAGATGAAAC 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 157 GTACCAATTAAACATGCTATGTGCTAGATGAGATGACTTAAGATGGCATCACTTA 216
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 GTACCAATTAAACATGCTATGTGCTAGATGAGATGACTTAAGATGGCATCACTTA 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 217 TTAAACCAAGCAATGATGATGATGAAAGACAGACAGACAGACTTAANT 276
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 TTAAACCAAGCAATGATGATGATGAAAGACAGACAGACAGACTTAANT 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 277 AACTAGTCATGAATGCTAG 297
 ||||||||||||||||||
 Db 241 AACTAGTCATGAATGCTAG 261
 ||||||||||||||||||

Search completed: October 14, 2004, 12:48:21
 Job time : 200 secs

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OM nucleic - nucleic search, using sw model

Run on: October 14, 2004, 12:03:47 ; Search time 1387.19 Seconds
 (without alignments)
 6393.544 Million cell updates/sec

Title: US-09-407-804A-9

Perfect score: 297
 Sequence: 1 atgtcaataataaacgaaa.....acttgatcatgaatgtag 297

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST:*

1: em_estba:*

2: em_esthum:*

3: em_estlin:*

4: em_estnu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pin:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_nus:*

24: em_gss_pro:*

25: em_gss_rtd:*

26: em_gss_png:*

27: em_gss_vr1:*

28: gb_ges1:++
29: gb_ges2:++

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
c 1	48	16.2	926	28	A2137368	A2137368 SP_0175_B
2	47.8	16.1	988	13	BK410403	BK410403 BK410403
3	47.2	15.9	1083	29	CNS00970	AL054505 Drosophila
c 4	45.8	15.4	1044	13	BK415231	BK415231 BK415231
5	45.6	15.4	328	28	A2923265	A2923265 4908-8f20
c 6	44.6	15.0	822	12	BK357887	BK357887 GA_Ea000
7	44.4	14.9	954	14	CA788983	CA788983 AGENCOURT
c 8	44.4	14.9	1101	29	CNS00178	AL060732 Drosophila
c 9	44.4	14.9	1198	13	BK395612	BK395612 BK395612
c 10	44.4	14.8	937	28	A2530244	A2530244 ENTBI12TF
c 11	43.6	14.7	700	28	BH371930	BH371930 AG-ND-132
c 12	43.4	14.6	1173	13	BK379866	BK379866 BK379866
13	43.4	14.6	1201	13	BK424465	BK424465 BK424465
14	43.4	14.5	1164	28	CC261365	CC261365 CH261-72H
15	42.6	14.3	842	10	BF617340	BF617340 HVSSEC001
c 16	42.4	14.3	509	28	B2842685	B2842685 CH240_276
c 17	42.4	14.3	588	29	BK168785	BK168785 Danilo ref
c 18	42.4	14.3	1002	28	B2695524	B2695524 SP_Ba006
c 19	42.2	14.2	761	14	CF282516	CF282516 AGENCOURT
c 20	42.2	14.2	876	28	BH164960	BH164960 ENTBY63TF
c 21	42.2	14.2	898	28	A2679345	A2679345 ENTBK48TF
c 22	42	14.1	763	10	BF126666	BF126666 601650942
23	42	14.1	1008	13	BK398691	BK398691 BK398691
c 24	42	14.1	1200	13	BK436510	BK436510 BK436510
25	41.8	14.1	519	28	A2525518	A2525518 244PBH11
c 26	41.8	14.1	571	28	A2526884	A2526884 260PB612
c 27	41.8	14.1	664	28	A2131173	A2131173 OSJNB5010
c 28	41.8	14.1	759	12	BJ375492	BJ375492 ENTB221TR
c 29	41.8	14.1	899	28	A2531765	A2531765 ENTB221TR
c 30	41.8	14.1	1027	28	A2668237	A2668237 ENTB205TR
31	41.8	14.1	1097	29	CNS01235	AL101650 Drosophila
c 32	41.6	14.0	706	28	BH954338	BH954338 cdb21b04.
33	41.6	14.0	924	28	A2674753	A2674753 ENTBU31TR
34	41.6	14.0	1189	13	BK456444	BK456444 BK456444
35	41.4	13.9	523	28	BH672321	BH672321 BOMH139TF
c 36	41.4	13.9	668	28	BH592678	BH592678 BOCG049TF
c 37	41.4	13.9	692	28	B2011251	B2011251 oel72a10.
38	41.4	13.9	874	28	A2673257	A2673257 ENTBM68TR
c 39	41.4	13.9	1101	29	CNS00807	AL072991 Drosophila
c 40	41.4	13.9	1234	12	BM911712	BM911712 AGENCOURT
c 41	41.2	13.9	556	28	BH686139	BH686139 BOMDB03TR
c 42	41.2	13.9	801	14	CA508813	CA508813 UI-R-FS0-
c 43	41.2	13.9	1101	29	CNS01790	AL108642 Drosophila
44	41	13.8	724	28	A2298940	A2298940 RPCI-23-1
45	41	13.8	920	29	CNS01UOL	AL168150 Tetradon

Search completed: October 14, 2004, 18:55:23
Job time : 1390.19 secs